

cell. The B chain binds to cell receptors and facilitates the
 entry of the B chain into the cell. The B chain is also responsible
 for cell agglutination (lectin activity). It binds to beta-2-
 galactopyranoside moieties.
 CC CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC SUBUNIT: Disulfide-linked dimer of A and B chains.
 CC DOMAIN: The B chain is composed of two domains, alpha and gamma.
 CC -1- The alpha domain is located in the N-terminal region (residues 45 AND THE
 CC -1- The gamma domain is located in the C-terminal region (residues 105-114).
 CC -1- INACTIVATING PROTEIN FAMILY: TYPE 2 RIP SUBFAMILY.
 CC -1- SIMILARITY: Contains 2 richin B-type lectin domains.
 CC -1- CAUTION: REF. 4 AND REF. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
 CC WITH THE SEQUENCE TRANSLATED FROM DNA (REF. 1, REF. 2 AND REF. 3).
 CC -1- DATABASE: NAME=Protein Spotlight;
 CC NOTE=Issue 31 of February 2003;
 CC WWW=ftp://www.expaasy.org/spotlight/articles/spl1031.html".
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb.ch).
 CC -----
 CC EMBL: X01109; CAA6639.1; -
 CC EMBL: X01109; CAA6639.1; -
 CC EMBL: X01388; CAA6230.1; -
 CC EMBL: A12892; CAA1058.1; -
 CC PIR: A24041; R1CSD.
 CC PDB: 2RA1; 31-JAN-94.
 CC PDB: 1APG; 31-JAN-94.
 CC PDB: 1PMP; 31-OCT-93.
 CC PDB: 1176; 14-JAN-98.
 CC PDB: 11PT; 14-JAN-98.
 CC PDB: 11FQ; 14-JAN-98.
 CC PDB: 11QS; 31-OCT-93.
 CC PDB: 10BT; 16-JUN-97.
 CC PDB: 1BR5; 02-SEP-98.
 CC PDB: 1BR6; 02-SEP-98.
 CC PDB: 1113; 16-JAN-02.
 CC PDB: 1114; 16-JAN-02.
 CC PDB: 1119; 16-JAN-02.
 CC GlycoSiteDB: P02879; -
 CC InterPro: IPR00772; Richin_B_lectin.
 CC Pfam: PF00450; RICHIN.
 CC Pfam: PF00161; RICHIN_1_lectin. 6.
 CC PRINTS: PR00396; SHIDARICHIN.
 CC SMART: SM00458; RICHIN; 2.
 CC PROSITE: PS00231; RICHIN_B_LECTIN; 2.
 CC PROSITE: PS00275; SHIGH_RICHIN; 1.
 CC Plant defense: Hydrolyase; Protein synthesis inhibitor; toxin; Repeat;
 CC Glycoprotein; Lectin; Signal; 3D-structure.
 CC SIGNAL 1 35
 CC CHAIN 36 302
 CC DOMAIN 36 302
 CC CHAIN 315 576
 CC DOMAIN 321 575
 CC REPEAT 331 373
 CC REPEAT 374 414
 CC REPEAT 417 449
 CC REPEAT 462 497
 CC REPEAT 501 540
 CC REPEAT 543 576
 CC REPEAT 578 610
 CC REPEAT 613 645
 CC REPEAT 648 680
 CC DISULFID 334 353
 CC INTERCHAIN.

FT DISULFID 377 394
 FT DISULFID 465 478
 FT DISULFID 508 522
 FT CARBOHYD 45 45
 FT CARBOHYD 271 271
 FT CARBOHYD 409 409
 FT CARBOHYD 449 449
 FT CARBOHYD 453 453
 FT CARBOHYD 551 551
 FT STRAND 41 47
 FT TURN 49 50
 Query Match 47.1%; Score 1231; DB 1; Length 576;
 Beat Local Similarity 49.1%; Pred. No. 7.7e-114;
 Matches 263; Conservative 74; Mismatches 179; Indels 20; Gaps 11;
 9 TQCTGKATFFPTLLRDVYSGS-FSNEPL-KQSTVSDAQRPVVEINQGNKX 66
 48 TGAATVSTVPIRVRKRLTADVRHILVLPKRVGLIN-QRILVELSHALSLV 105
 67 TLAIDVTVVYVYVQKQDQGYELR-DAPRGAE-THTFTGTRKSSIPKQSYXDLERYA 123
 106 TIALDVTVVYVYVQKQDQGYELR-DAPRGAE-THTFTGTRKSSIPKQSYXDLERYA 165
 124 GR-RDQIPPLGIXDLQSYVAL---RPGSTFRXANSLILTIQMSAARFPIIMKRXQ 179
 166 GNRKRNLSLQNGPRLAEALSLHTVSTGSLQPLTALSTICQPLSLKQYILRQK 225
 180 XINSQKSHLPQXVMELEFTGSGGCTGQVSTGQVNNPYKALIXGNFTLVNRRXYIA 239
 226 RIRVRSAPDPVITLENEMKRLSTAIQENQAFAPIQLOERNNSXFGYDVSLIL 285
 240 SLALMLVYCGERSSDVRVLYRPPVAD--DVYCSAEPFTRIVRGKXKXDVYAD 296
 286 IILMYRCAPPESSQ---FSLIRVPPVAVD-CNDPEFTRIVRGKXKXDVYAD 340
 297 DFDGNOIGLQVPSNMDDPOLATIKRDKITRENSSCLTITGTAQYVMAFQNFAYE 356
 341 RFRKNSLQVPCCKSLDANQVILKSDVITKNSKCLITVIGRQVYVMAFQNFAYE 400
 357 ACTIQVIXNGITLIPRSLVLAASGIKQITLVQTLDTLQCGMLAGNDAPAREVTV 416
 401 AFRQVIMDQGITLIPRSLVLAASGIKQITLVQTLDTLQCGMLAGNDAPAREVTV 460
 417 FRDLMSVXSVWVETXSSQXQXVMAVYGGGIRPRKQNDQCLTXGRDSVYVNIY 476
 461 LKALQVQNSQVWVETXSSQXQXVMAVYGGGIRPRKQNDQCLTXGRDSVYVNIY 519
 477 SCXSSXKQVRYPRVEXXILNXXXXXVQVQVAMPKRLTIIIPVTKXNNQWV 532
 520 SCQPSQQRWFRNGRITLVVSGVLVYVAPSPKQIIVLPHDDPQWVLEP 575
 RESULT 3
 ABR4 ABR4P STANDARD; ERT; 528 AA.
 ID ABR4 ABR4P
 AC P11140; P28599; 1.
 DT 01-JUN-1989 (Ref. 1).
 OR 01-JUN-1989 (Ref. 1).
 DE 28-PDB-2003 (Ref. 1).
 DE Abitin-4 precursor (Contains: Abitin-a A chain (RNA N-glycosidase))
 OS Abitin-4 precursor (Indian i-cortic) (Crab's eye).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 CC Eucoside I; Fabales; Fabaceae; Papilionoideae; Abraceae; Abrus.
 CC NCBI TaxID=3816;
 CC SOURCE FROM N.A.
 CC MEDLINE=3127266;
 CC HUNG C.H.; Lee M.-C.; Lee T.-C.; Lin J.-Y.

RT "Primary structure of three distinct isobabins determined by cDNA
 RT sequencing. Conservation and significance.";
 RT [2] Mol. Biol. 229:263-267 (1993).
 RN
 RP SEQUENCE OF 1-251.
 RA Funatsu G., Taguchi Y., Kameosono M., Yanaka M.;
 RT "The complete amino acid sequence of the A-chain of abrin-a, a toxic
 RT protein from the seeds of *Abrus precatorius*.";
 RT Agric. Biol. Chem. 52:1095-1097 (1988).
 RL
 RN SEQUENCE OF 1-251 FROM N.A.
 RP
 RX MEDLINE=91201323; PubMed=2016300;
 RA Evensen G., Mathiesen A., Sundan A.;
 RT "Direct molecular cloning and expression of two distinct abrin
 RT A-chains.";
 RT J. Biol. Chem. 266:6848-6852 (1991).
 RL
 RN [4]
 RP SEQUENCE OF 262-528.
 RX MEDLINE=92311656; PubMed=1505674;
 RA Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.;
 RT "The complete primary structure of abrin-a B chain.";
 RT FEBS Lett. 309:115-118 (1992).
 RL
 RP X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).
 RX MEDLINE=95331188; PubMed=7609980;
 RA Tahirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;
 RT "Crystal structure of abrin-a at 2.14 A.";
 RL J. Mol. Biol. 250:354-367 (1995).
 CC
 CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
 CC
 CC -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
 CC INHIBITS THE GROWTH OF ABRIN TO THE CELL MEMBRANE THAT
 CC PRECEDES ENDOCYTOSIS.
 CC
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC
 CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
 CC
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.
 CC
 CC -1- SIMILARITY: Contains 2 richin B-type lectin domains.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the European Bioinformatics Institute and the EMBL outstation -
 CC use by non-profit institutions as long as its copyright notice is
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC
 CC -----
 DR EMBL, N98344; AAA32624.1; ALT INIT.
 DR EMBL, X54872; -; NOT_ANNOTATED_CDS.
 DR FDB, JMBR, 077829-95; Ricin_B_lectin.
 DR JGI, JGI, 1900073; Ricin_B_lectin.
 DR InterPro, IPR001574; RIP.
 DR Pfam, PF00652; Ricin_B_lectin, 6.
 DR Pfam, PF00161; RIP_1.
 DR PRINTS, PRO0396; SHIGARICIN.
 DR SMART, SMO0458; RICIN, 2.
 DR PROSITE, PS00231; RICIN_B_LECTIN, 2.
 DR PROSITE, PS00275; SHIGA_RICIN, 1.
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 FM Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.
 RT CHAIN 1
 FT 1 251 ABRIN-A CHAIN.
 FT 252 1 LINKER PEPTIDE.
 FT 253 1 ABRIN-A B CHAIN.
 FT 254 1 ABRIN-A B CHAIN.
 FT 255 1 ABRIN-A B CHAIN.
 FT 256 1 ABRIN-A B CHAIN.
 FT 257 1 ABRIN-A B CHAIN.
 FT 403 527 RICIN B-TYPE LECTIN 2.
 FT
 FT REPEAT 283 325 1-ALPHA.
 FT REPEAT 326 366 1-BETA.
 FT REPEAT 369 401 1-GAMMA.
 FT REPEAT 414 449 2-ALPHA.
 FT REPEAT 452 483 2-BETA.
 FT ACT SITE 164 164
 FT DISULFID 247 269
 FT DISULFID 286 305
 FT DISULFID 329 346
 FT DISULFID 417 430
 FT DISULFID 456 473
 FT MOD RES 1
 FT CARRIAGE 361 361
 FT CONCORD 301 401
 FT CONCORD 302 401
 FT CONFLICT 298 298
 FT CONFLICT 427 427
 FT CONFLICT 467 467
 FT CONFLICT 483 483
 FT STRAND 5 8
 FT TURN 10 11
 FT HELIX 14 26
 FT STRAND 32 33
 FT STRAND 34 35
 FT STRAND 36 38
 FT STRAND 42 43
 FT HELIX 44 45
 FT STRAND 51 57
 FT STRAND 63 69
 FT TURN 70 72
 FT STRAND 75 79
 FT STRAND 83 86
 FT TURN 88 89
 FT TURN 92 93
 FT HELIX 94 97
 FT TURN 100 102
 FT STRAND 113 116
 FT TURN 117 118
 FT HELIX 119 126
 FT STRAND 124 126
 FT STRAND 129 129
 FT HELIX 131 142
 FT TURN 143 144
 FT HELIX 148 167
 FT STRAND 168 168
 FT HELIX 169 180
 FT STRAND 181 182
 FT STRAND 183 185
 FT HELIX 187 195
 FT TURN 197 197
 FT HELIX 199 207
 FT STRAND 212 220
 FT TURN 222 223
 FT STRAND 226 231
 FT TURN 232 233
 FT HELIX 235 239
 FT STRAND 240 240
 FT STRAND 243 243
 FT STRAND 246 248
 FT STRAND 249 252
 FT STRAND 256 259
 FT STRAND 262 284
 FT HELIX 286 289
 FT STRAND 290 292
 FT TURN 296 297
 FT HELIX 299 303
 FT STRAND 311 313
 FT STRAND 315 317
 FT STRAND 319 320
 FT TURN 322 325
 FT TURN 326 327

East Local Similarity	92.28;	Pred.No. 8.le-108;	
Matches	235;	Conservative	0; Mismatches 19; Indels 1;
QY	1	YERLRVYHTQTGXEYFRITLLRDYVSSGSFNEIPLRQSTIPVSDAQRFVLVELTN	60
DS	1	YERLRVYHTQTGXEYFRITLLRDYVSSGSFNEIPLRQSTIPVSDAQRFVLVELTN	60
QY	61	QGXDSXTHADVTNAYVYAYQGSQYIFRDAFPGASTHLFTGTTRXSLPFGXSXMLE	120
DS	61	QGXDSXTHADVTNAYVYAYQGSQYIFRDAFPGASTHLFTGTTRXSLPFGXSXMLE	120
QY	121	EYAGHEDDIPLGHTXOLQSVLXEPGSGTQXSQBSILLIOWISEAPAFNPLWREXQ	180
DS	120	EYAGHEDDIPLGHTXOLQSVLXEPGSGTQXSQBSILLIOWISEAPAFNPLWREXQ	179
QY	181	INSGXSEFLPDXMYLELSTNGQOSTQVHSTGCVGNFNPXELAIXXGNFVTLXNRXVIAS	240
DS	180	INSGXSEFLPDXMYLELSTNGQOSTQVHSTGCVGNFNPXELAIXXGNFVTLXNRXVIAS	239
QY	241	LAINLFWGGERPSS	255
DS	240	LAINLFWGGERPSS	254

RESULT 5

ABRC ABRCR

AC ID ABRC_ABRFR STANDARD; PRT; 562 AA.

IC 528590; 1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Abrin-c precursor [Contains: Abrin-c A chain (tRNA N-glycosidase) (EC 3.2.2.22); Abrin-c B chain].

OS Abrus precatorius (Indian locoweed) (Crab's eye).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Abrueae; Abrus.

CC NCBI_TaxId=3816;

RP

RP SEQUENCE FROM N.A.

RP TISSUE=Leaf.

RC MEDLINE=91266957; PubMed=2050149;

RC "Preprobrin; Lord J.M., Wawrzynczak E.J., Piatak M.;

RT "Preprobrin; genomic cloning, characterization and the expression of the A-chain in Escherichia coli.";

RL Eur. J. Biochem. 1987;723-732(11991);

CC -1- UNKNOWN: THE A-CHAIN IS A PROPEPTIDE FOR INHIBITING PROTEIN SUBUNITS BY REMOVING ADENINE FROM POSITION 4.324 OF 28 S RNA. THE SUBUNIT IS A RIBOSOMAL PROTEIN WITH A MOLECULAR WEIGHT OF 14.5 KDA.

CC THE B-CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.

CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS. EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).

CC -1- SIMILARITY: THE N-TERMINAL SECTION BELONGS TO THE RIBOSOME-SUBUNIT BINDING PROTEIN SUPERFAMILY.

CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.

CC

CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement> or send an email to license@isb-sib.ch).

CC

CC EMBL; X65026; GI5032402.1; .

CC EMBL; X65026; GI5032402.1; .

DR HGSP; P11140; IABR.

DR InterPro: IPR001574; RIP.

DR InterPro: IPR001574; RIP.

RESULT 7
AGGLUTININ
AC P06750; STANDARD; PRT; 564 AA.
DT 01-JAN-1988 (Rel. 06, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain].
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eudicots I; Malpighiales; Euphorbiaceae; Ricinus.
RX 111; taxid=3986;
RY SEQUENCE FROM N.A.
RA MEDLINE=86059449; PubMed=299130;
RA Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
RA "The primary sequence of Ricinus communis agglutinin. Comparison with ricin.";
RL J. Biol. Chem. 260:15682-15686(1985).
RP SEQUENCE OF 303-564.
RC TISSUE=Seed;
RA Araki T., Yoshioka Y., Funatsu G.;
RT "The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large grain castor bean seeds.";
RI Biochim. Biophys. Acta 872:277-285(1986).
RN [3]
RP SEQUENCE OF 303-337.
RX MEDLINE=80178723; PubMed=6768555;
RA Lin T.-S., Li S.-L.;
RT "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis";
RI Eur. J. Biochem. 105:453-459(1980).
RN [3]
CC -1- CATALYTIC ACTIVITY: Endonuclease.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC -1- INACTIVATING: Contains 2 ricin B-type lectin domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
DR ENBL; M12089; AAK33869.1; --
DR ENBL; S40368; AAB22584.1; --
DR PIR; A24261; RLC3AG.
DR HSSP; P02879; IIR6.
DR GlycoSuiteDB; P06750; --
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; P00396; SHIGARICIN.
DR PROSITE; PS00231; RLCIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 290 AGGLUTININ A CHAIN.
FT PROPEP 291 302 LINKER PEPTIDE.
FT CHAIN 303 564 AGGLUTININ B CHAIN.
FT DOMAIN 309 436 RICIN B-TYPE LECTIN 1.
FT DOMAIN 439 563 RICIN B-TYPE LECTIN 2.
FT REPEAT 319 361 1-ALPHA.
FT REPEAT 362 402 1-BETA.
FT REPEAT 403 437 1-GAMMA.

PT REPEAT 450 485 2-ALPHA.
PT REPEAT 489 528 2-BETA.
PT REPEAT 531 558 2-GAMMA.
FT ACT_SITE 200 200 BY SIMILARITY.
FT DISULFID 282 306 INTERCHAIN (BY SIMILARITY).
FT DISULFID 322 341 BY SIMILARITY.
FT DISULFID 365 382 BY SIMILARITY.
FT DISULFID 453 466 BY SIMILARITY.
FT DISULFID 492 509 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLNAC). (POTENTIAL).
FT CARBOHYD 37 37 N-LINKED (GLNAC). (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLNAC).
FT CARBOHYD 437 437 N-LINKED (GLNAC).
FT CONFLICT 331 331 F -> T (IN REF. 2).
FT CONFLICT 362 362 N -> D (IN REF. 2).
FT CONFLICT 374 374 R -> G (IN REF. 2).
FT CONFLICT 404 404 R -> T (IN REF. 2).
FT CONFLICT 552 552 F -> V (IN REF. 2).
SQ SEQUENCE 564 AA; 62351 MW; D455F2A72F609759 CRC64;
Query Match 42.4%; Score 1109.5; DB 1; Length 564;
Best Local Similarity 45.2%; Pred. No. 7.9e-14; Indels 19; Gaps 10;
Matches 242; Conservative 79; Mismatches 195;
QY 9 THQTGKYEPRFTLLRYYSSGS-PSNEIPLL-RQSTIPVSDAQRFVLVELTNOQDXX 66
DB 37 TADATVSTNFRVRSHTTGADVRHEIPVLPNRVGLPIS--QRFILVLSNHAELSV 94
QY 67 TAAIDVTKYVAYQGDQSYFLR-DAPRGAE--THLFTGTTTRASSLPFGXSXXDLERYA 123
DB 95 TLALDVTVNAYVCGRAGNSAYFFHPNQDEAETHLFTDQNSFTAFGNDRLDQLG 154
QY 124 GRDQIPGLGIQISVVAL---RFGSGSTXQASILLIOWISEARFPNLPKXQX 180
DB 155 GURENIEGTGLEDALNLYVYSTCTQIPTLANSFVCLQWISERARFQIEGEMTR 214
QY 181 INSGKSLPKDYMLELSTGSGQSTQVQHSVDGVNFXELAXXGNFVTLXNVRXVAS 240
DB 215 IRYNRERAPDSVITLNSMGLSLTAOSNQGFASIQLORRNGKXFNVDVSLPI 274
QY 241 LAIMEFYCCERPSSTVRYMPLVRPIAD---DVTCASSEFVRIYKXKXVYVDRDD 327
DB 275 IALNYTCAPPSSQ----FSLILFPVFNFRNDV-CHDFEPIVIRVGNGLCVDTGEE 329
QY 298 FHDGQIOLWPKSKNDNDQNTIKESYITNSGCLTIVGTAGVYVWFDCTAVREA 357
DB 330 FDEENPLQWPKCNTDNNQLWLTLEKSDITNSGKLTISKSPRQQWVYVNCSTATVGA 389
QY 358 TIHQIWNXGTTINFRNLVLAASSIGTTLVQTLDTLGGQWLAGNCTAPREVITGF 417
DB 390 TRNQIWNKTTINPRSGVLVLAATSGNCTKLTIVQTIYANSQWLPNTNQPFYTVGL 449
QY 418 RDLCEENKXGSWVETCKSXQXVXWALYIGDSIRPKQNDQCLTXGKDSVSTVINIVS 477
DB 450 YGKCIQANSGKRWLEDCSTSEKAEQ-QWALYAGSIRPQQRNDCMLTIDANIKGVKLS 508
QY 478 CSXKX 532
DB 509 CGPSSQQRWFKNDGTILNYGLVLDVRRSDPSLKLQIIVHFPFGNLQIWLJPL 563
RESULT 8
NIGB SAMMI
ID NIGB SAMMI STANDARD; PRT; 563 AA.
AC P31183; P31184; P93542;
DT 01-OCT-1993 (Rel. 27, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE (rRNA N-glycosidase) (EC 3.2.2.22); Nigrin B A chain
OS Samolus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

CC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
OK NCBI_taxid=4202;
RX SEQUENCE FROM N.A.
PC TISSUE=BAZ15449; PubMed=8647092;
PC MEDLINE=96215449; PubMed=8647092;
RA Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
RT "Characterization and molecular cloning of Sambucus nigra agglutinin V
RT (nigra b), a GalNAc-specific type-2 ribosome-inactivating protein
RL from the bark of elderberry (Sambucus nigra).";
RX Eur. J. Biochem. 237:505-513(1996).
RX [2]
CC SEQUENCE OF 26-49 AND 298-321.
RX TISSUE=BAZ15449; PubMed=8647092;
RX MEDLINE=96215449; PubMed=8647092;
RA Munoz R., Andueza J., Claveria L., Arizaga J.M., Rojo M.A., Iglesias R.,
RA Munoz R., Andueza J., Claveria L., Arizaga J.M., Rojo M.A., Iglesias R.,
RT "Isolation and partial characterization of Nigra B, a non-toxic
RT novel type 2 ribosome-inactivating protein from the bark of Sambucus
RL nigra L.";
RL Plant Mol. Biol. 22:1181-1186(1993).
CC -1- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAWALIAN
CC PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN
CC SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE
CC BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
CC ENDOCYTOSIS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC The European Bioinformatics Institute. There are no restrictions on its
CC modified and distributed by other institutions as long as its content is in no way
CC entitise requires a license agreement. (See <http://www.ebi.ac.uk/EMBL/blast/>)
CC or send an email to license@ebi.ac.uk)
CC EMBL; U41299; AAB39475.1; .
CC FIR; S37382; S37382.
CC InterPro; IPR000772; Ricin_B_lectin.
CC InterPro; IPR001574; RIP.
CC Pfam; PF00652; Ricin_B_lectin; 6.
CC Pfam; PF00161; RIP; 1.
CC SMART; SMART01386; SHIGARICIN.
CC SMART; SMART01386; SHIGARICIN.
CC PROSITE; PS00274; RIBIN_2; RIBIN_1.
CC PROSITE; PS00231; RIBIN_B_LECTIN; 2.
CC Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
CC Glycoprotein; Lectin; Signal.
CC SIGNAL 1 25
FT CHAIN 26 297 NIGRIN B A CHAIN.
FT CHAIN 298 563 NIGRIN B B CHAIN.
FT DOMAIN 298 563 NIGRIN B-B CHAIN.
FT DOMAIN 305 431 NIGRIN B-TYPE LECTIN 1.
FT REPEAT 316 356 RIBIN B-TYPE LECTIN 2.
FT REPEAT 357 397 1-ALPHA.
FT REPEAT 397 431 1-BETA.
FT REPEAT 431 462 2-GAMMA.
FT REPEAT 462 496 2-BETA.
FT REPEAT 496 524 2-GAMMA.
FT REPEAT 524 554 2-GAMMA.
FT ACT SITE 188 188 INTERCHAIN (BY SIMILARITY).
FT DISULFID 274 302 INTERCHAIN (BY SIMILARITY).
FT DISULFID 319 338 BY SIMILARITY.
FT DISULFID 360 377 BY SIMILARITY.
FT DISULFID 448 463 BY SIMILARITY.
FT DISULFID 489 506 BY SIMILARITY.

FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 537 537 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ CONFLICT 39 39 X -> V (IN REF. 2).
SQ SEQUENCE 563 AA; 62300 MW; F250CBE24621BF14 CRC64;
Query Watch 31.4%; Score 820.5; DB:1; Length 563;
Best Local Similarity 37.0%; Best NC: 2; e: 1.1;
Matches 197; Conservative 88; Mismatches 211; Indels 37; Gaps 16;
QY 17 YFRFTLLRXYSGSGFS-NEIFLLRQSTIPVSDAQRFVLVELTNGQXSDXAAIDVTNX 75
DB 43 YRDFSLNLRKTATGTYEVNGLFVLRES-EVQVKSFRVLPLNNGVTVLAVDVTNL 101
QY 76 YVVAQAGQSYPIADAPRGASTHFTGTTEXSSLPFGXSYDXDLERYAG-HRQDIPLGIX 134
DB 102 YVFAFGNRRNPFYKDAFVQKSMFVG-TQNTLSFTGNYDNLTAANTRRSIELGPS 160
QY 135 QLIQSVXALRFPGSTKACBRIILLIOMIGSEARFNPILKXQINSKSGKPDXYML 194
DB 161 PLDGAITSL-VHDSV--ARELLVILQWSEARFVLEQVRSILOASTFPAALML 216
QY 195 ELETSMGQOSTQVQHSITGV-----FNNPKRLAIXGNFVTLANVXKVASLAI 243
DB 217 SNNKSSMSLEIQAGNNVSPFGTVQLNLYDHTHLV---DNFELYK-----ITGIAI 269
QY 244 MLFVQGERPSSSVRYMPLVIR--PVIADDTVCASEPTVR-IVGRGXQVDRDDFFH 299
DB 270 LIFRCSS-PSYDNRMLPDLAGEKNYNDGTCTLRSTFTNIVRGDCLCVRNGYDT 328
QY 300 DNDQIOLNFKSNNDPQLMTIKDYTIKRSNGSLTGYTYGVYKIPQONTVREKTI 359
DB 329 DCTELQNEFCOTR-NQRTVPSDOTIRSMGKNTANGNSNIVFNCSTAEANIK 386
QY 360 MWIXWNTIIPNSMLVLAASSGKTITVQTLDTYLGQGLAGNDTAPREVTYVGRD 419
DB 387 MEVTDGSIINPSSGLVTPAPASHTILLENTYLAASQGTNNVNFVIVASIVGYKE 446
QY 420 LQMESN--XGSVVVTCCSXQXQXVLAAGDSIRFQKQDCLTXGRDSVSTVINVS 477
DB 447 MCLQSGENGVNMECEATSLQO-QNALYQDRTIVNSTGLCVITNGSKDLIILX 505
QY 478 CSXKXQGVFVFNKALINLXXXXXXQVQANPKLRIIVYATKCKRNOML 530
DB 506 CQGLP-SQWFFNSDGLVNPKSHVMDVRAVSLEIILPPTATGNPNQGV 557

RESULT 9
RIP2_BRYDI STANDARD; PRT: 282 AA.
ID RIP2_BRYDI
AC P98184; Q98800;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 41, Last annotation update)
DE 16-FEB-2003 (Rel. 41, Last annotation update)
DE Glycosylase (EC 3.2.2.22) [Inet].
OS Bryonia dioica (Red Bryonia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
OK NCBI_taxid=3652;
RN [1]
RP SEQUENCE FROM N.A.
RA Siegel C.B., Gawlak S.L., Marquardt H.;
RT "Bryodin 2 a ribosome-inactivating protein isolated from the plant
RL Bryonia dioica.";
RL Patent number US5597569, 28-JAN-1997.
RC SEQUENCE OF 22-42.
RC TISSUE=ROOT;
RX MEDLINE=95151812; PubMed=7849072;

RA Siegal C.B., Gavlak S.L., Chace D., Wolff E.A., Mixan B.,
RA Marquardt H.;
RA "Characterization of ribosome-inactivating proteins isolated from
RT Bryonia dioica and their utility as carcinoma-reactive
RT immunocytostatics"; J. Natl. Cancer Inst. 86:423-429 (1994).
CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1. INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; 134238; ; NOT ANNOTATED CDS.
CC HSSP; P09989; 1MRJ.
CC InterPro; IPR001574; RIP.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; P000396; SHIGARICIN
CC PROSITE; PS00275; SHIGA_RICIN; 1.
CC Kunitz defense protein domain; 1.
CC Multi-subunit; 1.
CC Multi-subunit family; Glycoprotein; Signal.
CC SIGNAL 1 21
CC CHAIN 22 282 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
CC FT ACT SITE 183 183 BY SIMILARITY.
CC FT CARBOHYD 25 25 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 282 AA; 30754 MW; C52B2F6A873769C CRC64;
CC
CC Query Match 12.3%; Score 322.5; DB 1; Length 282;
CC Best local similarity 36.4%; Fragment 2; se-24;
CC Matches 86; Conservative 37; Mismatches 100; Gaps 9;
CC
CC QY 13 TGKEYFRITLLRDYVSSG-PSNEIPLLRSTIPVSDAQFVLVNLNGDSTAAID 71
CC DB 32 TGATYKTFIRNLATLTVGTTPRVYDIPVLRNMAAGLA--RFQLVTLNNGESVTVLD 88
CC QY 72 VTNAYVAYQDQSYFIADAPGAEATHLFTGTXXSLFPXGYXDLRYAGH--PDQI 129
CC DB 89 VVNYVYVAYRAGTAYFIADASTENNVLPAGINEV-RLPYGNNGYGLTAGRISREMI 147
CC QY 130 PLGTQIQTSVYAL--XPQGSTQXQASILLIQVISEARFNFLARXKINCSXSF 187
CC DB 148 ELGFSEISSNIGMFFNPGTSV---PRAEVILQTVSEARFPYLEQVSE--NVGTGF 202
CC QY 188 LPDXVMELETSGQGSQTVQ--HSTDGVFNFXELALXGNFVTLXNVX--VIALSLAM 244
CC DB 203 KEDFAFLSLQANGSLSEQIQIATQAGGFARFVELATVSNTPFTVTVNSPVYKGIALL 262
CC QY 245 LF 246
CC DB 263 LY 264
CC
CC RESULT 10
CC RIPT-TRIKI
CC AC P09989 STANDARD; PRT; 289 AA.
CC DT 01-NOV-1989 (Rel. 10, Created)
CC DT 15-SEP-2003 (Rel. 42, Last sequence update)
CC DE Ribosome-inactivating protein alpha-trichosanthin precursor
CC OS (-RNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).
CC SE Trichosanthin kirilowii (Mongolian snake-guard).
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.

OX NCBI_TaxID=3677;
RN [1]_TaxID=3677;
RP SEQUENCE FROM N.A.
RC STRAIN-Maximowicz;
RX MEDLINE=91153657; PubMed=999291;
RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
RT "Cloning of trichosanthin cDNA and its expression in Escherichia
RT coli."; J. Biol. Chem. 265:8670-8674 (1990).
RN [2]
RP SEQUENCE FROM N.A. TISSUE=Leaf;
RC STRAIN-Maximowicz;
RX MEDLINE=90256790; PubMed=2341400;
RA Chow T., Feldman R.A., Lovett M., Piatak M.;
RT "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
RT type I ribosome-inactivating protein."; J. Biol. Chem. 265:8670-8674 (1990).
RN [3]
RP SEQUENCE OF 24-270.
RC STRAIN-Maximowicz; TISSUE=Tuberos root;
RX MEDLINE=90256789; PubMed=2341399;
RA Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
RA Wu P., Huang K., Piatak M.;
RT "Primary amino acid sequence of alpha-trichosanthin and molecular
RT cloning of trichosanthin cDNA and alpha-trichosanthin."; J. Biol. Chem. 265:8665-8669 (1990).
RN [4]
RP SEQUENCE OF 24-270.
RC TISSUE=Tuberos root;
RX Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
RA Tian G.Y., Ni C.Z.;
RT "Scientific evaluation of Tian Hua Pen (THP): history, chemistry and
RT application."; J. Natl. Cancer Inst. 86:789-798 (1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
RX MEDLINE=94344957; PubMed=8066085;
RA Zhou F., Fu Z., Chen M., Lin Y., Pan X.;
RT "Structure of trichosanthin at 1.88-A resolution."; Proteins 19:4-13 (1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RX MEDLINE=95344383; PubMed=7619000;
RA Huang Q., Liu S., Tang S.;
RT "Studies on chemical structures of active-centre geometry and
RT mechanism of action of two ribosome-inactivating proteins."; Biochem. J. 309:285-298 (1995).
RN [7]
CC -!- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
CC CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
CC INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
CC -!- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; M34858; AAA34207.1; -;
CC EMBL; J05434; AAA34206.1; -;
CC PIR; JT0566; RLTZT
CC PDB; 1MRJ; 07-FEB-95.
CC PDB; 1TCS; 10-JUL-95.
CC PDB; 1JGJ; 28-JAN-03.
CC PDB; 1NLI; 21-JAN-03.
CC PDB; 1Q22; 28-JAN-00.
CC InterPro; IPR001574; RIP.

DR PFAM; PF00161; RIP: 1.
 DR PRINTS; P000396; SHIGARICIN.
 DR PROSITE; P000275; SHIGA_RICIN; 1.
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
 FT Signal; 3D-structure.
 FT CHAIN 24 270

RIBOSOME-INACTIVATING PROTEIN ALPHA-
 TRICHOSANTHIN
 MISSING IN MATURE PROTEIN.
 BY SIMILARITY.
 IPLL -> IPLI (IN REF. 4).
 MISSING (IN REF. 4).
 I -> L (IN REF. 4).
 V -> VDAQENAVL (IN REF. 4).
 KI -> GL (IN REF. 4).
 K -> S (IN REF. 4).
 MS -> LMS (IN REF. 4).
 Q -> T (IN REF. 4).
 S -> T (IN REF. 2).
 MISSING (IN REF. 4).
 T -> M (IN REF. 2).
 FT PROPEP 271 289
 FT ACT SITE 183
 FT CONFLICT 57 60
 FT CONFLICT 82 84
 FT CONFLICT 87 87
 FT CONFLICT 92 92
 FT CONFLICT 143 144
 FT CONFLICT 196 196
 FT CONFLICT 215 215
 FT CONFLICT 231 231
 FT CONFLICT 234 234
 FT CONFLICT 246 246
 FT CONFLICT 247 247
 FT STRAND 25 28
 FT TURN 30 31
 FT HELIX 34 46
 FT TURN 47 47
 FT STRAND 50 54
 FT TURN 55 56
 FT STRAND 57 60
 FT HELIX 66 66
 FT STRAND 70 76
 FT TURN 78 79
 FT STRAND 82 88
 FT TURN 89 92
 FT STRAND 93 99
 FT TURN 100 101
 FT STRAND 102 105
 FT HELIX 109 114
 FT TURN 115 117
 FT TURN 120 121
 FT STRAND 124 124
 FT HELIX 134 134
 FT TURN 142 142
 FT HELIX 145 147
 FT STRAND 150 150
 FT TURN 152 163
 FT TURN 164 165
 FT HELIX 167 180
 FT TURN 181 181
 FT HELIX 182 186
 FT STRAND 187 187
 FT HELIX 188 192
 FT TURN 193 193
 FT STRAND 203 202
 FT HELIX 206 226
 FT TURN 227 230
 FT STRAND 231 239
 FT TURN 241 242
 FT STRAND 245 250
 FT TURN 251 252
 FT HELIX 254 258
 FT TURN 259 259
 FT STRAND 260 260
 FT TURN 263 263
 FT STRAND 265 265
 FT TURN 268 268
 FT STRAND 285 285
 FT TURN 288 288
 FT STRAND 289 289

Query Match 11.8%; Score 308.5; DB 1; Length 289;
 Best Local Similarity 34.7%; Pred. No. 6.3e-23;
 Matches 83; Conservative 49; Mismatches 94; Indels 13; Gaps 8;
 QY 13 TKXEYFRITLLRDYVSGSFSNEIPRLROSTIPVSDAQRFVLEMTNQXDSMTAIDV 72
 DB 33 TSSSYGVFTENLREKALPNERKLYDIPLLR--SSLFCS--QRVALTHLTNYADETISVAIDV 89

QY 73 TXXVTVVQADQSDQSVFLDA--PRGAEHLFTGTTXSLSPFXGYXDLERYACH-RDQIP 130
 DB 90 TVVIMGRAGDTSTIFFNEASATEAKVFKDMARKVFLPFGNRELTQTAQKRENP 149
 QY 131 LGIXQLQSVAXRPGSGTQXQASILILQIMSEARBNELWEXQXNGSKSLPD 190
 DB 150 LGLPALSATLFTFYVANS--AASALVLLQSTSEARVYKIQIGRVDK--TFLPS 205
 QY 191 XTMLELSTWQOSTQV--HSTGVFNFXRLAIXGNFVLXVRX--VIASLAILM 245
 DB 206 LAITLSEWSALSQIQIASTNNGQFSPVVLNAQNRVITNVDAGVVTNTALL 264

RESULT 11
 RIPT-TRIKI
 AD RIPT-TRIKI STANDARD; PRT: 289 AA.
 AC 478
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein Karasurin precursor (rRNA
 DE N-glycosidase) (EC 3.2.2.22).
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 RN [UniTaxId=3677]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Root tuber;
 RX MEDLINE=97356562; PubMed=9212998;
 RA Mizukami H., Iida K., Kondo T., Ogiwara Y.;
 RT "Cloning and bacterial expression of a gene encoding ribosome-
 RT inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
 RT kirilowii var. japonica.";
 RT Biol. Pharm. Bull. 20:711-713 (1997).
 RN [2]
 RN SEQUENCE OF 24,270
 RP MEDLINE=900922; PubMed=1914000;
 RA Takeda S., Takeda T., Kato Y., Wakabayashi K., Ogiwara Y.;
 RT "The complete amino acid sequence of an abortifacient protein,
 RT karasurin.";
 RT Chem. Pharm. Bull. 39:1244-1249 (1991).
 CC -1- FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC
 CC 60S RIBOSOMAL SUBUNITS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolase of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB000666; BAA21786.1; -
 CC FIR; JCS606; JCS606.
 CC FIR; J00393; J00393.
 CC HSP; E09989; INR3.
 CC INR; P000154; RIP.
 CC INR; P000154; RIP.
 CC PRINTS; P000396; SHIGARICIN.
 CC PROSITE; P000275; SHIGA_RICIN; 1.
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
 FT Signal; 1 21
 FT CHAIN 22 270
 FT CHAIN 24 270
 FT PROPEP 271 289

FT ACT SITE 183 183 BY SIMILARITY
 SQ SEQUENCE 289 AA; 31704 MW; 883D3E24288726 CRC64;
 Query Match 11.8%; Score 307.5; DB 1; Length 289;
 Best Local Similarity 35.6%; Pred. No. 7.9e-23;
 Matches 85; Conservative 45; Mismatches 96; Indels 13; Gaps 8;

DB 13 TQKPERFTLLRDYVSSGSPNEPILRQSTIVSDAQREVLVELTNGQKXKTAIDV 72
 QY 33 TSSSYGVISNKAALPEERKLDLELR-STLPGS--QRTALHLINVADETLVADLV 89
 DB 73 TSKYVAVQAGQSGYFLRDA-PRGAEFTLFTGTRKSLPFGXSYDLERVAGH-NDQIP 130
 DB 90 TNYVYVAVRTRDVSYPFESKSPPEXVILFKG--TRKTLPTGNYENLTQ-AAKTRF 144
 QY 131 LGIXOLIQSYVALKXPGSGSTXQARSILTIQMSBAAPFPLMXKQXNSKXSF 187
 DB 150 LGILPALSALITLTFYNNANS--ASALMTVLQSTISARVFLQOIGKRVK--TFEFS 205
 QY 191 XYVMBLETSNGQSGTVO--HSTDGVFNKXLAIXXGNFVTLXNVK--VIASLAIL 245
 DB 206 LATISLNSNSAKRQIOASTNGCFEFTFVVLINMQKQVITTVDAVGVINAIL 264

RESULT 12
 RIP2.MOMBA STANDARD; PRT; 286 AA.

AC P29339;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribosome-inactivating protein momordin II precursor (rRNA
 DE N 3,2,22)
 OS Momordica balsamina (Balsam. peac.)
 OC Eukaryota; Viridiplantae; Streptophyta; Eudicots; Rosidae;
 OC Spermatophyta; Magnoliopsida; eudicots; Rosidae;
 OC eurosid I; Cucurbitales; Cucurbitaceae; Momordica.
 NCBI_TaxID=3672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX DBLINK=93027170; PubMed=1408771;
 RT "Momordica", better "M";
 RL "balsamina", better "balsamina";
 RL Nucleic Acids Res 20:4662-4662(1992)
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch)
 CC
 CC EMBL; 212175; CA78166.1;
 DR PIR; S25560; S25560.
 DR FDB; ICF5; 07-JUN-99;
 DR InterPro; IPR01574; RIP.
 DR PAM; PF00161; RIP; 1.
 DR PROSITE; PS00275; STRANSACTIN.
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
 KW 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 286
 FT FT
 FT ACT SITE 181 181
 FT SEQUENCE 286 AA; 32031 MW; 3B89FFA5B25986 CRC64;

Query Match 11.1%; Score 291; DB 1; Length 286;
 Best Local Similarity 33.1%; Pred. No. 3.3e-21;
 Matches 84; Conservative 48; Mismatches 102; Indels 20; Gaps 10;

DB 13 TQKPERFTLLRDYVSSGSPNEPILRQSTIVSDAQREVLVELTNGQKXKTAIDV 72
 QY 33 TSSSYGVISNKAALPEERKLDLELR-STLPGS--QRTALHLINVADETLVADLV 89
 DB 73 TSKYVAVQAGQSGYFLRDA-PRGAEFTLFTGTRKSLPFGXSYDLERVAGH-NDQIP 130
 DB 90 TNYVYVAVRTRDVSYPFESKSPPEXVILFKG--TRKTLPTGNYENLTQ-AAKTRF 144
 QY 131 LGIXOLIQSYVALKXPGSGSTXQARSILTIQMSBAAPFPLMXKQXNSKXSF 187
 DB 145 LGILPALSALITLTFYNNANS--ASALMTVLQSTISARVFLQOIGKRVK--TFEFS 205
 QY 186 LBDYVMBLETSNGQSGTVO--HSTDGVFNKXLAIXXGNFVTLXNVK--VIASLAIL 245
 DB 201 KENLALISLEWQMSLSTQIPQAQNGKFNKLVLPKPGKQVNVSDGVVKNIL 260
 QY 246 FVCGEPSSSDVAY 259
 DB 261 LL-NSRSTADENP 273

RESULT 13
 RIP1.TRIIN STANDARD; PRT; 294 AA.

AC P56526; 092077;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 30-FEB-2003 (Rel. 41, Last annotation update)
 DE Type I ribosome-inactivating protein trichosanthin precursor (rRNA
 DE N 3,2,22) (RIP) (trichosanthin).
 OS Trichosanthes anguina (Snake gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; eudicots; Rosidae;
 OC eurosid I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 NCBI_TaxID=50544;
 RN [1]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE. AND CHARACTERIZATION.
 RC STRAIN=cv. Anguina; TISSUE=Seed;
 RX MEDLINE=9131006; PubMed=9931318;
 RA Chow L.-P., Chou W.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H.,
 RA Lin J.-Y.;
 RT "Trichosanthin", characterization and molecular cloning of trichosanthin,
 RT a nucleolar type I, ribosome-inactivating protein from the seeds of
 RT Trichosanthes anguina (Cucurbitaceae).
 RL Biochem. J. 338:211-219(1999).
 RN [2]
 RP SEQUENCE OF 20-264.
 RC TISSUE=Seed;
 RX Chow L.-P., Kano M., Lin J.-Y., Wang S.-H., Ueno Y., Tange A.;
 RL "Amino acid sequence of trichosanthin, a ribosomal-inactivating
 RL protein from Trichosanthes anguina seeds".
 RT J. Biomed. Sci. 3:178-186(1996).
 CC -1- FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPHOSPHORYLATING 28S RNA IN
 CC THE 80S RIBOSOME.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch)

Thu Dec 11 16:09:44 2003

us-09-601-667c-1.rpt

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 41.0829 Seconds

Title: US-09-601-667C-1 ; (without alignment)

Sequence: 1 YERLRVYHQTGXEYFR.....RRIIVPATKQKQWMPVX 533

Perfect score: 2616

Scoring table: BLOSUM62

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: sp_archaea: 2: sp_bacteria: 3: sp_fungi: 4: sp_human: 5: sp_invertebrate: 6: sp_mammal: 7: sp_mbc: 8: sp_orcellale: 9: sp_plant: 10: sp_protist: 11: sp_todent: 12: sp_virus: 13: sp_vertebrate: 14: sp_unclassified: 15: sp_virus: 16: sp_bacteriap: 17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2478	521	10	Q8XN6	Q8XN6 vitiscum albu
2	2224	521	10	Q8XN6	Q8XN6 vitiscum albu
3	1246	521	10	Q8XN6	Q8XN6 vitiscum albu
4	1243	47.5	580	Q8XN6	Q8XN6 vitiscum albu
5	1230	47.0	541	Q8XN6	Q8XN6 vitiscum albu
6	1197.5	45.8	549	Q8XN6	Q8XN6 vitiscum albu
7	1196.5	45.7	581	Q8XN6	Q8XN6 vitiscum albu
8	1137.5	43.5	528	Q8XN6	Q8XN6 vitiscum albu
9	1137.5	42.6	249	Q8XN6	Q8XN6 vitiscum albu
10	1094.5	41.8	254	Q8XN6	Q8XN6 vitiscum albu
11	1067.5	41.2	243	Q8XN6	Q8XN6 vitiscum albu
12	1054.5	40.3	246	Q8XN6	Q8XN6 vitiscum albu
13	1029.5	39.4	263	Q8XN6	Q8XN6 vitiscum albu
14	977.5	37.4	251	Q8XN6	Q8XN6 vitiscum albu
15	968.5	37.0	592	Q8XN6	Q8XN6 vitiscum albu

Result No.	Score	Query Match	Length	DB ID	Description
1	961.5	35.8	572	Q8XN6	Q8XN6 vitiscum albu
2	877.5	33.2	570	Q8XN6	Q8XN6 vitiscum albu
3	876.5	33.5	382	Q8XN6	Q8XN6 vitiscum albu
4	874	33.4	564	Q8XN6	Q8XN6 vitiscum albu
5	852.5	32.6	563	Q8XN6	Q8XN6 vitiscum albu
6	849.5	32.5	570	Q8XN6	Q8XN6 vitiscum albu
7	828.5	31.7	565	Q8XN6	Q8XN6 vitiscum albu
8	825.5	31.6	604	Q8XN6	Q8XN6 vitiscum albu
9	822.5	31.4	563	Q8XN6	Q8XN6 vitiscum albu
10	820.5	31.4	563	Q8XN6	Q8XN6 vitiscum albu
11	807	30.6	566	Q8XN6	Q8XN6 vitiscum albu
12	764.5	28.2	603	Q8XN6	Q8XN6 vitiscum albu
13	755	27.7	569	Q8XN6	Q8XN6 vitiscum albu
14	526.5	20.1	316	Q8XN6	Q8XN6 vitiscum albu
15	525.5	20.1	316	Q8XN6	Q8XN6 vitiscum albu
16	525.5	20.1	316	Q8XN6	Q8XN6 vitiscum albu
17	504.5	19.3	320	Q8XN6	Q8XN6 vitiscum albu
18	494.5	18.3	320	Q8XN6	Q8XN6 vitiscum albu
19	454.5	17.4	252	Q8XN6	Q8XN6 vitiscum albu
20	454.5	17.3	251	Q8XN6	Q8XN6 vitiscum albu
21	447.5	17.1	251	Q8XN6	Q8XN6 vitiscum albu
22	443.5	17.0	252	Q8XN6	Q8XN6 vitiscum albu
23	409.5	11.8	289	Q8XN6	Q8XN6 vitiscum albu
24	306	11.7	299	Q8XN6	Q8XN6 vitiscum albu
25	303.5	11.6	247	Q8XN6	Q8XN6 vitiscum albu

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	961.5	35.8	572	Q8XN6	Q8XN6 vitiscum albu
2	877.5	33.2	570	Q8XN6	Q8XN6 vitiscum albu
3	876.5	33.5	382	Q8XN6	Q8XN6 vitiscum albu
4	874	33.4	564	Q8XN6	Q8XN6 vitiscum albu
5	852.5	32.6	563	Q8XN6	Q8XN6 vitiscum albu
6	849.5	32.5	570	Q8XN6	Q8XN6 vitiscum albu
7	828.5	31.7	565	Q8XN6	Q8XN6 vitiscum albu
8	825.5	31.6	604	Q8XN6	Q8XN6 vitiscum albu
9	822.5	31.4	563	Q8XN6	Q8XN6 vitiscum albu
10	820.5	31.4	563	Q8XN6	Q8XN6 vitiscum albu
11	807	30.6	566	Q8XN6	Q8XN6 vitiscum albu
12	764.5	28.2	603	Q8XN6	Q8XN6 vitiscum albu
13	755	27.7	569	Q8XN6	Q8XN6 vitiscum albu
14	526.5	20.1	316	Q8XN6	Q8XN6 vitiscum albu
15	525.5	20.1	316	Q8XN6	Q8XN6 vitiscum albu
16	525.5	20.1	316	Q8XN6	Q8XN6 vitiscum albu
17	504.5	19.3	320	Q8XN6	Q8XN6 vitiscum albu
18	494.5	18.3	320	Q8XN6	Q8XN6 vitiscum albu
19	454.5	17.4	252	Q8XN6	Q8XN6 vitiscum albu
20	454.5	17.3	251	Q8XN6	Q8XN6 vitiscum albu
21	447.5	17.1	251	Q8XN6	Q8XN6 vitiscum albu
22	443.5	17.0	252	Q8XN6	Q8XN6 vitiscum albu
23	409.5	11.8	289	Q8XN6	Q8XN6 vitiscum albu
24	306	11.7	299	Q8XN6	Q8XN6 vitiscum albu
25	303.5	11.6	247	Q8XN6	Q8XN6 vitiscum albu

Thu Dec 11 16:09:44 2003

us-09-601-667c-1.rept

Page 2

Matches 483; Conservative 5; Mismatches 42; Indels 2; Gaps 2;
QY 1 YERLRATVHTGKCYFRFRITLLADYVSSGSENFILRLROSTIPVSDAQRVLTETN 60
DB 1 YERLRATVHTGKCYFRFRITLLADYVSSGSENFILRLROSTIPVSDAQRVLTETN 60
QY 61 QGDSXTAIDVYNNVYVAYQAGDSYFLRDPAGAEHLFTGTTRXSILPFXSYDLE 120
DB 61 QGDSXTAIDVYNNVYVAYQAGDSYFLRDPAGAEHLFTGTTRXSILPFXSYDLE 119
QY 121 RVAGHDQIPLOIQLQSVTLALRPGAKTRKQASLILQMTSEAPNFTLWEXOK 180
DB 121 RVAGHDQIPLOIQLQSVTLALRPGAKTRKQASLILQMTSEAPNFTLWEXOK 180
QY 181 INSGSFLPDVYMLETSMGQSTQVQSTGVFNNEKXLAIXGNFTLWEXVYAS 240
DB 181 INSGSFLPDVYMLETSMGQSTQVQSTGVFNNEKXLAIXGNFTLWEXVYAS 239
QY 241 LAIMLVCGERSSSDVRYWPLVIRPVADVTCSAEPVIRVGRXGXVDVADDDPH 300
DB 241 LAIMLVCGERSSSDVRYWPLVIRPVADVTCSAEPVIRVGRXGXVDVADDDPH 299
QY 301 GNQIQWPKSKNDPQVLTIRKXDTIRNSGCLTGYGTAGYVYVPCQNTAVREATV 360
DB 301 GNQIQWPKSKNDPQVLTIRKXDTIRNSGCLTGYGTAGYVYVPCQNTAVREATV 359
QY 361 QIRXNGTIIINPNSVLVLAASGKIGTTLVQCLDTLQCGWLANGTAPREVTYGFED 420
DB 361 QIRXNGTIIINPNSVLVLAASGKIGTTLVQCLDTLQCGWLANGTAPREVTYGFED 419
QY 421 QWESNKGWYVETCKSSQXQXVYVGDGSIKPKQNDQCLTXKQDSVSTVNIYSCX 480
DB 421 QWESNKGWYVETCKSSQXQXVYVGDGSIKPKQNDQCLTXKQDSVSTVNIYSCX 478
QY 481 XSKQWYVETCKSSQXQXVYVGDGSIKPKQNDQCLTXKQDSVSTVNIYSCX 532
DB 479 GSGQWYVETCKSSQXQXVYVGDGSIKPKQNDQCLTXKQDSVSTVNIYSCX 530
RESULT 2
Q9M243
ID Q9M243 PRELIMINARY; PRT; 565 AA.
AC 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE VCA precursor (EC 2.2.1.22) (RNA N-glycosylase)
OS Viscum album subsp. coloratum
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RS SEQUENCE FROM N.A.
RT "Clk N-B, Lys S, S, Viscum album subsp. coloratum (Korean mistletoe).";
RT Bioclin. Biophys. Res. Commun. 0 (2002)
CC -1- CATALYTIC ACTIVITY: ENDORIBOXYLIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF369661; ALA0417.1; -
DR InterPro; IPR000772; RICH_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; RICH_B_lectin; 6.
DR Pfam; PF00652; SHIGARICIN.
DR SMART; SM00458; RICH_B_lectin; 2.
DR PROSITE; PS00231; RICH_B_lectin; 2.
KW Hydroxylase, signal, toxin.
FT SIGNAL. 1
FT CHAIN. 23 273 VCA ALPHA CHAIN.
FT CHAIN. 309 565 VCA BETA CHAIN.
SQ SEQUENCE 565 AA; 62401 MW; 991E394DA0D5F11 CRC64;

Query Match 85.0%; Score 2224.5; DB 10; Length 565;
Best Local Similarity 81.8%; Pct. No. 1.4e-218;
Matches 439; Conservative 18; Mismatches 69; Indels 11; Gaps 4;
QY 1 YERLRATVHTGKCYFRFRITLLADYVSSGSENFILRLROSTIPVSDAQRVLTETN 60
DB 1 YERLRATVHTGKCYFRFRITLLADYVSSGSENFILRLROSTIPVSDAQRVLTETN 60
QY 61 QGDSXTAIDVYNNVYVAYQAGDSYFLRDPAGAEHLFTGTTRXSILPFXSYDLE 120
DB 61 QGDSXTAIDVYNNVYVAYQAGDSYFLRDPAGAEHLFTGTTRXSILPFXSYDLE 119
QY 121 RVAGHDQIPLOIQLQSVTLALRPGAKTRKQASLILQMTSEAPNFTLWEXOK 180
DB 121 RVAGHDQIPLOIQLQSVTLALRPGAKTRKQASLILQMTSEAPNFTLWEXOK 180
QY 181 INSGSFLPDVYMLETSMGQSTQVQSTGVFNNEKXLAIXGNFTLWEXVYAS 240
DB 181 INSGSFLPDVYMLETSMGQSTQVQSTGVFNNEKXLAIXGNFTLWEXVYAS 239
QY 241 LAIMLVCGERSSSDVRYWPLVIRPVADVTCSAEPVIRVGRXGXVDVADDDPH 300
DB 241 LAIMLVCGERSSSDVRYWPLVIRPVADVTCSAEPVIRVGRXGXVDVADDDPH 299
QY 301 GNQIQWPKSKNDPQVLTIRKXDTIRNSGCLTGYGTAGYVYVPCQNTAVREATV 360
DB 301 GNQIQWPKSKNDPQVLTIRKXDTIRNSGCLTGYGTAGYVYVPCQNTAVREATV 359
QY 361 QIRXNGTIIINPNSVLVLAASGKIGTTLVQCLDTLQCGWLANGTAPREVTYGFED 420
DB 361 QIRXNGTIIINPNSVLVLAASGKIGTTLVQCLDTLQCGWLANGTAPREVTYGFED 419
QY 421 QWESNKGWYVETCKSSQXQXVYVGDGSIKPKQNDQCLTXKQDSVSTVNIYSCX 480
DB 421 QWESNKGWYVETCKSSQXQXVYVGDGSIKPKQNDQCLTXKQDSVSTVNIYSCX 478
QY 481 XSKQWYVETCKSSQXQXVYVGDGSIKPKQNDQCLTXKQDSVSTVNIYSCX 532
DB 479 GSGQWYVETCKSSQXQXVYVGDGSIKPKQNDQCLTXKQDSVSTVNIYSCX 530
RESULT 3
Q94BM4
ID Q94BM4 PRELIMINARY; PRT; 560 AA.
AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
OS Rye 2 ribosome-inactivating protein cinnamomum II precursor
OS Cinnamomum cinnamomum (Caryophyllales)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Santalales; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RS SEQUENCE FROM N.A.
RT "Yang Q., Gong Z. Z., Liu W. Y.;
RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomum proteins and study of their expression
RT Submitted (Jun-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDORIBOXYLIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF039802; AAK2459.1; -
DR InterPro; IPR000772; RICH_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; RICH_B_lectin; 6.
DR Pfam; PF00652; SHIGARICIN.
DR SMART; SM00458; RICH_B_lectin; 2.
DR PROSITE; PS00231; RICH_B_lectin; 2.

Thu Dec 11 16:09:44 2003

us-09-601-667c-1.rsp1

Page 3

Hydrolase; Signal; Toxin.
FT SIGNAL 32 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CHAIN 33 580 CINNAMOIN II.
SQ SEQUENCE 580 AA; 6425 MW; 37242896CCECP6 CRC64;
Query Match 47.6%; Score 1246; DB 10; Length 580;
Best Local Similarity 50.4%; Pred. No. 1-9e-115; Indels 24; Gaps 13;
Matches 274; Conservative 69; Mismatches 175; DSKRFLVLSMMAADSPV 97
9 THQTKGKFRFTLLRDYSSGSGSSENEPIRLQ-STPYSPAPQFVHELTMOXGSKT 67
40 TKAKTSYQPIALRAQALSGSEPHGIPWERASTVP--DSKRFLVLSMMAADSPV 97
68 A-AIDVTNXYVAQKQDSYFIR-DAPRGAEHLFTCTTKXSLPEXSGSYDLERYAGH 125
98 ALAVDTNNAVVAARTGSGSSEFLREDNDPALEMLDPTKRY-TEPSSGYTLDERVAGE 156
126 -EDQTRGIXQLOSVALKXRG-OSTRQKASILLIOMISAPRNPILMKXQKINS 183
157 LRRELLMDPLENAISLMTSNMQKALARSILIVQVNAKVRFRILEKVESLIR 216
184 GXEFLPDXYMLELFTSMGQSGTOVQHSITD-GVFNKFXLAIXXGNPVLXNVR-XVIA 241
217 AEWFRDPFALSLFNKMSLSNAYQSQGVSFSEVFLSINRNPVYGSVDRIISGL 276
242 AMLFVQC--GERPSSDVRWVPLVIRVIAD-----DVTCSASEPTVXIVKXNM 289
277 AMLFPGSGSDTSDDQFIHLMIRPLADVADVDADNDPTCLOPFEPTVIRSGNG 336
290 XYVREDDPHDNDQLOLPKSNMPPNQLATIRKDDTIRNSGCLTYGTGAYVYMF 349
337 CVVDRGKNNKNGPIQWPCCKNSDVQQLATIRDDOTIRNSGCLTINQVSNADPVY 396
350 CNTAVREKTIWQKNGTIIMPESNVLAASSGIKGTLVYQTLDTYLDQGLAGNDIAP 409
397 CKPTVASTISQFWANGTIIMPQSLVLSSESGSPETLLVQANVYASRQMLAGNTEP 456
410 REVTVIGRDLQNSKXGVSWEVETCSXQKXKXALIGDSIRPKQNDQCLT-XGRDS 468
457 FVTSIVGRDLQKQNDKMMVVEGSSKED-KMLIPDSIRPKQNDQCLTSTDNHS 515
469 VSTVINIVSCSXKXQKRWVTEKALINLXXXXXVDVAQNMFKRLIITYPARGKPM 528
516 QGSIILISCSFGSQGRWVNDGTILNKXGLVMDVQSGNSPHOIIMPARGKPMQ 575
529 WLPV 532
576 WLPV 579

FT SIGNAL 32 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CHAIN 33 580 CINNAMOIN II.
SQ SEQUENCE 580 AA; 64421 MW; 940D10P0L7E558 CRC64;
Query Match 47.5%; Score 1243; DB 10; Length 580;
Best Local Similarity 50.4%; Pred. No. 3-8e-115; Indels 24; Gaps 13;
Matches 274; Conservative 71; Mismatches 175; DSKRFLVLSMMAADSPV 97
9 THQTKGKFRFTLLRDYSSGSGSSENEPIRLQ-STPYSPAPQFVHELTMOXGSKT 66
40 TKAKTSYQPIALRAQALSGSEPHGIPWERASTVP--DSKRFLVLSMMAADSPV 97
67 TPAIDVTNXYVAQKQDSYFIR-DAPRGAEHLFTCTTKXSLPEXSGSYDLERYAGH 124
98 ALAVDTNNAVVAARTGSGSSEFLREDNDPALEMLDPTKRY-TEPSSGYTLDERVAGE 156
126 -EDQTRGIXQLOSVALKXRG-OSTRQKASILLIOMISAPRNPILMKXQKINS 183
157 LRRELLMDPLENAISLMTSNMQKALARSILIVQVNAKVRFRILEKVESLIR 216
184 GXEFLPDXYMLELFTSMGQSGTOVQHSITD-GVFNKFXLAIXXGNPVLXNVR-XVIA 241
217 AEWFRDPFALSLFNKMSLSNAYQSQGVSFSEVFLSINRNPVYGSVDRIISGL 276
242 AMLFVQC--GERPSSDVRWVPLVIRVIAD-----DVTCSASEPTVXIVKXNM 289
277 AMLFPGSGSDTSDDQFIHLMIRPLADVADVDADNDPTCLOPFEPTVIRSGNG 336
290 XYVREDDPHDNDQLOLPKSNMPPNQLATIRKDDTIRNSGCLTYGTGAYVYMF 349
337 CVVDRGKNNKNGPIQWPCCKNSDVQQLATIRDDOTIRNSGCLTINQVSNADPVY 396
350 CNTAVREKTIWQKNGTIIMPESNVLAASSGIKGTLVYQTLDTYLDQGLAGNDIAP 409
397 CKPTVASTISQFWANGTIIMPQSLVLSSESGSPETLLVQANVYASRQMLAGNTEP 456
410 REVTVIGRDLQNSKXGVSWEVETCSXQKXKXALIGDSIRPKQNDQCLT-XGRDS 468
457 FVTSIVGRDLQKQNDKMMVVEGSSKED-KMLIPDSIRPKQNDQCLTSTDNHS 515
469 VSTVINIVSCSXKXQKRWVTEKALINLXXXXXVDVAQNMFKRLIITYPARGKPM 528
516 QGSIILISCSFGSQGRWVNDGTILNKXGLVMDVQSGNSPHOIIMPARGKPMQ 575
529 WLPV 532
576 WLPV 579

RESULT 4
ID Q94BM3 PRELIMINARY; PRT; 580 AA.
AC Q94BM3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamoin III precursor
OS Cinnamomum (Celastraceae)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI_TaxID=13429;
RN (1)
RP SEQUENCE FROM N. A.
RA Yang Q., Gong Z. Z., Liu W. Y.;
RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
genes encoding cinnamoin proteins and study of their expression
ST Submitted (JUN-2001) to the EMBL/GenBank/DBS databases
CC -!- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.

RESULT 5
ID Q41174 PRELIMINARY; PRT; 541 AA.
AC Q41174;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Protein A chain (EC 3.2.2.22) (RNA N-glycosidase)
OS Ricinus communis (Cecropiaceae)
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Rosales;
OC eustoids I; Malpighiales; Euphorbiaceae; Ricinus.

NCBI_TaxID=3986;
 (1)
 SEQUENCE FROM N.A.
 MEDLINE=9238377; PubMed=163311;
 Roberts L.M., Tregear J.W., Lord J.M.;
 "Molecular cloning of ricin."
 Targeted Diagn. Ther. 7:81-97(1992).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC EMBL: S40362; AB0592.1; -
 CC HSP: P02879; 186.
 DR Interpro: IPR000772; Ricin_B_lectin.
 DR Interpro: IPR001574; Ricin_B_lectin.
 DR Interpro: IPR001400; Somatostatin.
 DR Pfam: PF00652; Ricin_B_lectin; 6.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: P00396; SHIGARICIN.
 DR SMART: SM00458; RICIN; 2.
 DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
 DR PROSITE: PS50231; SHIGA_RICIN; 1.
 DR PROSITE: PS50231; SOMATOSTATIN_2; 1.
 DR Hydrobase: Toxin.
 DR NON TER
 FT
 SQ SEQUENCE 541 AA; 60281 MW; 2872CDEF12E39D CRC64;

Query Match 47.0%; Score 1230; DB 10; Length 541;
 Best Local Similarity 48.9%; Pred. No. 7.3e-117;
 Matches 262; Conservative 76; Mismatches 178; Indels 20; Gaps 11;

9 THQCTKXKYEPRITLLADYSSGS-FSNEEL-RCSTIPSDQNFVLEINQCKSX 66
 13 TAGATVOSTNFIKAVRHLITGADYHDIPLVLEINQCKSX 70
 67 TAAIDVNVXVVAQAGDSYFLR-DAFRAE-THLFTPTKXSLPFKXSYDLEKVA 123
 71 TLADVNAVVAQAGDSYFLR-DAFRAE-THLFTPTKXSLPFKXSYDLEKVA 130
 124 GH-RDQIPDIXOLGYSVAL--KPGSTKXASILLIOMISARAPPLMRKQ 179
 131 GNLAKETLHNGPFLKSLALYITGTOPLTAKSPICITOMISARAPPLMRKQ 190
 139 XINSKSPLEPKYMLKLTSSGQSTVOGSDTGVNPKALIXKNTVITLXNPKYIA 239
 191 RIRNRRAPDPSPVITLNSWGLSTALQSNQAFSPQIQRANSKSPSYDVGLIP 250
 240 SLAMLFVGERPSSDVAWVAVRPIAD--DYTSASEPTVLRKXKQVAVSD 296
 251 ILMATVRCAPFSSQ---ESLIRPVVENADY-CQDEPTVLRKXKQVAVSD 305
 297 DPHNGOICAFKSNQNDPQTLTKPTKXSSGCLTYGVTGATVLRKXKQVAVSD 356
 306 RFRNGVIAQFCKSNQNDPQTLTKPTKXSSGCLTYGVTGATVLRKXKQVAVSD 365
 357 ATTQVWNGITINPESNLVLAASGIGITLTVQTLDTVLQAGMLAGNDP 416
 366 ATQVWNGITINPESNLVLAASGIGITLTVQTLDTVLQAGMLAGNDP 425
 417 FRLDCESNGSVWETCCSQANOKXALYKGSIRPKONQCLTKRDSVYINIV 476
 426 LVLGCLQNSGQVWETCCSQANOKXALYKGSIRPKONQCLTKRDSVYINIV 484
 477 SCSSXXKQVWETCCSQANOKXALYKGSIRPKONQCLTKRDSVYINIV 532
 485 SCGASGQVWETCCSQANOKXALYKGSIRPKONQCLTKRDSVYINIV 540

RESULT 6
 ID 09PV22 PRELIMINARY; PRT; 549 AA.
 AC 09PV22
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 (2)
 SEQUENCE FROM N.A.
 MEDLINE=9238377; PubMed=163311;
 Roberts L.M., Tregear J.W., Lord J.M.;
 "Molecular cloning of ricin."
 Targeted Diagn. Ther. 7:81-97(1992).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC EMBL: S40362; AB0592.1; -
 CC HSP: P02879; 186.
 DR Interpro: IPR000772; Ricin_B_lectin.
 DR Interpro: IPR001574; Ricin_B_lectin.
 DR Interpro: IPR001400; Somatostatin.
 DR Pfam: PF00652; Ricin_B_lectin; 6.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: P00396; SHIGARICIN.
 DR SMART: SM00458; RICIN; 2.
 DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
 DR PROSITE: PS50231; SHIGA_RICIN; 1.
 DR PROSITE: PS50231; SOMATOSTATIN_2; 1.
 DR Hydrobase: Toxin.
 DR NON TER
 FT
 SQ SEQUENCE 549 AA; 60648 MW; 02607FE07CMA480 CRC64;

Query Match 45.8%; Score 1197.5; DB 10; Length 549;
 Best Local Similarity 48.8%; Pred. No. 1.6e-113;
 Matches 266; Conservative 71; Mismatches 183; Indels 25; Gaps 13;

9 THQCTKXKYEPRITLLADYSSGS-FSNEEL-RCSTIPSDQNFVLEINQCKSX 66
 13 TAGATVOSTNFIKAVRHLITGADYHDIPLVLEINQCKSX 70
 67 TAAIDVNVXVVAQAGDSYFLR-DAFRAE-THLFTPTKXSLPFKXSYDLEKVA 124
 71 TLADVNAVVAQAGDSYFLR-DAFRAE-THLFTPTKXSLPFKXSYDLEKVA 130
 124 GH-RDQIPDIXOLGYSVAL--KPGSTKXASILLIOMISARAPPLMRKQ 179
 131 GNLAKETLHNGPFLKSLALYITGTOPLTAKSPICITOMISARAPPLMRKQ 190
 139 XINSKSPLEPKYMLKLTSSGQSTVOGSDTGVNPKALIXKNTVITLXNPKYIA 239
 191 RIRNRRAPDPSPVITLNSWGLSTALQSNQAFSPQIQRANSKSPSYDVGLIP 250
 240 SLAMLFVGERPSSDVAWVAVRPIAD--DYTSASEPTVLRKXKQVAVSD 296
 251 ILMATVRCAPFSSQ---ESLIRPVVENADY-CQDEPTVLRKXKQVAVSD 305
 297 DPHNGOICAFKSNQNDPQTLTKPTKXSSGCLTYGVTGATVLRKXKQVAVSD 356
 306 RFRNGVIAQFCKSNQNDPQTLTKPTKXSSGCLTYGVTGATVLRKXKQVAVSD 365
 357 ATTQVWNGITINPESNLVLAASGIGITLTVQTLDTVLQAGMLAGNDP 416
 366 ATQVWNGITINPESNLVLAASGIGITLTVQTLDTVLQAGMLAGNDP 425
 417 FRLDCESNGSVWETCCSQANOKXALYKGSIRPKONQCLTKRDSVYINIV 476
 426 LVLGCLQNSGQVWETCCSQANOKXALYKGSIRPKONQCLTKRDSVYINIV 484
 477 SCSSXXKQVWETCCSQANOKXALYKGSIRPKONQCLTKRDSVYINIV 532
 485 SCGASGQVWETCCSQANOKXALYKGSIRPKONQCLTKRDSVYINIV 540

RESULT 6
 ID 09PV22 PRELIMINARY; PRT; 549 AA.
 AC 09PV22
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

	RESULT 7
	Q949M5 PRELIMINARY; FRT, 581 AA.
ID	Q949M5 (PRELIMINARY) 19 Created
AC	01-DEC-2003 13:11
DT	01-MAR-2003 (TRIBLEMEL) 23: Last annotation update)
DE	Type 2 ribosome-inactivating protein cinnamomin I precursor
EC	(EC 3.2.2.22) (RNA N-glycosidase).
OC	Cinnamomum Camphora (Camphor tree).
CC	Bakayevia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Equisetophyta; Laurales; Lauraceae; Cinnamomum.
RN	[1] RefSeq:U061429;
PN	SEQUENCE FROM N.A.
RA	Yang Q., Gong Z.Z., Liu M.Y.;
RT	"Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression patterns.";
RL	Submitted (JUN-2001) to the EMBL/GenBank/DDBS databases.
CC	-1- SPECIFIC ACTIVITY: ENDOPEPTIDASE OF THE N-GLYCOSIDIC BOND AT ONE -1- CATALYTIC ADENOSINE ON THE 28S RRNA.
DR	EMBL: AY033901; XAKY458.1; THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR	InterPro: IPRO00772; Richn_B_lectin.
DR	InterPro: IPRO01574; RIP.
DR	Pfam: PF00652; Richn_B_lectin; 5.
DR	Pfam: PF00161; RIP; 1.
DR	PRINTS: PR00396; SHIGAICIN.
DR	SMART: SMO0458; RICHN_2.
DR	PROSITE, PS50231; RICHN_LECTIN; 2.
FT	KDEL; Signal, 32.
FT	SIGNAL TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CHAIN 33 581 POTENTIAL CINNAMOMIN I.
SO	SEQUENCE 581 AA; 64215 MW; 683F5BF8FAAD196 CRC64;
Query Match	45.7%; Score 1196.5; DB:10; Length 581;
Best Local Similarity	48.8%; Pred. No. 2,26-113;
Matches	266; Conservative 70; Mismatches 184; Indels 25; Gaps 13
Dy	9 THQTGKAEHPITLDVDSGGSSNSRILPDR-STIPVSDAPVPLWNGDGS-X-66
Dy	40 TRNAKTSTGYETALPDQLASGESEPHGVPRSRSTVP-DSEKFLVELSNMAIDSVY-97
Dy	67 TTAIDVYNXVVAVOAGDGSPFYR-DAPRCATHTLTGTXTSGSLSEPFYGVDLERAG-124
Dy	98 TLAVDVNAVVAHVSCKSPFRKEDNPALENTLPDKRY-TPEPSYSVLDEAGVR-156
Dy	125 HSYGPICTGLXOISYKALRYR-QSTRXDAEAILIOMSEAARPPIWRKRXINS-183
Dy	157 RREILLTMDPLEMRISALMTSMNQGRALLASLIIVIGWAIVARFPIERFKGISIR-216
Dy	184 GKSPLEPKVATELTSSQGSGTOVGHSHD-GYNNRPKRALXXGMFVTLKNR-XVIASL-241
Dy	217 AEMEPDPDMALSLENRKASLSNVVQQSQNGYGFSSPELRISIKRRYVASYSRVISGL-276
Dy	242 LPMVTC--GEPPSSSTARYVPLRYRPND-----DYCSASFSTYRIYVKRM-289
Dy	277 ALMEPIFGSTEDSAASQDFDHMLMRPLIVDAVWALDANDDTCADEPFIYRSRGNL-336
Dy	350 XYVVEDDDFDNCQIQAMPSSNMPPNDLTTIXDKTIRSNQSCLTYGTGTAGVYWD-349
Dy	337 CVAYEDSKVNNANRQIQMWCKQSDVMQWLIEBGAHSKGCTKTSAGADVNYID-386
Dy	350 CYNRVRELATQHXKGTIRNPSTLVLAASGKCTITWOTDLTIQGTALANDTP-409
Dy	397 CRPTPLAASIHQFPANQIIIMPQSLVIVSASGSPRTLTVQANTIVABRQKLSANRP-456
Dy	410 REATTVGSPDLCKSSNGSWVSTCKSGSKANQXKMALYKDQDSITREPQCNO--CGLYRGND-467
Dy	457 FTVISVIGPNDLCQANGNDMMVVEECSSKAD-KMALYVDGSIIRHPDGPAPAFLLDNH-515

```

QY 468 SYSTVYIYSCSXKXSRVETFLMEKALINLXXXXXVXQANPELRRIIYPTATKXNO 525
Db 516 PGGIITIIISCSPPSSERFVFMMDQVILNKLGLWVDVXGNSPFLHQIITWPAIKRKH 575

QY 528 MMLPY 532
Db 576 EMULP 580

RESULT 8
Q06076 PRELIMINARY: RT, 528 AA.
AD 006076
ID 006076
DT 01-NOV-1995 (YEMRETEL, 01. Created)
DT 01-NOV-1996 (YEMRETEL, 01. Last annotation update)
DT 01-MAR-2003 (YEMRETEL, 23. Last annotation update)
DE Abtin-d IBC 3.2.2.22 (rRNA N-glycosidase) (fragment) .
OC Abtin precatorius (Indian lichenicolous) (Crab's eye) .
OC Eukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC Nuclei I; Fabales; Fabaceae; Papilionoideae; Abreae; Abtin.
OC NCBI_TaxId=3816;

CC SEQUENCE FROM N.A.
RX MEDLINE=91132798; PubMed=8421313;
RA Hung C-H, Lee M-C, Lee T-C, Lin J-Y,
RA "Primary structure of three distinct isobitins determined by cDNA
RT sequencing: conservation and significance."
RT J. Mol. Biol. 229:263-267(1993).
-1- GENALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
-1- SITES OF THE ADONISBONIN ON THE 26S RIBOM.
CC CC EMBL M93846; AAA32656.1.
DR HSRP; P11140; 1ABR.
DR InterPro; IPR000772; Stcin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Rlctn_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGALICIN.
DR SMART; SM00353; Rlctn1_2_LECTIN; 2.
DR PROSITE; PS00275; SHIG_Rlctn_1.
KW Hydroxylase; Toxin.

FT NON_TER 528 1
FT TER 528 1
SQ SEQUENCE 528 AA; 58870 MW; 62E2D42FB87F60F8 CRC64;

Query Match 43.5%; Score 1137.5; DB 10; Length 528;
Best Local Similarity 46.4%; Prid. No. 2,1e-107
Matches 242; Conservative 83; Mismatches 189; Indels 11; Gaps 9

QY 9 THQTGKGFERRITLPEYVSSGSSGSRPLRSTIYSPADQRFVLELTQDCXSKYA 68
Db 9 TBAATGSGVQGLITAIARQRLTGCIHIDIPVLPPTCYERRKRIIVELSSRESREIV 66
QY 69 AIDVTNXYVAYAGQDSYFLADAPRAETHLTGTTKASLPEYKSKYDLRYAGH RD 127
Db 67 GIDVTNXYVAYAGQDSYFLADAPRAETHLTGTTKASLPEYKSKYDLRYAGH RD 125
QY 128 QIDIKIQLIGVAAKPKGGSTGRQARSLITLQWISAPAFENPLMKROXINSKGF 187
Db 126 QIDIKIQLIGVAAKPKGGSTGRQARSLITLQWISAPAFENPLMKROXINSKGF 185
QY 188 LPEXVTELEFSSQGSQTVQSHSTGVFNNPKRAIXAGNFVTLKVA-KXVLSIALMF 246
Db 186 LPEXVTELEFSSQGSQTVQSHSTGVFNNPKRAIXAGNFVTLKVA-KXVLSIALMF 246
QY 247 VCGEPPSSGSSVPLVPIRPLVADQAFNVLISLRQGVVQSHSTGVFNNPKRAIXAGNF 305
Db 246 VCGEPPSSGSSVPLVPIRPLVADQAFNVLISLRQGVVQSHSTGVFNNPKRAIXAGNF 301
QY 306 LMSXSNKPNQMLWTKEDNTIISNGSCILTYGTATGAYVNIIDCQNAVREKATITWQIKWN 365

```

Thu Dec 11 16:09:44 2003

us-09-601-667c-1.rpt

Page 6

Db 302 AKKCKORLEKQWLTASDLTKNSKCLTEGTAAGNVAIVDCTSAVAKEATYMEIDN 361
Qy 366 GTTINPBNVYAAAGSGICGTLTQTLDTLQCGTLAGNDPAPRETYGPELQESN 425
Db 362 GTTINPBNVYAAAGSGICGTLTQTLDTLQCGTLAGNDPAPRETYGPELQESN 421
Qy 426 XGSAWVETCSQKQKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 485
Db 422 GSNVWADCNKKEQ-QVALYTDSSISVQTNMCLTSKQKQSPVAVACSNQMSQ 480
Qy 486 RYVPMKALITLKKKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 530
Db 481 RMLFQDSDISYSLDPMWMDVYKSDPSLQKILMPTLRKQKWL 525

RESULT 9

Q8RXH7 PRELIMINARY; PRT; 249 AA.
ID Q8RXH7
AC Q8RXH7
DT 01-OCT-2002 (TRENBERG, 21, Created)
DT 01-OCT-2002 (TRENBERG, 21, Last sequence update)
DT 01-MAR-2003 (TRENBERG, 21, Last annotation update)
DE Lectin chain A isoform 2 (EC 3.2.2.22) (RNA N-glycosidase)
OS (fragment)
OC Viscum album (European mistletoe)
OC Bukariyoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum
OX NCBI_TaxID=3972;
RN SOURCE FROM N.A.
RC TISSUE=leaf;
RA Paramasium M., Srinivasan A., Singh T.P.;
RT Viscum album (Indian) mRNA for Mistletoe lectin chain A, isoform 2,;
RL Submitted (Feb-2002) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOMYDOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF031187; F018705.1; -;
DR RefSeq; NM_001001274; RIF.
DR PIR; P01610; RIF; 1.
KW Hydroxylase; Toxin.
FT NON TER 1 1
FT NON TER 249 249
SQ SEQUENCE 249 AA; 27944 MW; 89FAFE78309A8183 CRC64;

Query Match 42.6%; Score 1113.5; DB 10; Length 249;
Best Local Similarity 89.2%; Pred. No. 2.1e-105;
Matches 229; Conservative 3; Mismatches 23; Indels 1; Gaps 1;

Qy 1 YERLAPVHTQTKGEYPRFTLLRDYVSSGSFNEPILQSTIPVSDQPFVLELN 60
Db 1 YERLAPVHTQTKGEYPRFTLLRDYVSSGSFNEPILQSTIPVSDQPFVLELN 60
Qy 61 QGKXSTALDYNKYVAVYQAGQSYFLDAPGATHTLFTGTRKSLPFXGSYDLE 120
Db 61 QGKXSTALDYNKYVAVYQAGQSYFLDAPGATHTLFTGTRKSLPFXGSYDLE 119
Qy 121 RYAGHDQIFLGICXOLIGVYALAKFGSGTRQARSLILQIMSEARNPILMKRX 180
Db 120 RYAGHDQIFLGICXOLIGVYALAKFGSGTRQARSLILQIMSEARNPILMKRX 179
Qy 181 INSGSEFLPDYVMELETSMQQSTOVQSTGVFNNPRLATXGKFTLKNRYAVIS 240
Db 180 INSGSEFLPDYVMELETSMQQSTOVQSTGVFNNPRLATXGKFTLKNRYAVIS 239
Qy 241 LAINLFCGSRPSS 250
Db 240 LAINLFCGSRPSS 249

RESULT 10

Q8LNQ6 PRELIMINARY; PRT; 254 AA.
ID Q8LNQ6
AC Q8LNQ6
DT 01-OCT-2002 (TRENBERG, 22, Created)
DT 01-OCT-2002 (TRENBERG, 22, Last sequence update)
DT 01-MAR-2003 (TRENBERG, 22, Last annotation update)
DE Lectin chain A isoform 1 (EC 3.2.2.22) (RNA N-glycosidase)
OS (fragment)
OC Viscum album subsp. coloratum
OC Bukariyoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum
OX NCBI_TaxID=15976;
RN SOURCE FROM N.A.
RC MEDLIB=21566752; PubMed=1170524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT cDNA cloning and sequence analysis of the lectin genes of the Korean
mistletoe (Viscum album coloratum).
RT Mol. Cells 12:215-220(2001).
RD SOURCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT Submitted (May-2002) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOMYDOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF508914; AA046932.1; -;
DR RefSeq; NM_00101574; RIF.
DR PIR; P80316; SHIGARICN.
KW Hydroxylase; Toxin.
FT NON TER 1 1
FT NON TER 254 254
SQ SEQUENCE 254 AA; 28446 MW; 6DB5C3B18F4AEEB0 CRC64;

Query Match 41.8%; Score 1094.5; DB 10; Length 254;
Best Local Similarity 85.9%; Pred. No. 1.9e-103;
Matches 219; Conservative 8; Mismatches 27; Indels 1; Gaps 1;

Qy 1 YERLAPVHTQTKGEYPRFTLLRDYVSSGSFNEPILQSTIPVSDQPFVLELN 60
Db 1 YERLAPVHTQTKGEYPRFTLLRDYVSSGSFNEPILQSTIPVSDQPFVLELN 60
Qy 61 QGKXSTALDYNKYVAVYQAGQSYFLDAPGATHTLFTGTRKSLPFXGSYDLE 120
Db 61 QGKXSTALDYNKYVAVYQAGQSYFLDAPGATHTLFTGTRKSLPFXGSYDLE 119
Qy 121 RYAGHDQIFLGICXOLIGVYALAKFGSGTRQARSLILQIMSEARNPILMKRX 180
Db 120 RYAGHDQIFLGICXOLIGVYALAKFGSGTRQARSLILQIMSEARNPILMKRX 179
Qy 181 INSGSEFLPDYVMELETSMQQSTOVQSTGVFNNPRLATXGKFTLKNRYAVIS 240
Db 180 INSGSEFLPDYVMELETSMQQSTOVQSTGVFNNPRLATXGKFTLKNRYAVIS 239
Qy 241 LAINLFCGSRPSS 255
Db 240 LAINLFCGSRPSS 254

RESULT 11

Q9W6E9 PRELIMINARY; PRT; 547 AA.
ID Q9W6E9
AC Q9W6E9
DT 01-OCT-2000 (TRENBERG, 15, Created)
DT 01-OCT-2000 (TRENBERG, 15, Last sequence update)
DT 01-MAR-2003 (TRENBERG, 23, Last annotation update)
DE P-procaspase-1 (EC 3.2.2.22) (RNA N-glycosidase).
GN AAG
OS Abrus precatorius (Indian licorice) (Crab's eye).

RA MEDLINE=2156752; PubMed=11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
R "CDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum)."
RL Mol. Cells 12:215-220(2001).
RN [2].
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- STRUCTURE: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF508191; PubMed=11710524; PubMed=11710524;
DR InterPro: IPR01574; RIF.
DR Pfam: PF00161; RIF.
DR PRINTS: PR00396; SHIGARICIN.
KM Hydrolase; Toxin.
FT NON TER 1
FT 249 1
SQ SEQUENCE 249 AA; 27821 MW; 3C5870F8338BDAB5 CRC64;

Query Match 40.3%; Score 1054.5; DB 10; Length 249;
Best Local Similarity 84.3%; Pred. No. 2,3e-59;
Matches 209; Conservative 13; Mismatches 25; Indels 1; Gaps 1;

QY 1 YERLRATVHTGKXKYEPRFILLADYVSSGSESNRPIRLROSTTPYSGARPTVLEIN 60
DB 1 YERLRATVHTGKXKYEPRFILLADYVSSGSESNRPIRLROSTTPYSGARPTVLEIN 60
QY 61 QGKDSXTAIDVNNXYVAVQAGDQSYFLADAPRGAEFTLFTGTXXSLSPFGSYXDL 120
DB 61 QGKDSXTAIDVNNXYVAVQAGDQSYFLADAPRGAEFTLFTGTXXSLSPFGSYXDL 120
QY 181 INSGXSELPDXYMLRLTSWGQOSTQVGSSTQYPRNXYLAXXGPTTANXXVYS 240
DB 181 INSGXSELPDXYMLRLTSWGQOSTQVGSSTQYPRNXYLAXXGPTTANXXVYS 240
QY 241 LAMMFVC 248
DB 241 LAMMFVC 247
DB 240 LAMMFVC 247

RESULT 14
Q8LXQ1 PRELIMINARY; RT; 263 AA.
AC Q8LXQ1
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Lactin chain B isoform 3 (Fragment).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
NCBI_TaxID=15976;
RN [1].
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- STRUCTURE: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF508191; PubMed=11710524; PubMed=11710524;
DR InterPro: IPR01574; RIF.
DR Pfam: PF00161; RIF.
DR PRINTS: PR00396; SHIGARICIN.
KM Hydrolase; Toxin.
FT NON TER 1
FT 251 1
SQ SEQUENCE 251 AA; 28090 MW; A11777489012E989 CRC64;

RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF508191; PubMed=11710524; PubMed=11710524;
DR InterPro: IPR000772; Ricin B lectin.
DR Pfam: PF06552; Ricin B lectin; 6.
DR SMART: SM00458; RICHN; 2.
DR PROSITE: PS0231; RICHN_B_LECTIN; 2.
FT NON TER 263
FT 263 1
SQ SEQUENCE 263 AA; 29071 MW; 3F9C4DA860F061D CRC64;

Query Match 39.4%; Score 1029.5; DB 10; Length 263;
Best Local Similarity 74.5%; Pred. No. 8.8e-97;
Matches 196; Conservative 19; Mismatches 47; Indels 1; Gaps 1;

QY 270 DVTCASEPTVIVIGKXKMYVDVDDFDGNGQIQMTSKSNNDENQMTIREDTIR 329
DB 1 DGTGTFSEPTVIVIGKXKMYVDVDDFDGNGQIQMTSKSNNDENQMTIREDTIR 329
QY 330 NSGCTTGTGAGTACVWVIFDQVTRPRTTQVKNQNTINPSSNIVLAASGCTGTT 389
DB 61 NSKCTTGTGAGTACVWVIFDQVTRPRTTQVKNQNTINPSSNIVLAASGCTGTT 389
QY 390 VQTDYTLGGMAGNTPAPRETTVIGFRLCHESNKGSWWETCKSSQXNXXALY 449
DB 121 VQTDYTLGGMAGNTPAPRETTVIGFRLCHESNKGSWWETCKSSQXNXXALY 449
QY 450 GSIRPKNQDCLTYGSDVSFTVINIVSCSXKXKRWFTNEXAIIINLCKXXXKDV 509
DB 180 GSIRPKNQDCLTYGSDVSFTVINIVSCSXKXKRWFTNEXAIIINLCKXXXKDV 509
QY 510 YPKRATITVPAKQKPYOMKPV 532
DB 240 NPSRRLITVPAKQKPYOMKPV 262

RESULT 15
Q8LXQ4 PRELIMINARY; RT; 251 AA.
AC Q8LXQ4
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Lactin chain A isoform 3 (Ec 3.2.2.22) (RNA N-Glycosidase)
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
NCBI_TaxID=15976;
RN [1].
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- STRUCTURE: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF508191; PubMed=11710524; PubMed=11710524;
DR InterPro: IPR01574; RIF.
DR Pfam: PF00161; RIF.
DR PRINTS: PR00396; SHIGARICIN.
KM Hydrolase; Toxin.
FT NON TER 1
FT 251 1
SQ SEQUENCE 251 AA; 28090 MW; A11777489012E989 CRC64;

Thu Dec 11 16:09:44 2003

us-09-601-667c-1.rpt

Page 9

```
Query Match      37.4%; Score 977.5; DB 10; Length 251;
Best Local Similarity 80.9%; Pred. No. 1.7e-91;
Matches 203; Conservative 7; Mismatches 36; Indels 5; Gaps 3;

QY 1 YERLRLVTHQITGKEFFRPIILRLDYSSSSSSSNEIPLRSTIPVSDAKRFVLYELN 60
DB 1 YERLRLVTHQITGKEFFRPIILRLDYSSSSSSSNDIPLPS-IPVSSAKRFVLYELN 59
QY 61 Q--GDSYTHAIDVTLXXVYAYQAGDSYELADPAGAEHLFTGTRSSSLPQSYX 117
DB 60 QGKMBDSITAIIDVTLVYAYQAGDSYELADPAGAEHLFTGTR-SSLPQSYX 118
QY 118 DIERVAGHRDQIFLGIXQLIGVXALXPGGSTRXQASLILQWISLAEAFNPILMEX 177
DB 119 DIERVAGHRDQIFLGIREPLIRSVSALDVPQGSTRAQSSIIIVQWISLAEAFNPILMEX 178
QY 178 RQINSQKSPLEPYVTLBELTSWQGSITQVGHSTGVFNNPKRLAIXXGNFTLXNTRXV 237
DB 179 RQINSQKSPLEPYVTLBELTSWQGSITQVGHSTGVFNNPKRLAIXXGNFTLXNTRXV 238
QY 238 IASLAIMLPYC 248
DB 239 IASLAIMLPYC 249
```

Search completed: December 11, 2003, 14:00:58
Job time : 44.0829 secs

Thu Dec 11 16:09:41 2003

us-09-601-667c-1.rag

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 : Search time 52.666 seconds

Title: US-09-601-667c-1
(without alignments)

Sequence: 1 YERILNVTHTQTEKYERF.....RRILVPTKPNQNMIPVX 533

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting filter 45 summaries

Database: A_Geneseq_19jun03.*

1:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2535	96.9	533	20	AAV25970
2	2535	96.9	533	20	AAV25973
3	2535	96.9	533	20	AAV25976
4	2519	96.3	531	20	AAV25979
5	2519	96.3	532	20	AAV25982
6	2505	95.8	564	18	AAV10021
7	2505	95.8	564	20	AAV90127
8	2157.5	83.6	551	23	AAV91450
9	1291	49.4	264	20	AAV25987

10	1291	49.4	264	20	AAV25988	Mistletoe lectin B
11	1291	49.4	265	20	AAV25990	Mistletoe lectin B
12	1291	49.4	265	20	AAV25993	Mistletoe lectin B
13	1290	49.3	264	20	AAV25986	Mistletoe lectin B
14	1290	49.3	264	20	AAV25990	Mistletoe lectin B
15	1290	49.3	265	20	AAV25996	Mistletoe lectin B
16	1289	49.3	265	20	AAV25992	Mistletoe lectin B
17	1289	49.3	264	20	AAV25989	Mistletoe lectin B
18	1286	49.2	265	20	AAV25995	Mistletoe lectin B
19	1286	49.2	264	20	AAV25978	Mistletoe lectin B
20	1286	49.2	264	20	AAV25972	Mistletoe lectin B
21	1286	49.2	264	20	AAV25985	Mistletoe lectin B
22	1277.5	48.8	264	20	AAV25991	Mistletoe lectin B
23	1277.5	48.8	264	20	AAV25982	Mistletoe lectin B
24	1267.5	48.5	263	19	AAV25991	Mistletoe lectin B
25	1267.5	48.5	264	18	AAV25992	Mistletoe lectin B
26	1267.5	48.5	264	18	AAV25993	Mistletoe lectin B
27	1267.5	48.5	264	19	AAV25990	Mistletoe lectin B
28	1267.5	48.5	264	19	AAV25996	Mistletoe lectin B
29	1261	47.1	574	10	AAV25989	Mistletoe lectin B
30	1261	47.1	576	18	AAV25992	Mistletoe lectin B
31	1261	47.1	576	21	AAV25993	Mistletoe lectin B
32	1261	47.1	576	22	AAV25990	Mistletoe lectin B
33	1261	47.1	576	22	AAV25996	Mistletoe lectin B
34	1260	47.0	565	22	AAV25991	Mistletoe lectin B
35	1260	47.0	565	22	AAV25992	Mistletoe lectin B
36	1260	47.0	565	22	AAV25993	Mistletoe lectin B
37	1260	47.0	565	22	AAV25990	Mistletoe lectin B
38	1260	47.0	565	22	AAV25996	Mistletoe lectin B
39	1260	47.0	565	22	AAV25991	Mistletoe lectin B
40	1260	47.0	565	22	AAV25992	Mistletoe lectin B
41	1260	47.0	565	22	AAV25993	Mistletoe lectin B
42	1260	47.0	565	22	AAV25990	Mistletoe lectin B
43	1260	47.0	565	22	AAV25996	Mistletoe lectin B
44	1260	47.0	565	22	AAV25991	Mistletoe lectin B
45	1260	47.0	565	22	AAV25992	Mistletoe lectin B

ALIGNMENTS

RESULT 1	AAV25970	standard; protein: 533 AA.
ID	AAV25970	
18-0CT-1999	(first entry)	
1	AAV25970	
2	AAV25970	
3	AAV25970	
4	AAV25970	
5	AAV25970	
6	AAV25970	
7	AAV25970	
8	AAV25970	
9	AAV25970	
10	AAV25970	
11	AAV25970	
12	AAV25970	
13	AAV25970	
14	AAV25970	
15	AAV25970	
16	AAV25970	
17	AAV25970	
18	AAV25970	
19	AAV25970	
20	AAV25970	
21	AAV25970	
22	AAV25970	
23	AAV25970	
24	AAV25970	
25	AAV25970	
26	AAV25970	
27	AAV25970	
28	AAV25970	
29	AAV25970	
30	AAV25970	
31	AAV25970	
32	AAV25970	
33	AAV25970	
34	AAV25970	
35	AAV25970	
36	AAV25970	
37	AAV25970	
38	AAV25970	
39	AAV25970	
40	AAV25970	
41	AAV25970	
42	AAV25970	
43	AAV25970	
44	AAV25970	
45	AAV25970	

VISCUM ALBUM

Key	Location/Qualifiers
Misc-difference 15	/label= Asp, Glu
Misc-difference 63	/label= Gly, Gln
Misc-difference 66	/label= Ile, Val
Misc-difference 75	/label= Leu, Ala
Misc-difference 107	/label= Asp, Arg or none
Misc-difference 111	/label= Asn, Thr
Misc-difference 117	/label= Pro, Thr

FT	Misc-difference	114	/label= Asp, Glu
FT	Misc-difference	141	/label= Ser, Thr
FT	Misc-difference	145	/label= Phe, Tyr
FT	Misc-difference	177	/label= Thr, Ala
FT	Misc-difference	180	/label= Ala, Tyr
FT	Misc-difference	185	/label= Tyr, Asp
FT	Misc-difference	191	/label= Val, Glu
FT	Misc-difference	224	/label= Ile, Phe
FT	Misc-difference	225	/label= Pro, Ser
FT	Misc-difference	232	/label= Thr, Ser
FT	Misc-difference	326	/label= Asp, Ser
FT	Misc-difference	327	/label= Asp, Ser
FT	Misc-difference	329	/label= Asn, Ser
FT	Misc-difference	325	/label= Cys, Arg
FT	Misc-difference	364	/label= Gly, Asn
FT	Misc-difference	426	/label= Gly, Asp
FT	Misc-difference	439	/label= Val, Asp
FT	Misc-difference	442	/label= Glu, Lys
FT	Misc-difference	443	/label= Gly or none
FT	Misc-difference	444	/label= Arg, Lys
FT	Misc-difference	454	/label= Cys, Ser, Val
FT	Misc-difference	450	/label= Ala, Gly
FT	Misc-difference	481	/label= Gly, Ala
FT	Misc-difference	483	/label= Ser, Gly
FT	Misc-difference	484	/label= Gly, Ser
FT	Misc-difference	493	/label= Gly, Tyr
FT	Misc-difference	500	/label= Asn, Ser, Thr, Lys
FT	Misc-difference	501	/label= Ser, Gly
FT	Misc-difference	502	/label= Leu, Pro
FT	Misc-difference	503	/label= Ala, Met
FT	Misc-difference	504	/label= Met, Val
FT	Misc-difference	533	/label= Pro, Phe
XX	DE19604210-AL		
XX	12-ATG-1999,		
XX			

	PF	03-FEB-1998;	98DE-1004210.
	PR	03-FEB-1998;	98DE-1004210.
	PA	(BIO-) BIOSYN ARGENIMITEU GMEH.	
	PI	Morris P, Stiefel T, Voelter W, Welters P,	
	PM	WP; 1999-44535/78.	
	PT	Preparation of mistletoe lectins in heterologous systems, particularly for use as anticancer agents and immunostimulants	
	XX	Claim 1; Page 25-26; 78pp; German.	
	CC	This invention describes a novel mistletoe lectin (I) and its fragments which have antitumor and immunostimulatory activity. The A-chain (MA) of the mistletoe lectin binds to, and inactivates, the 28S subunit of ribosomes. Non-toxic forms of (I) activate T-cell and macrophage mediated cytotoxicity against tumor cells. (II) fragments are used as adjuvants to stimulate immunity. (I) and its fragments are used as co-adjuvants to enhance the antigenicity of the cancer) and if they lack cytotoxicity, they can be used as adjuvants of the (immune response, particularly for oral administration along with antigens of the (tumor-associated, bacterial or viral). The method allows production of mistletoe lectin, and its individual chains, in many different isoforms and on a large scale, at any time of the year. Recombinant products are free from toxins present in natural mistletoe extracts. This sequence represents a consensus sequence of the mistletoe lectin described in the specification.	
	XX	Sequence 533 Ab;	
	Query Match	96.9%; Score 2355; D5 20; Length 533;	
	Best Local Similarity	100.0%; Pred. No. 1,7e-270;	
	Matches 532;	Conservative 0; Mismatches 20; Indels 0; Gaps 0;	
OY	1	YERLRLVTHQTKGYEFREITLLRDVSSPSFSENPILRSGTTPVSADRPVLVELTN 60	
DB	1	YERLRLVTHQTKGYEFREITLLRDVSSPSFSENPILRSGTTPVSADRPVLVELTN 60	
OY	61	OGKDSYALDVTNYVAQAQGOSYFLRAPRGTFPHFGTTXSGSLPFGSXNTE 120	
DB	61	OGKDEXTAIDVTNYVAQAQGOSYFLRAPRGATFHFGTTXSLSPFGSXNTE 120	
OY	121	RVGHRGRCQCEGLKOLIOSYALRKPGCGSTXOARSLIIIONISEAASFPLIMKXOX 180	
DB	121	RVGHRGRCEGLGIKOLIOSYALKPGCGSTXOARSIIIIIONISEAASFPLIMKXOX 180	
OY	161	INSGASTLDXYMLETSNGSQOSTOVCHSDGVFNFXELAXXONFVTLXNRVIAS 240	
DB	161	INSGASTLDXYMLETSNGSQOSTOVCHSDGVFNFXELAXXONFVTLXNRVIAS 240	
OY	241	LAIMLPVCEGEPPSSSPNRYLPYLRPYADVDGCAASEPTVYIGRGXGDVDRDDPH 300	
DB	241	LAIMLPVCEGEPPSSSPVRYLPYPYADVDGCAASEFTVALIGRGXGDVDRDDPH 300	
OY	301	GNGQLMPKSKNDPNQWLMIXGXDTIRSNOSCLTTGGYAGCYVMFPICVAVRBATW 360	
DB	301	GNGQLMPKSKNDPNQWLTXGXDTIRSNOSCLTTGYAYGVMMPCGTAVRBATW 360	
OY	361	GTRXGRTIRSRYSVLAASGIKTTLVOTQDNTLCQHLASNDIPRRBTWIFGFDL 420	
DB	361	GTRXGRTIRSRYSVLAASGIKETTLVQTLDITLQGSXNSDPFRBBTWIFYFDL 420	
OY	421	CHEKSXSIVWEVCESQOMXQXALVEYGSGIRPKONDCCIXGRASYTVINIYSCSX 480	
DB	421	CHEKSXSIVWEVCESQOMXQXALVEYGSGIRPKONDCCIXGRASYTVINIYSCSX 480	
OY	461	XKXQRWVYTBKAIAINI KKKXXXDVAAQANFKLRRIIYFATGKGNOMPLEV 532	
DB	461	XKXQRWVYTBKAIALINKKKXXXDVAAQANKLRRIIYFATGKGNOMPLEV 532	

Thu Dec 11 16:09:41 2003

us-09-601-667c-1.rag

Page 3

[illegible]

FT	/label= Gly, none
FT	Misc-difference 443
FT	/label= Arg, Lys
FT	Misc-difference /label= Cys, Ser, Val
FT	Misc-difference 480
FT	/label= Ala, Gly
FT	Misc-difference 481
FT	/label= Gly, Ala
FT	Misc-difference 493
FT	/label= Ser, Gly
FT	Misc-difference 494
FT	/label= Gly, Ser
FT	Misc-difference 493
FT	/label= Gly, Tyr
FT	Misc-difference 500
FT	/label= Asn, Ser, Thr, Lys
FT	Misc-difference 501
FT	/label= Ser, Gly
FT	Misc-difference 502
FT	/label= Leu, Pro
FT	Misc-difference 503
FT	/label= Ala, Met
FT	Misc-difference 504
FT	/label= Met, Val
FT	Misc-difference 533
FT	/label= Pro, Phe
XX	
XX	DEL9804210-AL.
PD	12-AUG-1999.
PF	03-FEB-1998/ 98DE-1004210.
XX	
XX	03-FEB-1998; 98DS-1004210.
PR	(BIOS) BIOSYN ARZNEIMITTEL GMBH.
XX	
PL	Morris P, Stiebel T, Voelter W, Welters P;
DR	WPI; 1999-445335/38.
XX	
XX	Preparation of mistletoe lectins in heterologous systems,
XX	particularly for use as anticancer agents and immunostimulants
XX	
XX	Claim 4; Page 28-29; 78pp; German.
CC	
CC	This invention describes a novel mistletoe lectin (I) and its fragments
CC	which have antitumor and immunostimulatory activity. The A-chain (WLA)
CC	of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC	r ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
CC	lymphokine-associated macrophage-mediated cell growth. Particularly
CC	cancers) and if they lack cytotoxicity, to increase the strength of the
CC	immune response, particularly to a co-administered antigen
CC	(tumour-associated, bacterial or viral). The method allows production of
CC	mistletoe lectin, and its individual chains, in many different isoforms
CC	and on a large scale, at any time of the year. Recombinant products are
CC	free from toxins present in natural mistletoe extracts. This sequence
CC	specification.
XX	
XX	
SQ	Sequence 533 AA:
Query Match	96.9%; Score 2535; DB 20; Length 533;
Best Local Similarity	100.0%; Pred. No. 1..76-270;
Matches 532; Conservative	0; Mismatches 0; Indels 0; Gaps 0
db	1 YERLRLRVHTGTCXVYFFITLLADVVSSGSFANEPLILAGSTIPVADNAPFVLEIN 60
OY	1 YERLRLRVHTGTCXVYFFITLLADVVSSGSFANEPLILAGSTIPVADNAPFVLEIN 60
QY	61 QGDSDKNAIDVTYYVAAYDADDQSFLNDAPFGAETHLFTGTIRKASLPKPSGVYDLE 120

Dd		61	GQMSKSTALADIVNNVYVAWGCGEFLMDAPRGAETLPTGTWRKSLSLPKASVDLE	120
Qy		121	RKAHQDQIEPLGKLIOGVVALPKFGSTRQAASIIILIMSEAAHPNLIKMKOX	180
Dd		121	RKAHQDQIEPLGKLIOGVVALPKFGSTRQAASIIILIMSEAAHPNLIKMKOX	180
Qy		181	INXSKSLPEPWYLELTSMQGGSTGVGFVNPRRLAAXKGFFPLTKANREVLAS	240
Dd		181	INXSKSLPEPWYLELTSMQGGSTGVGFVNPRRLAAXKGFFPLTKANREVLAS	240
Qy		241	LAILMFLPGERPSSSDVPFVWPIRVPIADVTCASAEFTVIRVAKGXQVADDDHFH	300
Dd		241	LAILMFLPGERPSSSDVPFVWPIRVPIADVTCASAEFTVIRVAKGXQVADDDHFH	300
Qy		301	GNQGLMPKSNNDPDLMTIKELTINSNGCLITTYGTAGYYVMFDCAVAREATVI	360
Dd		301	GNQGLMPKSNNDPDLMTIKELTINSNGCLITTYGTAGYYVMFDCAVAREATVI	360
Qy		361	QIWKNGTIIPRSNIYVLAASGIIGTLTVQLIDVTYGKMLANDPPEVITYGFIDL	420
Dd		361	QIWKNGTIIPRSNIYVLAASGIIGTLTVQLIDVTYGKMLANDPPEVITYGFIDL	420
Qy		421	CHEKNKSWNETCVASSONKXMAALYGRSPRPKONDQCITKRGDSVTVINVSCKX	480
Dd		421	CHEKNKSWNETCVASSONKXMAALYGRSPRPKONDQCITKRGDSVTVINVSCKX	480
Qy		481	KXXQRVPTMEKAIILNKXXXXXDPAQNPKEIRIIITPATKCKPNOMLEV	532
Dd		481	KXXQRVPTMEKAIILNKXXXXXDPAQNPKEIRIIITPATKCKPNOMLEV	532
RESULT 3				
AATZ5976				
AA125976				
AA25976:				
Xx		18-OCT-1999	(first entry)	
Xx		Mistletoe lectin protein consensus sequence 3.		
Xx		Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;		
Xx		ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;		
Xx		lymphokine-producing macrophages; uncontrolled cell growth; treatment;		
Xx		cancer; cytotoxicity; antigen; isoform.		
Xx		Viscum album.		
Xx		Key	Location/Qualifiers	
Ft		Misc-difference 15	/label= Asp, Glu	
Ft		Misc-difference 63	/label= Gly, Gln	
Ft		Misc-difference 66	/label= Ile, Val	
Ft		Misc-difference 75	/label= Leu, Ala	
Ft		Misc-difference 107	/label= Asp, none	
Ft		Misc-difference 113	/label= Asn, Thr	
Ft		Misc-difference 117	/label= Pro, Thr	
Ft		Misc-difference 124	/label= Asp, Glu	
Ft		Misc-difference 145	/label= Ser, Thr	
Ft		Misc-difference 152	/label= Phe, Tyr	
Ft		Misc-difference 177	/label= Thr, Ala	
Ft		Misc-difference 180	/label= Ala, Tyr	
Ft		Misc-difference 185	/label= Ala, Glu	
Ft		Misc-difference 191	/label= Val, Met	
Ft		Misc-difference 219	/label= Ile, Phe	
Ft		Misc-difference 224	/label= Pro, Ser	
Ft		Misc-difference 225	/label= Pro, Thr	
Ft		Misc-difference 232	/label= Thr, Ser	
Ft		Misc-difference 236	/label= Asp, Ser	
Ft		Misc-difference 287	/label= Asn, Ser	
Ft		Misc-difference 290	/label= Cys, Arg	
Ft		Misc-difference 325	/label= Gly, Asn	
Ft		Misc-difference 354	/label= Gly, Asp	
Ft		Misc-difference 426	/label= Gly, Gln	
Ft		Misc-difference 435	/label= Val, Asp	
Ft		Misc-difference 439	/label= Gln, Lys	
Ft		Misc-difference 442	/label= Gly, none	
Ft		Misc-difference 443	/label= Arg, Lys	
Ft		Misc-difference 464	/label= Cys, Ser, Val	
Ft		Misc-difference 480	/label= Ala, Gly	
Ft		Misc-difference 481	/label= Gly, Ala	
Ft		Misc-difference 483	/label= Ser, Gly	
Ft		Misc-difference 484	/label= Gly, Ser	
Ft		Misc-difference 493	/label= Gly, Tyr	
Ft		Misc-difference 500	/label= Asn, Ser, Thr, Lys	
Ft		Misc-difference 501	/label= Ser, Gly	
Ft		Misc-difference 502	/label= Leu, Pro	
Ft		Misc-difference 503	/label= Ala, Met	
Ft		Misc-difference 533	/label= Met, Val	
Ft		Misc-difference 533	/label= Pro, Phe	
Pd		DE19804210-A1.		
Pd		12-RUG-1999.		
Pd		03-FEB-1998; 98DE-1004210.		
Pd		03-FEB-1998; 98DE-1004210.		
Pd		(BLOS) BLOSYN ANZENMUTTEL GMBH.		
Pd		Morris F, Sclafel T, Voelter W,		
Pd		Welters P,		
Pd		WEI, 1999-44535/38.		

XX Preparation of mistletoe lectins in heterologous systems.
 PT particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 40; Page 37-38; 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC the ribosome. Non-cytotoxic forms of (I) activate T-cell and (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a consensus sequence of the mistletoe lectin described in the
 CC specification.
 XX
 XX Sequence 533 AA;
 SQ

Query Match 96.3%; Score 2519; DB 20; Length 533;
 Best Local Similarity 100.0%; Pred. No. 1.7e-270;
 Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YERLRVTHQGTGAEFFETLLRDVYSSGSFSEIPLRQSTIPVSDMORFVLELTN 60
 DB 1 YERLRVTHQGTGAEFFETLLRDVYSSGSFSEIPLRQSTIPVSDMORFVLELTN 60
 QY 61 GGRNRYTAIDVNNYVAVYQAGDSYFLADPRGATHTLFTGTXSAPKXSYXDE 120
 DB 61 GGRNRYTAIDVNNYVAVYQAGDSYFLADPRGATHTLFTGTXSAPKXSYXDE 120
 QY 61 GGRNRYTAIDVNNYVAVYQAGDSYFLADPRGATHTLFTGTXSAPKXSYXDE 120
 DB 61 GGRNRYTAIDVNNYVAVYQAGDSYFLADPRGATHTLFTGTXSAPKXSYXDE 120
 QY 121 RYAGHDQIPGIGXOLIGSVAXLRXGSTRXQASILLLOMISBAARNPILWRXRX 180
 DB 121 RYAGHDQIPGIGXOLIGSVAXLRXGSTRXQASILLLOMISBAARNPILWRXRX 180
 QY 121 RYAGHDQIPGIGXOLIGSVAXLRXGSTRXQASILLLOMISBAARNPILWRXRX 180
 DB 121 RYAGHDQIPGIGXOLIGSVAXLRXGSTRXQASILLLOMISBAARNPILWRXRX 180
 QY 181 INSXSRIPDXNWLRLTSMQSGSTOVGHSTGVNPNRRLAIKXGNFTLVNRYVLS 240
 DB 181 INSXSRIPDXNWLRLTSMQSGSTOVGHSTGVNPNRRLAIKXGNFTLVNRYVLS 240
 QY 181 INSXSRIPDXNWLRLTSMQSGSTOVGHSTGVNPNRRLAIKXGNFTLVNRYVLS 240
 DB 181 INSXSRIPDXNWLRLTSMQSGSTOVGHSTGVNPNRRLAIKXGNFTLVNRYVLS 240
 QY 241 LAIMLPVCGRPSSSDYRWPEVIRPVADDTCSASEPTVRAIVGXKXKVVVDODPHD 300
 DB 241 LAIMLPVCGRPSSSDYRWPEVIRPVADDTCSASEPTVRAIVGXKXKVVVDODPHD 300
 QY 241 LAIMLPVCGRPSSSDYRWPEVIRPVADDTCSASEPTVRAIVGXKXKVVVDODPHD 300
 DB 241 LAIMLPVCGRPSSSDYRWPEVIRPVADDTCSASEPTVRAIVGXKXKVVVDODPHD 300
 QY 301 GNOIQLMPSKSNNDPNQWLTIRKDXITISNSGCLTGYTGAGVYVIFDQNVARENTW 360
 DB 301 GNOIQLMPSKSNNDPNQWLTIRKDXITISNSGCLTGYTGAGVYVIFDQNVARENTW 360
 QY 361 GNOIQLMPSKSNNDPNQWLTIRKDXITISNSGCLTGYTGAGVYVIFDQNVARENTW 420
 DB 361 GNOIQLMPSKSNNDPNQWLTIRKDXITISNSGCLTGYTGAGVYVIFDQNVARENTW 420
 QY 361 GNOIQLMPSKSNNDPNQWLTIRKDXITISNSGCLTGYTGAGVYVIFDQNVARENTW 420
 DB 361 GNOIQLMPSKSNNDPNQWLTIRKDXITISNSGCLTGYTGAGVYVIFDQNVARENTW 420
 QY 421 CMEKSNQSWWETCKSSQXKXKXWALYGDGSIKPKXQKQCLTKGDSVATVIVSCSX 480
 DB 421 CMEKSNQSWWETCKSSQXKXKXWALYGDGSIKPKXQKQCLTKGDSVATVIVSCSX 480
 QY 481 KXKXQWTFNEMALILMLKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 532
 DB 481 KXKXQWTFNEMALILMLKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 532

RESULT 4

AA25979 standard; Protein: 531 AA.
 AA25979;

XX 18-OCT-1999 (first entry)
 XX Mistletoe lectin I protein fragment.
 DE

XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MLA; immunity;
 KW particularly for use as anticancer agents and immunostimulants
 KW cancer; cytotoxicity; antigen; isoform; lectin I.
 XX
 XX Vascum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (B10S-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX MPI, 1999-44535/38.
 XX N-58DB; AA69103.
 PT Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 7; Fig 18; 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC the ribosome. Non-cytotoxic forms of (I) activate T-cell and (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a mistletoe lectin I protein fragment.
 CC
 CC Sequence 531 AA;
 SQ
 Query Match 96.3%; Score 2519; DB 20; Length 531;
 Best Local Similarity 92.5%; Pred. No. 1e-268;
 Matches 492; Conservative 0; Mismatches 38; Indels 2; Gaps 2;
 QY 1 YERLRVTHQGTGAEFFETLLRDVYSSGSFSEIPLRQSTIPVSDMORFVLELTN 60
 DB 1 YERLRVTHQGTGAEFFETLLRDVYSSGSFSEIPLRQSTIPVSDMORFVLELTN 60
 QY 61 GGRNRYTAIDVNNYVAVYQAGDSYFLADPRGATHTLFTGTXSAPKXSYXDE 120
 DB 61 GGRNRYTAIDVNNYVAVYQAGDSYFLADPRGATHTLFTGTXSAPKXSYXDE 120
 QY 61 GGRNRYTAIDVNNYVAVYQAGDSYFLADPRGATHTLFTGTXSAPKXSYXDE 120
 DB 61 GGRNRYTAIDVNNYVAVYQAGDSYFLADPRGATHTLFTGTXSAPKXSYXDE 120
 QY 121 RYAGHDQIPGIGXOLIGSVAXLRXGSTRXQASILLLOMISBAARNPILWRXRX 180
 DB 121 RYAGHDQIPGIGXOLIGSVAXLRXGSTRXQASILLLOMISBAARNPILWRXRX 180
 QY 121 RYAGHDQIPGIGXOLIGSVAXLRXGSTRXQASILLLOMISBAARNPILWRXRX 180
 DB 121 RYAGHDQIPGIGXOLIGSVAXLRXGSTRXQASILLLOMISBAARNPILWRXRX 180
 QY 181 INSXSRIPDXNWLRLTSMQSGSTOVGHSTGVNPNRRLAIKXGNFTLVNRYVLS 240
 DB 181 INSXSRIPDXNWLRLTSMQSGSTOVGHSTGVNPNRRLAIKXGNFTLVNRYVLS 240
 QY 181 INSXSRIPDXNWLRLTSMQSGSTOVGHSTGVNPNRRLAIKXGNFTLVNRYVLS 240
 DB 181 INSXSRIPDXNWLRLTSMQSGSTOVGHSTGVNPNRRLAIKXGNFTLVNRYVLS 240
 QY 241 LAIMLPVCGRPSSSDYRWPEVIRPVADDTCSASEPTVRAIVGXKXKVVVDODPHD 300
 DB 241 LAIMLPVCGRPSSSDYRWPEVIRPVADDTCSASEPTVRAIVGXKXKVVVDODPHD 300
 QY 241 LAIMLPVCGRPSSSDYRWPEVIRPVADDTCSASEPTVRAIVGXKXKVVVDODPHD 300
 DB 241 LAIMLPVCGRPSSSDYRWPEVIRPVADDTCSASEPTVRAIVGXKXKVVVDODPHD 300
 QY 301 GNOIQLMPSKSNNDPNQWLTIRKDXITISNSGCLTGYTGAGVYVIFDQNVARENTW 360
 DB 301 GNOIQLMPSKSNNDPNQWLTIRKDXITISNSGCLTGYTGAGVYVIFDQNVARENTW 360
 QY 361 GNOIQLMPSKSNNDPNQWLTIRKDXITISNSGCLTGYTGAGVYVIFDQNVARENTW 420
 DB 361 GNOIQLMPSKSNNDPNQWLTIRKDXITISNSGCLTGYTGAGVYVIFDQNVARENTW 420

Thu Dec 11 16:09:41 2003

us-09-601-667c-1.rag

Page 7

Query Match 95.88; Score 2505; DB 18; Length 564;
Best Local Similarity 91.98; Pred. No. 3.9e-267;
Matches 489; Conservative 2; Mismatches 39; Indels 2; Gaps 2;

QY 1 YERLRLVHTQTGKVEFRFTLLRDVYSSGSFSNE:PLLRQSTIPVSDAQRFVVELTN 60
DB 34 YERLRLVHTQTGKVEFRFTLLRDVYSSGSFSNE:PLLRQSTIPVSDAQRFVVELTN 93
QY 61 QGDSKTLAIDVTKYVVAQAGSYFLADAPRCAFTLFTGTTRSS:LPKSGSYDLE 120
DB 94 QGDSKTLAIDVTKYVVAQAGSYFLADAPRCAFTLFTGTTRSS:LPKSGSYDLE 152
QY 121 RYAGHDDQIPGIGDLOSVTLAFPGSGSTRQASSTILLQMSAARFPIWBARQY 180
DB 153 RYAGHDDQIPGIGDLOSVTLAFPGSGSTRQASSTILLQMSAARFPIWBARQY 212
QY 181 INSGKSPFDXWMELETSWQOSTVOHSTGVNNEPKALIXANFTVLXNRYVYAS 240
DB 213 INSGKSPFDXWMELETSWQOSTVOHSTGVNNEPKALIXANFTVLXNRYVYAS 272
QY 241 LAIWLFCGERPSSSDYRWPIVIRPVADDTCSASEPTVRIYGNKXNDVDDDFD 300
DB 273 LAIWLFCGERPSSSDYRWPIVIRPVADDTCSASEPTVRIYGNKXNDVDDDFD 332
QY 301 GNOIOLMPKSNNDPQWLTIKRDXTIRNSGCLTYGTAGYVWIPDCNVAEBATW 360
DB 333 GNOIOLMPKSNNDPQWLTIKRDXTIRNSGCLTYGTAGYVWIPDCNVAEBATW 392
QY 361 QIWNKGTINRANVLAASGKGTITLTVQILDTTIGGMLAGNDLAPREVTYIGRDL 420
DB 393 QIWNKGTINRANVLAASGKGTITLTVQILDTTIGGMLAGNDLAPREVTYIGRDL 452
QY 421 CHESNGSWWETCSQXKXKXALYDGSIRPKOMQOCLTXGSDSVATVNIYSCX 480
DB 453 CHESNGSWWETCSQXKXKXALYDGSIRPKOMQOCLTXGSDSVATVNIYSCX 511
QY 481 XSKXQWVFTNEXALINLKKXXXDVQAQPKRLRIITYPATKPNQWMLPV 532
DB 512 GSGQKRVFTNEXALINLKKXXXDVQAQPKRLRIITYPATKPNQWMLPV 563

RESULT 7
AAM90127
ID AAM90127 standard; Protein; 564 AA.
XX
AC AAM90127;
XX
DT 20-MAR-2003 (updated)
DT 30-APR-1999 (first entry)
XX
XX Mistletoe lectin prepro-protein.
DB
KW MW; mistletoe lectin; MW; transgenic plant; glycosylation;
KW dimer; immunotoxin; large-scale production; diagnosis; therapeutic;
KW cancer.
XX
OS Viscum album.
OS
XX EP864388-A1.
XX
XX 16-DEC-1998.
XX
XX 26-JUN-1995; 98EP-0105660.
XX
XX 26-JUN-1995; 95EP-0105949.
XX 26-JUN-1995; 98EP-0105660.
XX
XX (MADU) MADAYS KOELN AG.
XX
XX Baur A., Eck J., Lentzen H., Zinke H.
XX
XX KPI, 1999-026582/03.

DR N-PsDB; AAV74182.
XX
XX New transgenic plant expressing mistletoe lectin - useful for
XX producing recombinant lectin in e.g. cancer diagnosis and therapy
XX
XX Claim 1a; Fig 4c; 10pp; German.
XX
XX This invention describes a novel transgenic plant transformed with a
XX vector capable of encoding a mistletoe (Viscum album) lectin
XX also describes a polypeptide produced by a plant where the polypeptide
XX embodies at least one enzymatic modification other than the glycosylation
XX modification of mistletoe lectin dimer and immunotoxin comprising the
XX polypeptide or the polypeptide dimer. The plants are used for large-scale
XX production of mistletoe lectin for diagnostic or therapeutic purposes
XX (e.g. in cancer therapy). This sequence represents the mistletoe lectin
XX used in the method of the invention.
XX (updated on 20-MAR-2003 to correct PF field.)
SQ
Sequence 564 AA.
Query Match 95.88; Score 2505; DB 20; Length 564;
Best Local Similarity 91.98; Pred. No. 3.9e-267;
Matches 489; Conservative 2; Mismatches 39; Indels 2; Gaps 2;

QY 1 YERLRLVHTQTGKVEFRFTLLRDVYSSGSFSNE:PLLRQSTIPVSDAQRFVVELTN 60
DB 34 YERLRLVHTQTGKVEFRFTLLRDVYSSGSFSNE:PLLRQSTIPVSDAQRFVVELTN 93
QY 61 QGDSKTLAIDVTKYVVAQAGSYFLADAPRCAFTLFTGTTRSS:LPKSGSYDLE 120
DB 94 QGDSKTLAIDVTKYVVAQAGSYFLADAPRCAFTLFTGTTRSS:LPKSGSYDLE 152
QY 121 RYAGHDDQIPGIGDLOSVTLAFPGSGSTRQASSTILLQMSAARFPIWBARQY 180
DB 153 RYAGHDDQIPGIGDLOSVTLAFPGSGSTRQASSTILLQMSAARFPIWBARQY 212
QY 181 INSGKSPFDXWMELETSWQOSTVOHSTGVNNEPKALIXANFTVLXNRYVYAS 240
DB 213 INSGKSPFDXWMELETSWQOSTVOHSTGVNNEPKALIXANFTVLXNRYVYAS 272
QY 241 LAIWLFCGERPSSSDYRWPIVIRPVADDTCSASEPTVRIYGNKXNDVDDDFD 300
DB 273 LAIWLFCGERPSSSDYRWPIVIRPVADDTCSASEPTVRIYGNKXNDVDDDFD 332
QY 301 GNOIOLMPKSNNDPQWLTIKRDXTIRNSGCLTYGTAGYVWIPDCNVAEBATW 360
DB 333 GNOIOLMPKSNNDPQWLTIKRDXTIRNSGCLTYGTAGYVWIPDCNVAEBATW 392
QY 361 QIWNKGTINRANVLAASGKGTITLTVQILDTTIGGMLAGNDLAPREVTYIGRDL 420
DB 393 QIWNKGTINRANVLAASGKGTITLTVQILDTTIGGMLAGNDLAPREVTYIGRDL 452
QY 421 CHESNGSWWETCSQXKXKXALYDGSIRPKOMQOCLTXGSDSVATVNIYSCX 480
DB 453 CHESNGSWWETCSQXKXKXALYDGSIRPKOMQOCLTXGSDSVATVNIYSCX 511
QY 481 XSKXQWVFTNEXALINLKKXXXDVQAQPKRLRIITYPATKPNQWMLPV 532
DB 512 GSGQKRVFTNEXALINLKKXXXDVQAQPKRLRIITYPATKPNQWMLPV 563

RESULT 8
AB879450
ID AB879450 standard; Protein; 551 AA.
XX
XX AB879450;
XX
XX 08-JUL-2002 (first entry)
XX
XX Galactose-recognition mistletoe lectin.
XX

XX	Mistletoe; galactose-recognising mistletoe lectin, MIII.	
XS	Viscum album.	
OS	Key	Location/Qualifiers
PH	Misc-difference 221	/note= "Encoded by A1C"
PT	Misc-difference 251	/note= "Encoded by T1T"
PT	Misc-difference 344	/note= "Encoded by T1C"
PT	Misc-difference 380	/note= "Encoded by GCC"
PT	Misc-difference 418	/note= "Encoded by GTG"
PN	DE10044027-A1.	
PD	14-MAR-2002.	
PD	06-SEP-2000; 2000DE-1044027.	
PS	06-SEP-2000; 2000DE-1044027.	
PR	(VISC-) VISCUM AG.	
PA	Klaeff S;	
PI	Claim 1; Fig 1; 6pp; German.	
XX	WPI; 2002-316737/36.	
DR	N-PSDB; ABL56947.	
XX	New nucleic acid encoding preprotein of mistletoe lectin, useful as diagnostic and therapeutic agents, also encodes polypeptide -	
PT	diagnostic and therapeutic agents, also encodes polypeptide -	
XX	Claim 1; Fig 1; 6pp; German.	
CC	The invention relates to a nucleic acid molecule (ABL56947) that encodes a preprotein (A5B79450) which, after maturation, has the biological activity of the galactose-recognising mistletoe lectin (MIII). The MIII encodes nucleic acid molecule, primers specific to it or complements of it, and encoded (oligonucleotide) polypeptides are useful as diagnostic and therapeutic agents.	
XX	Sequence 551 AA;	
50	Query Match 83.6%; Score 2187.5; DB 23; Length 551; Best Local Similarity 83.8%; Pred. NO. 4,1e-232; Matches 429; Conservative 14; Mismatches 62; Indels 7; Gaps 3	
OY	1 YERLALRYTQTCXKXPRFLTADYVSSGSRNFIPLIOGCTPIPSDAPFVLELN 60	
DB	3 YERLALRYHTQTDDEYFATLTLDADYVSSGSRNFIPLIOGCTPIPSDAPFVLELN 93	
OY	61 QGXDSEALADYTKXVYVAYVADQSYFLDAPGAGATLFTGTGXSIPXSGSYDLE 120	
DB	94 QGDSSTLADYDTLVYVAYVADQSYFLDAPGAGATLFTGTGXSIPXSGSYDLE 152	
OY	121 RYAGHROGFIKQILGSDVALRPGSGTRVQARSTILLQISBAPRNLTMRGX 180	
DB	153 RYAGRHDPIDGIEELIGSVALRPGSGTRVQARSTILLQISBAPRNLTMRGX 212	
OY	181 INSGXSEFDPXVTLLELTSGQOQSYOVGHSTGCVFNNPRLATIXGNFTLVNRYKVIS 240	
DB	213 INSGSEFDPXVTLLELTSGQOQSYOVGHSTGCVFNNPRLATIXGNFTLVNRYKVIS 272	
OY	241 LAMTFVGRBESSRIRWELVIRLVNSGANDVDVTCMSBPRKVERGQGLCTVRD 295	
DB	273 LAMTFVGRBESSRIRWELVIRLVNSGANDVDVTCMSBPRKVERGQGLCTVRD 332	
OY	296 DPHDSDNOLQLPESNNDPNQVATLTKDXTLRNSGSLCTVYGAGVYVNLFOCHTAVR 355	
DB	333 GKPHNNGIQLWFKCFVDPQWQVRRDQTLRSNGSLCTVYGAGVYVNLFOCHTAVR 392	

Oy		366	EATIMQVWNTGIINFRSNNVLAAASGICKGLTITVQLDTLTAAGSMIAANDYARREVTIV	418
Dy		393	EATIMQVWNTGIINFRSNNVLAAASGICGTLTITVQTYSIAGOMIAANDYARREVTIV	452
Oy		416	GREDICENSKASVWFETCKSSQKNXKXAKLVGNRSIFPCNQDCLTKAGDSVSTVINI	475
Dy		453	GRDCIKEMNBSAVSWFETCKSSQKNXKXAKLVGNRSIFPCNQDCLTKAGDSVSTVINI	511
Oy		476	VSCSXSXXQRWFFNEKALILMKXXXXADA	507
Dy		512	VSCSXSISQQRWFFNEGTILLMNGGVMDVA	543
		RESULT 9		
ID		AAZ5987		
TD		AAZ5987 standard; Protein; 264 AA.		
DI		AAZ5987;		
TI		18-OCT-1999 (first entry)		
DX		Mistletoe lectin B2 protein fragment.		
KX		Mistletoe lectin, antitumor; immunostimulant; A-chain; MAb; immunity;		
KW		lysozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;		
KM		lymphokine-producing macrophage; uncontrolled cell growth; treatment;		
KX		cancer; cytotoxicity; antigen; isoform; lectin B2.		
OX		Viscum album.		
PX		DEL9804210-A1.		
PD		12-AUG-1999.		
KX		03-FEB-1998; 98DE-1004210.		
FX		03-FEB-1998; 98DE-1004210.		
KX		(BIOS) BIOSYN ARKANGMTTEL QHSH.		
KX		Morris P, Stiefel T, Voelter W, Welters P.		
PI		WFI; 1999-445935/38.		
DR		N-PSDB: AA209111.		
KX		Preparation of mistletoe lectins in heterologous systems,		
FX		particularly for use as anticancer agents and immunostimulants		
B3		Claim 9; Fig 9B; 78pp; German.		
KX		This invention describes a novel mistletoe lectin (I) and its fragments		
CC		which have antitumor and immunostimulatory activity. The A-chain (MLA)		
CC		of the mistletoe lectin binds to, and inactivates, the 28S subunit of		
CC		ribosomes. Non-cytotoxic forms of (I) activate T-cell and		
CC		lymphokine-producing macrophages, so stimulate immunity. (I) and its		
CC		fragments are used to treat uncontrolled cell growth (particularly		
CC		cancers), and if they lack cytotoxicity, to increase the length of the		
CC		immune-associated bacterial or viral). The method allows production of		
CC		mistletoe lectin, and its individual chains, in many different isoforms		
CC		and on a large scale, at any time of the year. Recombinant products are		
CC		free from toxins present in natural mistletoe extracts. This sequence		
CC		represents a fragment of a mistletoe lectin B2 protein.		
SO		Sequence 264 AA:		
		Query Match 49.4%; Score 1291; DB 20; Length 264;		
		Best Local Similarity 92.4%; Pctd No. 1,3e-133;		
		Hatches 243; Conservative 20; Mismatches 20; Indels 0; Gaps 0		
Dy		270 DDTGSAASEPFAVVRKKXKVADDDPFDDNDIQUMSPSSNNPNOLWTKEKHTRIS	329	
Dy		1 DDTGSASEPFAVVRKVSXNVVDVDDDPFDNDIQUMSPSSNNPNOLWTKEKHTRIS	60	

QY 330 MNSCLTGYGYAGVYVWIFDGNRAVEATITWIMKNTIIMPBSMLVLAASGIGKTTLT 389
 DB 61 MNSCLTGYGYAGVYVWIFDGNRAVEATITWIMKNTIIMPBSMLVLAASGIGKTTLT 120
 QY 390 VQTLDTLGGWLAGNDTAPREVTIYGRDLCHESXKGSVWVETCKSSQXKXWALYGD 449
 DB 121 VQTLDTLGGWLAGNDTAPREVTIYGRDLCHESXKGSVWVETCKSSQXKXWALYGD 180
 QY 450 GSIRPKQKODCLTGRBDSVTVINIVSCSXKXKQWVFTNEXALINLAKXXXXVYQA 509
 DB 181 GSIRPKQKODCLTGRBDSVTVINIVSCSXKXKQWVFTNEXALINLAKXXXXVYQA 240
 QY 510 NPKLRITITPATGKPKQKMLPV 532
 DB 241 NPKLRITITPATGKPKQKMLPV 263

RESULT 10

AYZ5988
 ID AYZ5988 standard; Protein: 264 AA.

AYZ5988;
 18-OCT-1999 (first entry)

DE Mistletoe lectin B3 protein fragment.
 KW Mistletoe; lectin; antitumor; immunostimulant; A-chain; MDA; immunity;
 ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;
 lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 cancer; cytotoxicity; antigen; isoform; lectin B3.

OS Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P. Stiefel T. Voelter W. Welters P;
 XX WPI: 1999-44535/36.
 XX N-PSDB: AA209112.

PT Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants
 PS Claim 9; Fig 10B; 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 26S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and its
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B3 protein.

Sequence 264 AA;
 Query Match 49.4%; Score 1291; DE 20; Length 264;
 Best Local Similarity 92.4%; Pred. No. 1.3e-133;

Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 270 DNVTCGSAEPTVRIYGRKXKQWVYRDDPFDNQCILMPSKNNNDPQWATYKPDYTR 329
 DB 1 DNVTCGSAEPTVRIYGRKXKQWVYRDDPFDNQCILMPSKNNNDPQWATYKPDYTR 60
 QY 330 MNSCLTGYGYAGVYVWIFDGNRAVEATITWIMKNTIIMPBSMLVLAASGIGKTTLT 389
 DB 61 MNSCLTGYGYAGVYVWIFDGNRAVEATITWIMKNTIIMPBSMLVLAASGIGKTTLT 120
 QY 390 VQTLDTLGGWLAGNDTAPREVTIYGRDLCHESXKGSVWVETCKSSQXKXWALYGD 449
 DB 121 VQTLDTLGGWLAGNDTAPREVTIYGRDLCHESXKGSVWVETCKSSQXKXWALYGD 180
 QY 450 GSIRPKQKODCLTGRBDSVTVINIVSCSXKXKQWVFTNEXALINLAKXXXXVYQA 509
 DB 181 GSIRPKQKODCLTGRBDSVTVINIVSCSXKXKQWVFTNEXALINLAKXXXXVYQA 240
 QY 510 NPKLRITITPATGKPKQKMLPV 532
 DB 241 NPKLRITITPATGKPKQKMLPV 263

RESULT 11

AYZ5994
 ID AYZ5994 standard; Protein: 265 AA.

AYZ5994;
 18-OCT-1999 (first entry)

DE Mistletoe lectin B3 variant protein fragment.
 KW Mistletoe; lectin; antitumor; immunostimulant; A-chain; MDA; immunity;
 ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;
 lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 cancer; cytotoxicity; antigen; isoform; lectin B3.

OS Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P. Stiefel T. Voelter W. Welters P;
 XX WPI: 1999-44535/36.
 XX N-PSDB: AA209118.
 PT Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants
 PS Disclosure; Fig 16B; 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 26S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and its
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B3 protein.

XX Sequence 265 AA;
SQ
Query Match 49.4%; Score 1291; DB 20; Length 265;
Best Local Similarity 92.4%; Pred. No. 1,3e-133;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
OY 270 DVVTCASAEPTVRIYVGRKXGVAVRDDEPDGQIQIOLPFSKSNNDPQQLMTIKEDYTRS 329
DB 1 DVVTCASAEPTVRIYVGRKXGVAVRDDEPDGQIQIOLPFSKSNNDPQQLMTIKEDYTRS 60
OY 330 NSGCLITVGTAGVYVMEFCNTAVREXITWQXNGTINPSSNLVLAASSGIKGTTLT 389
DB 61 NSGCLITVGTAGVYVMEFCNTAVREXITWQXNGTINPSSNLVLAASSGIKGTTLT 120
OY 390 VQTLDTYLLGGMLAGNDAPREVTIYGRDLCKESNGSVWVETCSQXQXKXALYGD 449
DB 121 VQTLDTYLLGGMLAGNDAPREVTIYGRDLCKESNGSVWVETCSQXQXKXALYGD 180
OY 450 GSIRPKONODCLTVGRDSVSTVINIVSCSXKXKXQVFTNEXAILNLKXXXXXDVAA 509
DB 181 GSIRPKONODCLTVGRDSVSTVINIVSCSXKXKXQVFTNEXAILNLKXXXXXDVAA 240
OY 510 NPKLRILIIYPAFGKPNQWMLPV 532
DB 241 NPKLRILIIYPAFGKPNQWMLPV 263

RESULT 12

AAV25993
ID AAV25993 standard; Protein; 265 AA.

XX AAV25993;

18-OCT-1999 (first entry)

Mistletoe lectin B2 variant protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MAb; immunity;
XX ribozyme 288 subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B2.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelker W, Welters P;

XX WPI: 1999-44535/38.

XX N-PSDB; AA209117.

XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants

XX Disclosure; Fig 15B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MAA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancer) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a variant mistletoe lectin B2 protein.
XX
SQ Sequence 265 AA;
Query Match 49.4%; Score 1291; DB 20; Length 265;
Best Local Similarity 92.4%; Pred. No. 1,3e-133;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 270 DVVTCASAEPTVRIYVGRKXGVAVRDDEPDGQIQIOLPFSKSNNDPQQLMTIKEDYTRS 329
DB 1 DVVTCASAEPTVRIYVGRKXGVAVRDDEPDGQIQIOLPFSKSNNDPQQLMTIKEDYTRS 60
OY 330 NSGCLITVGTAGVYVMEFCNTAVREXITWQXNGTINPSSNLVLAASSGIKGTTLT 389
DB 61 NSGCLITVGTAGVYVMEFCNTAVREXITWQXNGTINPSSNLVLAASSGIKGTTLT 120
OY 390 VQTLDTYLLGGMLAGNDAPREVTIYGRDLCKESNGSVWVETCSQXQXKXALYGD 449
DB 121 VQTLDTYLLGGMLAGNDAPREVTIYGRDLCKESNGSVWVETCSQXQXKXALYGD 180
OY 450 GSIRPKONODCLTVGRDSVSTVINIVSCSXKXKXQVFTNEXAILNLKXXXXXDVAA 509
DB 181 GSIRPKONODCLTVGRDSVSTVINIVSCSXKXKXQVFTNEXAILNLKXXXXXDVAA 240
OY 510 NPKLRILIIYPAFGKPNQWMLPV 532
DB 241 NPKLRILIIYPAFGKPNQWMLPV 263

RESULT 13

AAV25986
ID AAV25986 standard; Protein; 264 AA.

XX AAV25986;

18-OCT-1999 (first entry)

Mistletoe lectin B1 protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MAb; immunity;
XX ribozyme 288 subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B1.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelker W, Welters P;

XX WPI: 1999-44535/38.

XX N-PSDB; AA209110.

XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants

XX Claim 9; Fig 8B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MAA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of

CC ribosomes. Non-cytotoxic forms of (1) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (1) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC produced from transgenic animals. This sequence represents a fragment of a
 CC mistletoe lectin B1 protein.

XX Sequence 264 AA;

Query Match 49.3%; Score 1290; DB 20; Length 264;

Best Local Similarity 92.4%; Pred. No. 1.6e-133;

Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

DB 270 DDTCSASEPTVRIYKXKAVVVDVDDPHDQNOIQLPKSNDDPQMLTKIKDXTIRS 329
 1 DDTCSASEPTVRIYKXKAVVVDVDDPHDQNOIQLPKSNDDPQMLTKIKDXTIRS 60
 QY 330 NSCLTGYGTAGVYVIMFDCAVAREATIMQIXNGTIIIPASNLVLAASGKKTTLT 389
 DB 61 NSCLTGYGTAGVYVIMFDCAVAREATIMQIXNGTIIIPASNLVLAASGKKTTLT 120
 QY 390 VQTLDTLGGWLAGNDTPAPEVTIYGFRLDMSKSGSVVETCSQXQXNALYGD 449
 DB 121 VQTLDTLGGWLAGNDTPAPEVTIYGFRLDMSKSGSVVETCSQXQXNALYGD 180
 QY 450 GSIRPKNOPOCLTXGSDSVETIVIVCSXSGXGQVFTNEXAIIINLKXXXXVDAQ 509
 DB 181 GSIRPKNOPOCLTXGSDSVETIVIVCSXSGXGQVFTNEXAIIINLKXXXXVDAQ 240
 QY 510 NPKLRRIIIPATKRNQWMLPV 532
 DB 241 NPKLRRIIIPATKRNQWMLPV 263

RESULT 14

AAV25990 ID AAV25990 standard; Protein: 264 AA.

XX AAV25990;

DB 18-OCT-1999 (first entry)

XX Mistletoe lectin B5 protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;

XX cancer; cytotoxicity; antigen; isoform; lectin B5.

XX Viscum album.

XX DB19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelker W, Walters P;

XX WPI; 1999-44535/38.

XX N-PSDB; AA209114.

XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX

BS Claim 9; Fig 12B; 78pp; German.

XX This invention describes a novel mistletoe lectin (1) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (MIA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (1) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (1) and its
 XX fragments are used to treat uncontrolled cell growth (particularly
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX free from toxins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a mistletoe lectin B5 protein.

XX Sequence 264 AA;

Query Match 49.3%; Score 1290; DB 20; Length 264;

Best Local Similarity 92.4%; Pred. No. 1.6e-133;

Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

DB 270 DDTCSASEPTVRIYKXKAVVVDVDDPHDQNOIQLPKSNDDPQMLTKIKDXTIRS 329
 1 DDTCSASEPTVRIYKXKAVVVDVDDPHDQNOIQLPKSNDDPQMLTKIKDXTIRS 60
 QY 330 NSCLTGYGTAGVYVIMFDCAVAREATIMQIXNGTIIIPASNLVLAASGKKTTLT 389
 DB 61 NSCLTGYGTAGVYVIMFDCAVAREATIMQIXNGTIIIPASNLVLAASGKKTTLT 120
 QY 390 VQTLDTLGGWLAGNDTPAPEVTIYGFRLDMSKSGSVVETCSQXQXNALYGD 449
 DB 121 VQTLDTLGGWLAGNDTPAPEVTIYGFRLDMSKSGSVVETCSQXQXNALYGD 180
 QY 450 GSIRPKNOPOCLTXGSDSVETIVIVCSXSGXGQVFTNEXAIIINLKXXXXVDAQ 509
 DB 181 GSIRPKNOPOCLTXGSDSVETIVIVCSXSGXGQVFTNEXAIIINLKXXXXVDAQ 240
 QY 510 NPKLRRIIIPATKRNQWMLPV 532
 DB 241 NPKLRRIIIPATKRNQWMLPV 263

RESULT 15

AAV25996 ID AAV25996 standard; Protein: 265 AA.

XX AAV25996;

DB 18-OCT-1999 (first entry)

XX Mistletoe lectin B5 variant protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;

XX cancer; cytotoxicity; antigen; isoform; lectin B5.

XX Viscum album.

XX DB19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelker W, Walters P;

XX WPI; 1999-44535/38.

Thu Dec 11 16:09:41 2003

us-09-601-667c-1.rag

DR N-PSDB; AA209120.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
PS Disclosure; Fig 185; 78pp; German.
XX
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen production of
CC (tumour associated) peptides. (I) and its fragments are used to produce
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B5 protein.
XX
SQ Sequence 265 AA;
Query Match 49.3%; Score 1290; DB 20; Length 265;
Best Local Similarity 92.4%; Pred. No. 1.6e-133;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 270 DMTCSASPTVRIYGRKXGVYDPPDHPDNGIQLPKSKNDPQMLTKIKDITRS 329
Db 1 DDTCSASPTVRIYGRKXGVYDPPDHPDNGIQLPKSKNDPQMLTKIKDITRS 60
Qy 330 NSCLTYGTAGVYVIMPDNTAVRENTIQIXGTLINPRSLVLAASGKGTLLT 389
Db 61 NSCLTYGTAGVYVIMPDNTAVRENTIQIXGTLINPRSLVLAASGKGTLLT 120
Qy 390 VQTLDTLQGMLAGNDPAPEVYTIYGRDLQMSXGSAWVETCSQXQXWALYGD 449
Db 121 VQTLDTLQGMLAGNDPAPEVYTIYGRDLQMSXGSAWVETCSQXQXWALYGD 180
Qy 450 GSTPRKQKQCLTKRBSVSTINIVSCSXKXKRWTFNEXAIIKXXXXXQVQA 509
Db 181 GSTPRKQKQCLTKRBSVSTINIVSCSXKXKRWTFNEXAIIKXXXXXQVQA 240
Qy 510 NPKLRRIIIPATGKPNQWMLPV 532
Db 241 NPKLRRIIIPATGKPNQWMLPV 263

Search completed: December 11, 2003, 14:07:40
Job time : 35.669 secs

Thu Dec 11 16:09:42 2003

us-09-601-667c-1.rapb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 14:01:14 / Search time 34.348 Seconds
(without alignment)

2866.029 Million cell updates/sec

Title: US-09-601-667C-1
Perfect score: 2616
Sequence: 1 YERLRRLVHTQTKYKFRP.....RRILYPAIKGNQMLPFYX 533

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 684280 seqs, 185993659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: /cgn2_6/prodata/1/pubpa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpa/PCUS_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpa/US06_PUB.pep.*
4: /cgn2_6/prodata/1/pubpa/US07_PUB.pep.*
5: /cgn2_6/prodata/1/pubpa/US07_PUB.pep.*
6: /cgn2_6/prodata/1/pubpa/US08_PUB.pep.*
7: /cgn2_6/prodata/1/pubpa/US08_PUB.pep.*
8: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
9: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
12: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
13: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
15: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
16: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
17: /cgn2_6/prodata/1/pubpa/US60_PUBCOMB.pep.*
18: /cgn2_6/prodata/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1267.5	48.5	263	9	US-09-347-064-10
2	1267.5	48.5	267	9	US-09-347-064-4
3	1231	47.1	576	12	US-10-083-336A-1
4	1135.3	44.2	252	9	US-09-347-064-8
5	1135.3	44.0	252	9	US-09-347-064-2
6	1135.3	44.0	252	9	US-09-347-064-8
7	1135.3	44.0	252	9	US-09-347-064-2
8	1135.3	44.0	252	9	US-09-347-064-8
9	1135.3	44.0	252	9	US-09-347-064-2
10	1135.3	44.0	252	9	US-09-347-064-8
11	1135.3	44.0	252	9	US-09-347-064-2
12	1135.3	44.0	252	9	US-09-347-064-8
13	1135.3	44.0	252	9	US-09-347-064-2
14	1135.3	44.0	252	9	US-09-347-064-8
15	1135.3	44.0	252	9	US-09-347-064-2
16	1135.3	44.0	252	9	US-09-347-064-8
17	1135.3	44.0	252	9	US-09-347-064-2
18	1135.3	44.0	252	9	US-09-347-064-8
19	1135.3	44.0	252	9	US-09-347-064-2
20	1135.3	44.0	252	9	US-09-347-064-8
21	1135.3	44.0	252	9	US-09-347-064-2
22	1135.3	44.0	252	9	US-09-347-064-8
23	1135.3	44.0	252	9	US-09-347-064-2
24	1135.3	44.0	252	9	US-09-347-064-8
25	1135.3	44.0	252	9	US-09-347-064-2
26	1135.3	44.0	252	9	US-09-347-064-8
27	1135.3	44.0	252	9	US-09-347-064-2
28	1135.3	44.0	252	9	US-09-347-064-8
29	1135.3	44.0	252	9	US-09-347-064-2
30	1135.3	44.0	252	9	US-09-347-064-8
31	1135.3	44.0	252	9	US-09-347-064-2
32	1135.3	44.0	252	9	US-09-347-064-8
33	1135.3	44.0	252	9	US-09-347-064-2
34	1135.3	44.0	252	9	US-09-347-064-8
35	1135.3	44.0	252	9	US-09-347-064-2
36	1135.3	44.0	252	9	US-09-347-064-8
37	1135.3	44.0	252	9	US-09-347-064-2
38	1135.3	44.0	252	9	US-09-347-064-8
39	1135.3	44.0	252	9	US-09-347-064-2
40	1135.3	44.0	252	9	US-09-347-064-8
41	1135.3	44.0	252	9	US-09-347-064-2
42	1135.3	44.0	252	9	US-09-347-064-8
43	1135.3	44.0	252	9	US-09-347-064-2
44	1135.3	44.0	252	9	US-09-347-064-8
45	1135.3	44.0	252	9	US-09-347-064-2

15	280	10.7	247	12	US-10-375-209A-34	Sequence 34, App1
16	277	10.4	251	12	US-10-127-890-102	Sequence 102, App
17	272	10.4	251	12	US-10-127-890-102	Sequence 102, App
18	272	10.4	251	12	US-10-127-890-102	Sequence 102, App
19	272	10.4	251	12	US-10-127-890-102	Sequence 102, App
20	271.5	10.4	332	9	US-09-765-527-251	Sequence 251, App
21	271	10.4	251	12	US-10-127-890-99	Sequence 99, App1
22	270	10.3	316	12	US-10-074-596-1	Sequence 1, App1
23	269	10.3	251	12	US-10-127-890-100	Sequence 100, App
24	269	10.3	251	12	US-10-127-890-105	Sequence 105, App
25	268	10.2	251	9	US-09-765-527-247	Sequence 247, App
26	268	10.2	251	12	US-10-127-890-2	Sequence 2, App1
27	268	10.2	251	12	US-10-127-890-103	Sequence 103, App
28	268	10.2	251	12	US-10-127-890-106	Sequence 106, App
29	268	10.2	251	12	US-10-127-890-108	Sequence 108, App
30	268	10.2	507	12	US-10-127-890-11	Sequence 11, App1
31	267	10.2	251	12	US-10-127-890-109	Sequence 109, App
32	267	10.2	251	12	US-10-127-890-109	Sequence 109, App
33	265	10.1	251	12	US-10-127-890-107	Sequence 107, App
34	265	10.1	293	9	US-09-765-527-253	Sequence 253, App
35	265	10.1	309	9	US-09-765-527-253	Sequence 253, App
36	264.5	10.1	198	12	US-10-083-336A-3	Sequence 3, App1
37	264.5	10.1	198	12	US-10-083-336A-7	Sequence 7, App1
38	264.5	10.1	199	12	US-10-083-336A-5	Sequence 5, App1
39	264.5	10.1	200	12	US-10-083-336A-10	Sequence 10, App1
40	264.5	10.1	199	12	US-10-127-890-7	Sequence 7, App1
41	261	9.6	182	12	US-10-083-336A-9	Sequence 9, App1
42	242.5	9.3	188	12	US-10-083-336A-2	Sequence 2, App1
43	242.5	9.3	188	12	US-10-083-336A-6	Sequence 6, App1
44	242.5	9.3	189	12	US-10-083-336A-6	Sequence 6, App1
45	242.5	9.3	190	12	US-10-083-336A-11	Sequence 11, App1

ALIGNMENTS

RESULT 1	US-09-347-064-10	Application US/09347064A
Sequence 10, App1	US-09-347-064-10	
Patent No. US20020045208A1		
GENERAL INFORMATION:		
APPLICANT: Eck, Jürgen		
APPLICANT: Schmidt, Arno		
APPLICANT: Zinke, Holger		
TITLE OF INVENTION: Recombinant Fusion Proteins Based on		
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the		
TITLE OF INVENTION: Viscum		
TITLE OF INVENTION: Viscum		
CURRENT APPLICATION NUMBER: US/09/347, 064A		
CURRENT FILING DATE: 1999-07-02		
EARLIER FILING DATE: 1999-01-02		
EARLIER FILING DATE: 1999-01-02		
EARLIER FILING DATE: 1997-01-02		
NUMBER OF SEQ ID NOS: 38		
SOFTWARE: PatentIn Ver. 2.1		
SEQ ID NO: 10		
LENGTH: 263		
QUERY: Viscum album		
US-09-347-064-10		
Query Match	48.5%	Score 1267.5; DB 9; Length 263;
Best Local Similarity	91.6%	Pred. No. 1.7e-112;
Matches 241; Conservative 1; Mismatches 20; Indels 1; Gaps 1;		
QY	270	DVTCASAPPTVIVGKXGKVDKDDPHGQGLQWPKSKNDPQWMTIKKDDYTR 329
DB	1	DVTCASAPPTVIVGKXGKVDKDDPHGQGLQWPKSKNDPQWMTIKKDDYTR 329
QY	330	NKSCLTGTYAGTVMIPPCNTAVKATVWQIWKNGTIIIPRSNVLWLAASSGKQITLT 389
DB	61	NKSCLTGTYAGTVMIPPCNTAVKATVWQIWKNGTIIIPRSNVLWLAASSGKQITLT 389

Thu Dec 11 16:09:42 2003

us-09-601-667c-1.rapb

Page 3

/ SEQ ID NO 8
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Viscum album
US-09-347-064-8

Query Match
Best Local Similarity 44.2%; Score 115.5; DB 9; Length 252;
Best Local Similarity 91.7%; Pred. No. 1,36-119;
Matches 233; Conservative 1; Mismatches 19; Indels 1; Gaps 1;

QY 1 YERLRATVHTQTEKYEPRITLLADYSSGSFSNEIFLLRQSTIPVSDAQRFVLVELTN 60
DB 1 YERLRATVHTQTEKYEPRITLLADYSSGSFSNEIFLLRQSTIPVSDAQRFVLVELTN 60
QY 61 QGDSXTALIDVTNYVAVAGQSYFLDAPRGAETHLFTGTRKSLPFYGSYDLE 120
DB 61 QGDSXTALIDVTNYVAVAGQSYFLDAPRGAETHLFTGTRKSLPFYGSYDLE 119
QY 121 RYAGHRDQIPGIGDQILQSVTLAPFGSTTQASILLIOMISEKAPFPLMRKRX 180
DB 121 RYAGHRDQIPGIGDQILQSVTLAPFGSTTQASILLIOMISEKAPFPLMRKRX 179
QY 181 INSGASFLPDVYMLELFTSMGQSTVOYHSTGVFNPRFLAIPRGNFVTLNVDVINS 240
DB 181 INSGASFLPDVYMLELFTSMGQSTVOYHSTGVFNPRFLAIPRGNFVTLNVDVINS 239
QY 241 LAIMLFVCGERP 253
DB 241 LAIMLFVCGERP 252

RESULT 5
US-09-347-064-2
/ Sequence 2, Application US/09347064A
/ Patent No. US20020045208A1
/ GENERAL INFORMATION:
/ APPLICANT: Eck, Jürgen
/ APPLICANT: Schmidt, Arno
/ APPLICANT: Zinke, Holger
/ TITLE OF INVENTION: Recombinant Fusion Proteins Based on
/ TITLE OF INVENTION: album
/ FILE REFERENCE: 09282-5
/ CURRENT APPLICATION NUMBER: US/09/347,064A
/ CURRENT FILING DATE: 1999-07-02
/ EARLIER APPLICATION NUMBER: PCT/EP98/00009
/ EARLIER FILING DATE: 1998-01-02
/ EARLIER APPLICATION NUMBER: EP 97 10 0012.0
/ EARLIER FILING DATE: 1997-01-02
/ NUMBER OF SEQ ID NOS: 38
/ SOURCE: Patent in Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Viscum album
US-09-347-064-2

Query Match
Best Local Similarity 44.0%; Score 115.5; DB 9; Length 252;
Best Local Similarity 91.7%; Pred. No. 1,36-119;
Matches 231; Conservative 1; Mismatches 19; Indels 1; Gaps 1;

QY 1 YERLRATVHTQTEKYEPRITLLADYSSGSFSNEIFLLRQSTIPVSDAQRFVLVELTN 60
DB 1 YERLRATVHTQTEKYEPRITLLADYSSGSFSNEIFLLRQSTIPVSDAQRFVLVELTN 61
QY 61 QGDSXTALIDVTNYVAVAGQSYFLDAPRGAETHLFTGTRKSLPFYGSYDLE 120
DB 61 QGDSXTALIDVTNYVAVAGQSYFLDAPRGAETHLFTGTRKSLPFYGSYDLE 120
QY 121 RYAGHRDQIPGIGDQILQSVTLAPFGSTTQASILLIOMISEKAPFPLMRKRX 180
DB 121 RYAGHRDQIPGIGDQILQSVTLAPFGSTTQASILLIOMISEKAPFPLMRKRX 180

QY 181 INSGASFLPDVYMLELFTSMGQSTVOYHSTGVFNPRFLAIPRGNFVTLNVDVINS 240
DB 181 INSGASFLPDVYMLELFTSMGQSTVOYHSTGVFNPRFLAIPRGNFVTLNVDVINS 240
QY 241 LAIMLFVCGERP 252
DB 241 LAIMLFVCGERP 252

RESULT 6
US-10-282-935-3
/ Sequence 3, Application US/10282935
/ Publication No. US20030143193A1
/ GENERAL INFORMATION:
/ APPLICANT: VITETTA, ELLEN S.
/ APPLICANT: GHETTE, VICTOR F.
/ APPLICANT: SWALLSHAW, JOAN
/ APPLICANT: BALUNA, ROXANA G.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
/ TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
/ FILE REFERENCE: US/08/8405 US/10/282,935
/ CURRENT FILING DATE: 2002-10-29
/ PRIOR APPLICATION NUMBER: 09/538,873
/ PRIOR FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: 60/126,826
/ PRIOR FILING DATE: 1999-03-30
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: Patent in Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 251
/ TYPE: PRT
/ ORGANISM: Abrus precatorius
US-10-282-935-3

Query Match
Best Local Similarity 41.7%; Score 454.5; DB 12; Length 251;
Best Local Similarity 41.7%; Pred. No. 5,6e-42;
Matches 105; Conservative 34; Mismatches 88; Indels 25; Gaps 6;

QY 9 THQOTKYEPRITLLADYSSGSFSNEIFLLRQSTIPVSDAQRFVLVELTNQGXDTA 68
DB 9 THQOTKYEPRITLLADYSSGSFSNEIFLLRQSTIPVSDAQRFVLVELTNQGXDTA 66
QY 69 AIDVTNYVAVAGQSYFLDAPRGAETHLFTGTRKSLPFYGSYDLEKRYAGH-RD 127
DB 69 AIDVTNYVAVAGQSYFLDAPRGAETHLFTGTRKSLPFYGSYDLEKRYAGH-RD 125
QY 120 QIPGIGDQILQSVTLAPFGSTTQASILLIOMISEKAPFPLMRKRXINSGAS 187
DB 120 QIPGIGDQILQSVTLAPFGSTTQASILLIOMISEKAPFPLMRKRXINSGAS 185
QY 188 LPDXYMLELFTSMGQSTVOYHSTGVFNPRFLAIPRGNFVTLNVDVINS 236
DB 188 LPDXYMLELFTSMGQSTVOYHSTGVFNPRFLAIPRGNFVTLNVDVINS 235
QY 237 VIALIMLFVCG 248
DB 237 VIALIMLFVCG 247

RESULT 7
US-10-282-935-1
/ Sequence 1, Application US/10282935
/ Publication No. US20030143193A1
/ GENERAL INFORMATION:
/ APPLICANT: VITETTA, ELLEN S.
/ APPLICANT: GHETTE, VICTOR F.
/ APPLICANT: SWALLSHAW, JOAN G.
/ APPLICANT: BALUNA, ROXANA G.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
/ TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
/ FILE REFERENCE: US/08/8405
/ CURRENT APPLICATION NUMBER: US/10/282,935

Thu Dec 11 16:09:42 2003

us-09-601-667c-1.rapb

Page 4

CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/558, 873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126, 826
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent Ver. 2.1
SEQ ID NO: 1
LENGTH: 267
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-282-935-1

Query Match 14.4%; Score 377.5; DB 12; Length 267;
Best Local Similarity 38.8%; Pred. No. 2.3e-33;
Matches 99; Conservative 41; Mismatches 104; Indels 11; Gaps 7;

9 THQTGKXFRFTLLADYSSGS-FSNRPLL-RGSTIPNSDAPRYVLENGQDX 66
13 TAGATVQSYTNFIRVGRITLTGADVREHFLVPRVQGLFN--QRTLVLSNHAELSV 70
67 TLAIDVTNXXVYVYVADQSYFLR-DAPRGAE--THLFTGTRXSLPFKGSYXDLERYA 123
71 TLAIDVTNXXVYVYVADQSYFLR-DAPRGAE--THLFTGTRXSLPFKGSYXDLERYA 123
124 GH-RDQIPGIXOLIOSVYAL--KPGGSTRXQARSILILQMSAPARNPILMRXQ 179
131 GNLRENTIELNGPLEFASLSALVYISGTCQPLFLASFLICIDMSAPKQVILSGERT 190
180 XNSGKSFIPDXVYLELFTSGQCGSTQVQHSCTGQVFNPKRLAXGNVTLLXNPRVYA 239
191 RIRYNRSAPDPVITLNSMRSLTAIOESNGAFASFPICORNGSFSYVDSILIP 250
240 SLALMFVCGERRSS 254
251 IIALMYRCAPRESS 265

RESULT 8
US-10-127-890-1
Sequence 1, Application US/10127890
Patent No. US2001068136A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESS: McAndrews, Heald & Malloy, Ltd.
SUITE 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-MAY-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/06/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 1990-03-30
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70, P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-127-890-1

Query Match 14.4%; Score 377.5; DB 12; Length 267;
Best Local Similarity 38.8%; Pred. No. 2.3e-33;
Matches 99; Conservative 41; Mismatches 104; Indels 11; Gaps 7;
9 THQTGKXFRFTLLADYSSGS-FSNRPLL-RGSTIPNSDAPRYVLENGQDX 66
13 TAGATVQSYTNFIRVGRITLTGADVREHFLVPRVQGLFN--QRTLVLSNHAELSV 70
67 TLAIDVTNXXVYVYVADQSYFLR-DAPRGAE--THLFTGTRXSLPFKGSYXDLERYA 123
71 TLAIDVTNXXVYVYVADQSYFLR-DAPRGAE--THLFTGTRXSLPFKGSYXDLERYA 123
124 GH-RDQIPGIXOLIOSVYAL--KPGGSTRXQARSILILQMSAPARNPILMRXQ 179
131 GNLRENTIELNGPLEFASLSALVYISGTCQPLFLASFLICIDMSAPKQVILSGERT 190
180 XNSGKSFIPDXVYLELFTSGQCGSTQVQHSCTGQVFNPKRLAXGNVTLLXNPRVYA 239
191 RIRYNRSAPDPVITLNSMRSLTAIOESNGAFASFPICORNGSFSYVDSILIP 250
240 SLALMFVCGERRSS 254
251 IIALMYRCAPRESS 265

RESULT 9
US-09-792-793A-39
Sequence 3, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DISEASES
TITLE OF INVENTION: OTHER INFORMATION: CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent Ver. 2.0
SEQ ID NO: 39
LENGTH: 247
TYPE: PRT
ORGANISM: Trichosanthens killowii
US-09-792-793A-39
Query Match 11.8%; Score 308.5; DB 10; Length 247;
Best Local Similarity 34.7%; Pred. No. 1e-25; 94; Indels 13; Gaps 8;
Matches 83; Conservative 49; Mismatches 94; Indels 13; Gaps 8;

Thu Dec 11 16:09:42 2003

us-09-601-667c-1.rpb

Page 5

13 TCKEYFPTTLADYVSSGFSNIPILKOSTIPVSDAQFVLYELNKGXSKXTALIDV 72
10 TSSSYGVFISNLRKALPBERKLYDIPILR-SLPGS--QRYALHILNADETISVALIDV 66
73 TNYVYVQAGDQSYFLSDA-PRGAETHLFTGTXSLEPFYGSYXDLERYAGH-RDQIP 130
67 TNYVYVQAGDQSYFLSDA-PRGAETHLFTGTXSLEPFYGSYXDLERYAGH-RDQIP 126
131 LGIXOLQSYVXALXPGSGSTXQASSTILLIOMISAAENPILMRKXINSCKSEFLPD 190
127 LGIPALDSAITTLFTYNNNS--ASALMWLIQSTSEARKEFLEQJGKRVK--TFLPS 182
191 XYMLELSTMGQSTQVQ--HSTQVFNPNPKALIXGNFVILNXYKX--VIASIAIML 245
183 LAIISLNSMSALSNOIQAISTNOCFESPVVILNNOQVATITVDAVTSNIALIL 241

RESULT 10
US-10-375-209A-39
Sequence 39, Application US/10375209A
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601E
CURRENT APPLICATION NUMBER: US/10/375,209A
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 247
TYPE: PRT
ORGANISM: Trichosantheus kiliowii
US-10-375-209A-39

Query Match 11.8%; Score 308.5; DB 12; Length 247;
Best Local 34.7%; Pred. No. 1.e-25; Indels 13; Gaps 8;
Matches 83; Conservative 49; Mismatches 95;

13 TCKEYFPTTLADYVSSGFSNIPILKOSTIPVSDAQFVLYELNKGXSKXTALIDV 72
10 TSSSYGVFISNLRKALPBERKLYDIPILR-SLPGS--QRYALHILNADETISVALIDV 66
73 TNYVYVQAGDQSYFLSDA-PRGAETHLFTGTXSLEPFYGSYXDLERYAGH-RDQIP 130
67 TNYVYVQAGDQSYFLSDA-PRGAETHLFTGTXSLEPFYGSYXDLERYAGH-RDQIP 126
131 LGIXOLQSYVXALXPGSGSTXQASSTILLIOMISAAENPILMRKXINSCKSEFLPD 190
127 LGIPALDSAITTLFTYNNNS--ASALMWLIQSTSEARKEFLEQJGKRVK--TFLPS 182
191 XYMLELSTMGQSTQVQ--HSTQVFNPNPKALIXGNFVILNXYKX--VIASIAIML 245
183 LAIISLNSMSALSNOIQAISTNOCFESPVVILNNOQVATITVDAVTSNIALIL 241

RESULT 11
US-10-127-890-6
Sequence 6, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Studenka, Gary M.
TITLE OF INVENTION: Immunocoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 172
CORRESPONDENCE ADDRESS:
ADDRESSER: McGraw-Hill, Inc.
STREET: 500 West Madison Street, 34th floor

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-PC/MS DOS
SOFTWARE: Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 23-Apr-2002
CLASSIFICATION: Unknown
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 31,516
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
MOLECULAR WEIGHT: 247
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-127-890-6

Query Match 11.7%; Score 306.5; DB 12; Length 247;
Best Local 34.3%; Pred. No. 1.e-25; Indels 13; Gaps 8;
Matches 82; Conservative 49; Mismatches 95;

13 TCKEYFPTTLADYVSSGFSNIPILKOSTIPVSDAQFVLYELNKGXSKXTALIDV 72
10 TSSSYGVFISNLRKALPBERKLYDIPILR-SLPGS--QRYALHILNADETISVALIDV 66
73 TNYVYVQAGDQSYFLSDA-PRGAETHLFTGTXSLEPFYGSYXDLERYAGH-RDQIP 130
67 TNYVYVQAGDQSYFLSDA-PRGAETHLFTGTXSLEPFYGSYXDLERYAGH-RDQIP 126
131 LGIXOLQSYVXALXPGSGSTXQASSTILLIOMISAAENPILMRKXINSCKSEFLPD 190
127 LGIPALDSAITTLFTYNNNS--ASALMWLIQSTSEARKEFLEQJGKRVK--TFLPS 182
191 XYMLELSTMGQSTQVQ--HSTQVFNPNPKALIXGNFVILNXYKX--VIASIAIML 245
183 LAIISLNSMSALSNOIQAISTNOCFESPVVILNNOQVATITVDAVTSNIALIL 241

RESULT 12
US-10-280-679B-4
Sequence 4, Application US/10280679B
Publication No. US20030150019A1
GENERAL INFORMATION:
APPLICANT: Biogen Inc.
TITLE OF INVENTION: Monoclonal Antibody Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 172
CORRESPONDENCE ADDRESS:
ADDRESSER: Biogen Inc.
STREET: 1400 Massachusetts Avenue, 14th floor

Thu Dec 11 16:09:42 2003

us-09-601-667c-1.rapb

```
/ CURRENT FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: 09/557,941
/ PRIOR FILING DATE: 2000-04-24
/ PRIOR APPLICATION NUMBER: 08/484,341
/ PRIOR FILING DATE: 1995-06-07/923,692
/ PRIOR APPLICATION NUMBER: 07/737,899
/ PRIOR FILING DATE: 1991-01-16
/ PRIOR APPLICATION NUMBER: 07/641,617
/ PRIOR FILING DATE: 1991-07-26
/ PRIOR APPLICATION NUMBER: 07/737,899
/ PRIOR FILING DATE: 1991-08-01
/ PRIOR APPLICATION NUMBER: 07/310,881
/ PRIOR FILING DATE: 1989-02-17/160,766
/ PRIOR APPLICATION NUMBER: 07/160,766
/ PRIOR FILING DATE: 1988-02-26
/ PRIOR APPLICATION NUMBER: 07/160,771
/ REMAINING PRIOR APPLICATION DATA REMOVED - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO: 4
/ TYPE: PRT
/ LENGTH: 289
/ ORGANISM: Chinese cucumber protein alpha-trichosanthin
US-10-280-679E-4

Query Match
Best Local Similarity 34.3%; Score 301.5; DB 12; Length 289;
Matches 82; Conservative 48; Mismatches 96; Indels 13; Gaps 8;

Cy 13 TCEYFFPTILRDYSSGSSFSNIPILRQSTIPSDQSFVYVLTNQGKXSTALDY 72
Db 33 TSSSYGFISMLRKALPNERKYDIPILR-SELPGS--QVYALHITNVADETISVALDY 89

Cy 73 TXYVYAYQADQOSYTLDA-PRGATLFTGTXXSLPEFYGSYXDLERYAGH-RDQIP 130
Db 90 TNYVWGTIRASRTIFENASATEKATVFKDAKRVTLPEISNTERLQDAGKRENIIP 149

Cy 131 ICHYGLQSYVYALRXRGSTRKQASLILITOMISARRPILMRKXQINSQSPED 190
Db 150 LGLPLDASITLTFYNNMS--RASAALWLIQSTEARAKFKFBOQIGRVDK--TFIPS 205

Cy 191 XYWLALSTWQSGSTQVQ--HSTDGVFNNPKXLAIXGNFVTLXVYEX--VYASLAIL 245
Db 206 IALISLNSMNSLSKQIQIQAISTNQGFETPVVILNMQQRMTVTVDAQVTSIALLL 264

RESULT 13
US-10-127-890-4
Sequence 4: Application US/10127890
Publication No. US2003016196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
SCIENTIST: McAndrews, Hald & Malloy, Ltd.
STREET: 150 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/127,890
/ FILING DATE: 12-Apr-2002
/ INVENTOR: Unknown
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/06/646,360
/ FILING DATE: 13-May-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-May-1994
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-May-1993
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-Dec-1992
/ APPLICATION NUMBER: 07/901,707
/ FILING DATE: 07/182,192
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-Nov-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70,74
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
/ MOLECULE TYPE: protein
/ TOPOLOGY: linear
/ TYPE: amino acid
/ LENGTH: 263 amino acids
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-127-890-4

Query Match
Best Local Similarity 33.1%; Score 291; DB 12; Length 263;
Matches 84; Conservative 48; Mismatches 102; Indels 20; Gaps 10;

Cy 13 TCEYFFPTILRDYSSGSSFSNIPILRQSTIPSDQSFVYVLTNQGKXSTALDY 72
Db 10 TXYVYAYQADQOSYTLDA-PRGATLFTGTXXSLPEFYGSYXDLERYAGH-RDQIP 130

Cy 70 ICHYGLQSYVYALRXRGSTRKQASLILITOMISARRPILMRKXQINSQSPED 190
Db 64 ICHYGLQSYVYALRXRGSTRKQASLILITOMISARRPILMRKXQINSQSPED 190

Cy 128 QIPGLQSYVYALRXRGSTRKQASLILITOMISARRPILMRKXQINSQSPED 190
Db 122 NIDGLQSYVYALRXRGSTRKQASLILITOMISARRPILMRKXQINSQSPED 190

Cy 138 LFDYVLELSTWQSGSTQVQ--HSTDGVFNNPKXLAIXGNFVTLXVYEX--VYASLAIL 245
Db 178 LFDYVLELSTWQSGSTQVQ--HSTDGVFNNPKXLAIXGNFVTLXVYEX--VYASLAIL 245

Cy 246 FYCGERPSSSPVAY 259
Db 238 IL-NSRASPADENF 250

RESULT 14
US-10-127-890-111
Sequence 4: Application US/10127890
Publication No. US2003016196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
SCIENTIST: McAndrews, Hald & Malloy, Ltd.
STREET: 150 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

Thu Dec 11 16:09:42 2003

US-09-601-667c-1.rapb

STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
SEQ ID: 1
TITLE: PCT/US94/05348
OPERATING SYSTEM: PC/DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/06/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: 12-MAY-1994
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/986,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
ADDRESS: 200-70, P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-127-890-111
Query Match 10.7%; Score 281; DB 12; Length 251;
Best Local Similarity 33.7%; Pred. No. 1,2e-22;
Matches 85; Conservative 34; Mismatches 113; Indels 20; Gaps 7;
QY 8 VTHQTKXEFYFILLRDY--VSSGSENEIFLLROSTIPVSDAQRVLYELINQGXG 64
DB 5 VSFSGCATYIYVNLMLRVLKPKGNSHILPKKADDPKKA--FVLVALSNDGQ 62
QY 65 SYTAALIVTNKVVYVQAQDQSYFLPAPGAEZTLFTGTRXSLPFKGSYDLERYAG 124
DB 125 HRPQPLGIXOL--IGSVAXALXPGSGTRXQASILLITOMISEARF---NPLIRX 177
QY 125 HRPQPLGIXOL--IGSVAXALXPGSGTRXQASILLITOMISEARF---NPLIRX 177
DB 122 YRETTDGIETPLRIGIKLDENAIQNTKPTBIASLSLVQWVSEARFTPIENQIRNP 181
QY 178 ROKINSKSLPDXVWLELFTSWQSQSTVQV--TGVFNNPRLAIXGNFTLXNRX 236
DB 192 QQRK-----PANNTISLENKGLSPQIRTSANGWFSVALELRANGKKYVAVDQ 235
QY 237 VHSALIMFVC 248
DB 236 VKKIALIKFVC 247

RESULT 15
US-09-792-793A-34
Sequence 34, Application US/09792793A
Patent No. US20020168370A1

GENERAL INFORMATION:
APPLICANT: BIONOLA, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DANA
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO: 347
TYPE: PRT
ORGANISM: Bionola diolca
US-09-792-793A-34
Query Match 10.7%; Score 280; DB 10; Length 247;
Best Local Similarity 32.0%; Pred. No. 1.5e-22;
Matches 79; Conservative 52; Mismatches 98; Indels 18; Gaps 9;
QY 7 RVTHTQTKXEFYFILLRDYVSSGSENEIFLLROSTIPVSDAQRVLYELINQGXG 66
DB 5 RUSGATF--TSYGVFLNRLALPEKRYNIFLRS--ISGGRYTLHLNVADEIT 60
QY 67 THAIDTNKVVYVQAQDQSYFLPAPGAEZTLFTGTRXSLPFKGSYDLERYAG 125
DB 61 SYAVDTNVLIMGLADQVTFPBAKSTBAKVFEDAKKQYLYSONERLQZAK 120
QY 126 -RQIPPLGIXOLIGSVAXALXPGSGTRXQASILLITOMISEARFPILEXROXINS 184
DB 121 IRENIFPLGIPALDSITTLVYVYTS--AASALVLLOSTASARKEFEQIGKVDK- 177
QY 185 XSLPLDXVWLELFTSWQSQSTVQ--HSTDGVNNPRLAIXGN---FVLNVRXVI 238
DB 178 -TFPSLATISLNNMALSNOIQLASTNQPESF--VLLDNRQKRVSTNARSVVT 234
QY 239 ASIALIMFVC 245
DB 235 SWIALIL 241

Search completed: December 11, 2003, 14:48:46
Job time : 35.348 secs

Thu Dec 11 16:09:42 2003

US-09-601-667C-1.rat

Page 1

GenCode version 5.1.6
Copyright (c) 1995 - 2003 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 18.4536 Seconds
(without alignments)

1222.073 Million cell updates/sec

Title: US-09-601-667C-1

Sequence: 1 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 533

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: /csm2_6/prodata/1/iaa/5A.COMB.pep.*
2: /csm2_6/prodata/1/iaa/5B.COMB.pep.*
3: /csm2_6/prodata/1/iaa/5C.COMB.pep.*
4: /csm2_6/prodata/1/iaa/5D.COMB.pep.*
5: /csm2_6/prodata/1/iaa/5E.COMB.pep.*
6: /csm2_6/prodata/1/iaa/5F.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2505	95.8	564	3	US-08-776-059-35
2	1267.5	48.5	263	3	US-08-776-059-43
3	1267.5	48.5	264	3	US-08-776-059-33
4	1155.5	44.2	253	3	US-08-776-059-31
5	1108.5	42.4	340	1	US-08-378-781A-77
6	1107.5	42.4	335	1	US-08-778-789-33
7	1073.5	42.6	351	4	US-08-538-873-33
8	454.5	17.4	250	1	US-08-378-781A-71
9	447	17.1	250	1	US-08-485-786-71
10	447	17.1	250	1	US-08-356-786-10
11	404.5	15.5	534	2	US-08-356-786-10
12	377.5	14.4	267	1	US-07-990-430-16
13	377.5	14.4	267	1	US-07-990-430-16
14	377.5	14.4	267	1	US-08-218-332-16
15	377.5	14.4	267	1	US-08-483-313-16
16	377.5	14.4	267	1	US-08-483-313-16
17	377.5	14.4	267	1	US-08-477-484-1
18	377.5	14.4	267	2	US-08-646-360-1
19	377.5	14.4	267	2	US-08-318-793D-61
20	377.5	14.4	267	2	US-08-839-765-1
21	377.5	14.4	267	3	US-09-136-389-1
22	377.5	14.4	267	4	US-09-610-838-1
23	377.5	14.4	267	4	US-09-538-873-1
24	377.5	14.4	267	5	PC1-US92-09487-1
25	377.5	14.4	268	2	US-08-356-786-8
26	377.5	14.4	268	2	US-08-356-786-8
27	373.5	14.3	290	1	US-08-485-286-27

28	373.5	14.3	280	6	5248606-4
29	373.5	12.3	252	1	US-08-378-781A-74
30	373.5	11.8	267	1	US-08-488-286-74
31	306.5	11.7	247	1	US-08-477-484B-6
32	306.5	11.7	247	1	US-08-477-484B-6
33	306.5	11.7	247	1	US-08-477-484B-6
34	306.5	11.7	247	1	US-08-477-484B-6
35	306.5	11.7	247	3	US-08-635-765-6
36	306.5	11.7	247	3	US-08-136-389-6
37	306.5	11.7	247	4	US-07-923-838-6
38	306.5	11.7	247	4	US-07-923-838-6
39	301.5	11.5	289	1	US-08-184-237-4
40	301.5	11.5	289	2	US-08-482-820-4
41	301.5	11.5	289	3	US-08-483-341-4
42	301.5	11.5	289	3	US-08-483-502-4
43	301.5	11.5	289	4	US-09-726-651A-4
44	291	11.1	263	1	US-07-901-707-4
45	291	11.1	263	1	US-07-988-430-4

ALIGNMENTS

Result 1
US-08-776-059-35
Sequence 35, Application US/0876059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: ECK, Axel
APPLICANT: ECK, Peter
TITLE: OXIDATION OF A PROTEIN
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776,059B
CURRENT FILING DATE: 1999-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 9510949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 36
SEQUENCE OF SEQ ID NOS: 2.0
LENGTH: 564
TYPE: PRT
ORGANISM: Viscum album

Query Match 95.8% Score 2505, DB 3, Length 564;
Best Local Similarity 91.9% Pred. No. 8.1e-274;
Matches 489; Conservative 2; Identical 39; Gaps 2;

1 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
2 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
3 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
4 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
5 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
6 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
7 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
8 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
9 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
10 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
11 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
12 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
13 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
14 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
15 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
16 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
17 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
18 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
19 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
20 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
21 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
22 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
23 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
24 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
25 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
26 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
27 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
28 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
29 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
30 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
31 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
32 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
33 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
34 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
35 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
36 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
37 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
38 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
39 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
40 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
41 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
42 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
43 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
44 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60
45 YERLALRYHOTGKXKXFR.....RLIIYPAQKPNQMLPVX 60

Thu Dec 11 16:09:42 2003

us-09-601-667c-1.rai

Page 2

Db 333 GAGCIGLQAMPSKSNNDPPQGLMTT KNDGRTIRSGSCLTGYTGTVGVYVIEDCNTHREXTLM 392

Qy 361 QIQMGKGTILNPSMLVAAASGSGKFTLYQGLDTVQGMKANDPPEEVTIYGRDL 420

Db 393 QIQMGKGTILNPSMLVAAASGSGKFTLYQGLDTVQGMKANDPPEEVTIYGRDL 450

Qy 421 QMSKSGSVWVSTCKSGSQANQXXMALVYDGSIRFQNMOCCLTKSGLDSTVINAVSCSX 480

Db 453 QMSKSGSVWVSTCKSGSQANQ-RMALVYDGSIRFQNMOCCLTKGSDVSEVINAVSCSA 510

Qy 481 XSXXQRAVFNFXKALINLQXXXQXXDVADNPKLRRIIYPAATGPKNQMLPV 532

Db 512 GSSGGRWVFPMNGALINLKNGLAMVDVADNPKLRRIIYPAATGPKNQMLPV 563

RESULT 2: 25-059-43
 US-08-776-059-43
 ? Sequence 43, Application US/08776059B
 ? Patent No. 6271368
 GENERAL INFORMATION:
 APPLICANT: LENTZEN, Hans
 APPLICANT: ECK, Jürgen
 APPLICANT: HILGER, Holger
 APPLICANT: ZIMM, Jörgen
 TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
 FILE REFERENCE: 674503-2003
 CURRENT APPLICATION NUMBER: US/08/776, 059B
 CURRENT FILING DATE: 1999-06-19
 EARLIER APPLICATION NUMBER: PCT/E96/02273
 EARLIER FILING DATE: 1996-06-25
 EARLIER APPLICATION NUMBER: 95109949.8
 EARLIER FILING DATE: 1995-06-25
 NUMBER OF SEQ ID NOS: 56
 SEQ ID NOS: 1-56
 SEQ ID NOS: 4, Patent in Ver. 2.0
 LENGTH: 263
 TYPE: PRT
 ORGANISM: Viscum album
 US-08-776-059-43

	Query Match	Similarity	48.5%	Score 1267.5	DB 3	Length 263
	Best Local	Similarity	91.6%	Pred. No. 1.2e-114		
	Matches	270	Conservative	1	Mismatches 20	Indels 1
					Gaps 1	
QY	210	DVDTCSAEEPTPIYVSKXKNDVDRDDDFDQNOIOLMFSKNSNDNOLMTIRDDTTS	325			
Ds	1	DDTSSSESTPIYVSKXKNDVDRDDDFDQNOIOLMFSKNSNDNOLMTIRDDTTS	60			
QY	330	NSGSCLTGTGTGTVGVWVWIPDCNAVEATITWQWNGTITNRSNVLVAASISGIGTTL	385			
Ds	61	NSGSCLTGTGTGTVGVWVWIPDCNAVEATITWQWNGTITNRSNVLVAASISGIGTTL	120			
QY	330	VQRTLVYTLGGCMALNDVTAPEVTVYGFRLCMESNGSGVWELTCSQNGV	445			
Ds	121	VQRTLVYTLGGCMALNDVTAPEVTVYGFRLCMESNGSGVWELTCSQNGV	172			
QY	450	GSTRPROMQDCLXGSDVSEVYVNVVSCSXSKXQWVFTNEKALIMLKKXXKXDVQAQ	505			
Ds	180	GSTRPROMQDCLXGSDVSEVYVNVVSCSXSKXQWVFTNEKALIMLKKXXKXDVQAQ	235			
QY	510	NPKLRRIITIPATKPKMCMVTV 532				
Ds	240	NPKLRRIITIPATKPKMCMVTV 262				

```

RESULT 3
US-08-776-059-33
; Sequence 33. Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
; APPLICANT: LENTZEN, Hans
; APPLICANT: ECK, Jürgen

```

Applicant:	BAUR, Axel
Inventor:	ZINK, Holger
Title of Invention:	RECOMBINANT MISTOLENE LECTIN (RML)
File Reference:	674503-2003
Current Application Number:	US/08/776,0598
Publication Number:	US/2004/0126003A1
Earlier Application Number:	PCT/EP96/02273
Earlier Filing Date:	1996-06-25
Earlier Application Number:	95109945-8
Earlier Filing Date:	1995-06-26
Number of Seq ID NOS:	56
Software:	PatentIn Ver. 2.0
Seq ID No:	324
Type:	PIRT
Organism:	Vibrium alburn
US-08-776-059-33	
Query Match	48.5%; Score 1267.5; DB 3; Length 264;
Best Local Similarity	91.6%; Freq. No. 1.2e-134; Indels 1; Gaps 1
Matches 241:	Conservative 1; Mismatches 20; Indels 1; Gaps 1
D1	2 DVTGSAASPTVTRVGRMGCVDRVDDPRDQIQIQLMPKSKNNPQGLATIKRQDITRS 61
D2	330 NSSCLTYVYAGVYVMI.FPCVTAIVRATVQIWMVGTIINRSNLVLAASSGIKOTLT 389
D3	62 NSSCLTITITAGVYKMFECVTAIVRATVQIWMVGTIINRSNLVLAASSGIKOTLT 121
D4	390 VQIDLTLDGGMALNGMDA.PEAVTYGPDLCIENSMKSVYEWECSSQXQXWMLAVD 449
D5	122 VQIDLTLDGGMALNGMDA.PEAVTYGPDLCIENSMKSVYEWECVSSQKQK.RMLAYGD 180
D6	450 GSIRPNNDQCLTKGRDYSVTVINIVSCSXSSXQWRVTFVEAALINIKXXXXVDVQA 509
D7	181 GSIRPNNDQCLTKGRDYSVTVINIVSCSXSSQWRVTFVEAALINIKXXXXVDVQA 246
D8	510 NPELARIITVPAKSGKNOMLEPV 532
D9	241 NPELARIITVPAKSGKNOMLEPV 263

RESULT 4
US-08-776-059-31
Sequence 31, Application US/08776059E
GENERAL INFORMATION:
APPLICANT: LEWTEEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: ZINKE, Axel
APPLICANT: BAHR, Holger
TITLE OF INVENTION: SECRETINANT MISTLETOE LETTIN (PML)
FILE REFERENCE: CY 0802003
CURRENT APPLICATION NUMBER: US/08/776,059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/32273
EARLIER FILING DATE: 1996-06-25
EARLIER PUBLICATION NUMBER: 2409949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 253
ORGANISM: Vicia cum album
US-08-776-059-31

```

Query Match      44.2%; Score 1155.5; DB 3; Length 253;
Best Local Similarity 91.7%;
                    Pred. No. 4,96-1224;
Matches 232; Conservative 19; Indels 1; Gaps 1

```

Db 2 YERIKLVHTGTEGFEFTLLADYVSSGSFSENIPLRQSTIPVSDQRFLVETLM 61
QY 61 QGKSKTALIDVTNXYVVAQAGDSYFLADAPGAEHTLFTGTXXSLFPKGSYDLE 120
Db 62 QGDSITRALIDVTNXYVVAQAGDSYFLADAPGAEHTLFTGTXXSLFPKGSYDLE 120
QY 131 RYAGHRDQIPGIXOLIOGYALRXPQSTKXASLIIILOMISFAPRPILNEXOX 180
Db 121 RYAGHRDQIPGIXOLIOGYALRXPQSTKXASLIIILOMISFAPRPILNEXOX 180
QY 181 INSGXSLFDXVWLBLETSWQOSTOVGSHSTGVFNNPRLAIXXGNFTLXNXXVYAS 240
Db 181 INSGXSLFDXVWLBLETSWQOSTOVGSHSTGVFNNPRLAIXXGNFTLXNXXVYAS 240
QY 241 LAMLFVCGERPS 253
Db 241 LAMLFVCGERPS 253

RESULT 5
US-08-378-761A-77
Sequence 77, Application us/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESSES:
ADDRESS: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-761A-77

Query Match 42.4%, Score 1109.5, DB 1, Length 540;
Best Local Similarity 45.2%, Field N 3.5e-185, Indels 19, Gaps 10,
Matches 242, Conservative 79, NMatches 195,
QY 9 THQTGKYEFTLLRQVSSGS-FSENIPL-RQSTIPVSDQSFVYVETLNGQDX 66
Db 13 TADAVESYTFIRAVRSHLTGADVREHIVLPKRGVLRIS-QRFLVLESNADSLV 70
QY 67 TLAIDVTNXYVVAQAGDSYFLADAPGAEHTLFTGTXXSLFPKGSYDLE 123

Db 71 TLAIDVTNXYVVAQAGDSYFLADAPGAEHTLFTGTXXSLFPKGSYDLE 130
QY 124 GHRODQIPGIXOLIOGYALRXPQSTKXASLIIILOMISFAPRPILNEXOX 180
Db 131 GRFENIEIGFLEIAISALYYSTGQIPLTASFMCIOMISAPFOYIEGMRTR 190
QY 181 INSGXSLFDXVWLBLETSWQOSTOVGSHSTGVFNNPRLAIXXGNFTLXNXXVYAS 240
Db 191 INSGXSLFDXVWLBLETSWQOSTOVGSHSTGVFNNPRLAIXXGNFTLXNXXVYAS 240
QY 241 LAMLFVCGERPS 253
Db 251 LAMLFVCGERPS 253
QY 298 FPDGNOIOLMPEKSNPNQMLMTIKEDXTIRNSGCLTGYTGYVYVMI FDCNFAVRA 357
Db 306 FPDGNOIOLMPEKSNPNQMLMTIKEDXTIRNSGCLTGYTGYVYVMI FDCNFAVRA 357
QY 358 TIMQVXNGTILNPSNVLAAASGIKOTLTVOTLDYTLGQGLAGNDIAPREVITYGF 417
Db 366 TIMQVXNGTILNPSNVLAAASGIKOTLTVOTLDYTLGQGLAGNDIAPREVITYGF 417
QY 418 BELQMSXGSIYVETKSGXQXNXYLVAGSGIFLQVNTVAVSQMLPTNQPFVYIVEL 425
Db 426 YGVCLOANSQVWLEDCTSEKAEQ-QWALYASGIFRQGNRCLITDANKETIVYALS 484
QY 478 CSXXSXKQVWFNEXXALINLKXXXDVQANPRLRIIYVATGKNCNMWLPV 532
Db 485 CGPSSQQRWPFNDGIIINLVNVLVYRSDPRLKQIIVHPHGNINQMLPL 539

RESULT 6
US-08-385-286-77
Sequence 77, Application US/08485286
Patent No. 5646026
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESSES:
ADDRESS: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,286
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid

Thu Dec 11 16:09:42 2003

us-09-601-667c-1.fai

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-77

Query Match 42.4%; Score 1109.5; DB 1; Length 540;
Best Local Similarity 45.2%; Pred. No. 2,56-116;
Matches 242; Conservative 79; Mismatches 195; Indels 19; Gaps 10;

QY 9 TQQTGKEFFRITLNDYVSGS-FSENIPIL-RQSTIPVSDAQRFVLVETNCGKDX 66
DB 13 TADAVESYTNFIRAVRSHITGADVHEHIVLPNRYVGLIS--QFPIIVELSNHLEISV 70
QY 67 TAAIDVTNRYVAYQAGQSYFLR-DAPRAE--THTFTGTRKSSLPFGSGYXDLERVA 123
DB 71 TAAIDVTNRYVAYQAGQSYFLR-DAPRAE--THTFTGTRKSSLPFGSGYXDLERVA 130
QY 124 GRRDQPLGIXQILGQSYAL--XPGGASTKXKASILLIIONISEAARFPIIMKXKX 180
DB 131 GRENTELGTPELEDAISALVYVSTCTQIPLTRAPFVCIQWISBAARFPIIMKXKX 190
QY 181 INSGXSLPDXMLETSNGQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQST 240
DB 191 IRYNRSRPPDSEVITLNSGWRSLAIOESNGAPASPLQDRENGSKENYVDSILPT 250
QY 241 LAIMFVCGERRSSDVAKRYLPIVAD--DTCASAPRYVYKXKMYRDRD 297
DB 251 LAIMFVCGERRSSDVAKRYLPIVAD--DTCASAPRYVYKXKMYRDRD 305
QY 298 FHDGNOIOLMPSKANDPNOITREKXITRNSGCLTGYTAQVYVIMPCNLYVEE 357
DB 306 FHDGNOIOLMPSKANDPNOITREKXITRNSGCLTGYTAQVYVIMPCNLYVEE 365
QY 358 TIWQVWNGTIIINRSNIVLAASSGIGTITVLTDTLGGWLANDPAREVITYG 417
DB 366 TFWQVWNGTIIINRSNIVLAASSGIGTITVLTDTLGGWLANDPAREVITYG 425
QY 418 RDIENESGWTWTCSSXONKXALYGGSPRONOCITGSDSYNTINYS 477
DB 426 YGWCQNSGXWLEDTSEKAEQ-QVALYADSGIHPQQRNDCLTDANIKGVVILS 484
QY 478 CSXSSXQWVFTNEKALINLKXXXXDVAKMFKRLRIIYVATGKXNQMLFV 532
DB 485 CGPSSGQWVFTNEKALINLKXXXXDVAKMFKRLRIIYVATGKXNQMLFV 539

RESULT 7
US-08-776-059-39
Sequence 39; Application US/087760598
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: BAIR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 6/4503-2003
CURRENT APPLICATION NUMBER: US/08/776-0598
CURRENT FILING DATE: 1999-06-27
EARLIER FILING DATE: 1998-06-25
EARLIER APPLICATION NUMBER: 9510949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
LENGTH: 235
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-39

Query Match 41.0%; Score 1073.5; DB 3; Length 235;
Best Local Similarity 51.9%; Pred. No. 7,86-113;

Matches 217; Conservative 0; Mismatches 18; Indels 1; Gaps 1;
QY 18 FRTITLNDYVSGS-FSENIPIL-RQSTIPVSDAQRFVLVETNCGKDXTRAIDVTNRY 77
DB 1 FRTITLNDYVSGS-FSENIPIL-RQSTIPVSDAQRFVLVETNCGKDXTRAIDVTNRY 60
QY 78 VAYQAGQSYFLR-DAPRAE--THTFTGTRKSSLPFGSGYXDLERVA 137
DB 61 VAYQAGQSYFLR-DAPRAE--THTFTGTRKSSLPFGSGYXDLERVA 119
QY 138 QSYXALRPGGASTKXKASILLIIONISEAARFPIIMKXKXGSLPEKXMLE 197
DB 120 QSYXALRPGGASTKXKASILLIIONISEAARFPIIMKXKXGSLPEKXMLE 179
QY 198 TSNQGSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQST 253
DB 180 TSNQGSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQST 235

RESULT 8
US-09-538-873-3
Sequence 3; Application US/09538873
Patent No. 6565500
GENERAL INFORMATION:
APPLICANT: CHITZ, VICTOR F.
APPLICANT: CHITZ, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
FILE REFERENCE: US/09/538,873
CURRENT APPLICATION NUMBER: US/09/538,873
CURRENT FILING DATE: 2000-03-30
EARLIER FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: 60/126,926
EARLIER FILING DATE: 1999-03-30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 251
TYPE: PRT
ORGANISM: Atrus pectorius
US-09-538-873-3

Query Match 17.4%; Score 454.5; DB 4; Length 251;
Best Local Similarity 41.7%; Pred. No. 6,4e-43; Indels 25; Gaps 6;
Matches 105; Conservative 34; Mismatches 88;

QY 9 TQQTGKEFFRITLNDYVSGS-FSENIPIL-RQSTIPVSDAQRFVLVETNCGKDXTRA 68
DB 9 TQQTGKEFFRITLNDYVSGS-FSENIPIL-RQSTIPVSDAQRFVLVETNCGKDXTRA 66
QY 69 AIDVTNRYVAYQAGQSYFLR-DAPRAE--THTFTGTRKSSLPFGSGYXDLERVA 127
DB 67 AIDVTNRYVAYQAGQSYFLR-DAPRAE--THTFTGTRKSSLPFGSGYXDLERVA 125
QY 128 QPPLGIXQILGQSYAL--XPGGASTKXKASILLIIONISEAARFPIIMKXKXGSP 187
DB 126 QPPLGIXQILGQSYAL--XPGGASTKXKASILLIIONISEAARFPIIMKXKXGSP 185
QY 188 LDDXMLETSNGQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQST 236
DB 186 LDDXMLETSNGQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQSTQVQST 235
QY 237 VIANSALMFPVC 248
DB 236 VIANSALMFPVC 247

RESULT 9
US-08-378-761A-71
Sequence 71; Application US/08378761A
Patent No. 633934
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: BAIR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 6/4503-2003
CURRENT APPLICATION NUMBER: US/08/378-761A
CURRENT FILING DATE: 1999-06-27
EARLIER FILING DATE: 1998-06-25
EARLIER APPLICATION NUMBER: 9510949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 71
LENGTH: 235
TYPE: PRT
ORGANISM: Viscum album
US-08-378-761A-71

Thu Dec 11 16:09:42 2003

us-09-601-667c-1.xai

Page 5

APPLICANT: WALSH, TERENCE A
 APPLICANT: HEY, TIMOTHY D
 TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
 TITLE OF INVENTION: RIBOSOME FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSER: ANDREA T. BOWUCKI
 STREET: 9330 ZIONSVILLE ROAD
 CITY: INDIANAPOLIS
 STATE: IN
 COUNTRY: US
 ZIP: 46268
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CORRESPONDENCE ADDRESS:
 APPLICATION NUMBER: US/08-378,761A
 FILING DATE: 26-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BOWUCKI, ANDREA T
 REGISTRATION NUMBER: 33651
 REFERENCE/DOCKET NUMBER: 382728
 TELEPHONE: (317) 337-4846
 INFORMATION FOR SEQ. ID NO.: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-378-761A-71

Query Match 11.1%; Score 447; DB 1; Length 250;
 Best Local Similarity 41.7%; Pred. No. 4,55-42;
 Matches 105; Conservative 34; Mismatches 87; Indels 26; Gaps 7;

Db 9 THGTYGKYEPRFTLLADVYSSGSFNEPLPLRQSTPIPVSDAQRFLVETLNQKDSYTA 68
 9 IENATIGSTGKQIFALNREK-RGGLNHLDPVDF-TLQERNKIVTALSPTSIEV 66
 Oy AIDMYNNVYVAQAGQSGYFLPAPRAGAEHLFTGTKASLPFGYSYDLERYARH-RD 127
 Db 67 GLIVNMYVVAARAGTQSGYFLPAPRASSASDPYLFGTDO-HSLPFGYGLERNAHQSKQ 125
 Oy 128 QHILGKQLQSGVYALRFGSGSTKQKARSILILQIMISEAFARFNLMRKQKINSKSP 187
 Db 126 QHILGKQLQSGVYALRFGSGSTKQKARSILILQIMISEAFARFNLMRKQKINSKSP 185
 Oy 188 ILEPYHMETLETFNQGQSGTQVGHSTGCVNNPYRLALIXGNGFVLIANYKX----- 236
 Db 186 QPAPAMSLSENMM-DMLRQVQESVDQTFPRQ-----VTLNIRNEPVIDSLSP 234
 Oy 237 VIASLAIMFLVC 248
 Db 235 TVALVLAFLVC 246

RESULT 10
 US-08-485-286-71
 ; Sequence 71, Application US/08485286
 ; Patent No. 2846026 564119
 ; GENERAL INFORMATION:
 ; APPLICANT: WALSH, TERENCE A
 ; APPLICANT: HEY, TIMOTHY D
 ; APPLICANT: MORGAN, ALICE ER
 ; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

APPLICANT: WALSH, TERENCE A
 APPLICANT: HEY, TIMOTHY D
 TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
 TITLE OF INVENTION: PROTEIN-SOURCE FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ANDREA T. BOWUCKI
 STREET: 9330 ZIONSVILLE ROAD
 CITY: INDIANAPOLIS
 STATE: IN
 COUNTRY: US
 ZIP: 46268
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CORRESPONDENCE NUMBER: US/08/378,761A
 FILING DATE: 26-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BOWUCKI, ANDREA T
 REGISTRATION NUMBER: 33651
 REFERENCE/DOCKET NUMBER: 382728
 TELEPHONE: (317) 337-4846
 INFORMATION FOR SEQ. ID NO.: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-378-761A-71

Query Match 11.1%; Score 447; DB 1; Length 250;
 Best Local Similarity 41.7%; Pred. No. 4,55-42;
 Matches 105; Conservative 34; Mismatches 87; Indels 26; Gaps 7;

Db 9 THQGTGYEYRFTLLADVYSSGSFNEPLRLQSTPIPVSDAQRFLVETLNQKDSYTA 68
 9 TEGATSGSTQKQIFALNREK-RGGLHDLVLPDPT-TLQERNKIVTALSPTSIEV 66
 Oy AIDPNKYYVVAQAGQSGYFLPAPRAGAEHLFTGTKASLPFGYSYDLERYARH-RD 127
 Db 67 GLIVNAYVVAARAGTQSGYFLPAPRASSASDPYLFGTDO-HSLPFGYGLERNAHQSKQ 125
 Oy 128 QHILGKQLQSGVAFLEKFGSGSTKQKARSILILQIMISEAFARFLIMKROKINSKSP 187
 Db 126 QHILGKQLQSGVAFLEKFGSGSTKQKARSILILQIMISEAFARFLIMKROKINSKSP 185
 Oy 188 LPEYHMETLETFNQGQSGTQVGHSTGCVFNPPYRLALIXGNGFTLIANYKX----- 236
 Db 186 QPAPAMSLSENNM-DNLKQVQESVDQTFPRQ-----VTLNIRNEPVIDSLSP 234
 Oy 237 VIASLAIMFLVC 248
 Db 235 TVALVLAFLVC 246

RESULT 10
 US-08-485-286-71
 ; Sequence 71, Application US/08485286
 ; Patent No. 2846026 564119
 ; GENERAL INFORMATION:
 ; APPLICANT: WALSH, TERENCE A
 ; APPLICANT: HEY, TIMOTHY D
 ; APPLICANT: MORGAN, ALICE ER
 ; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pletcher, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pletcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 336
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-10

Query Match 15.5%; Score 404.5; DB 2; Length 534;
Best Local Similarity 27.8%; Pred. No. 9.1e-37;
Matches 142; Conservative 76; Mismatches 170; Indels 123; Gaps 22;
DB 9 THQTTGAEYFRFTLLDNYVSSGS-FSNEIFLL-RGSTIVSDAQRVYVETLNGKDXK 66
16 TGAATVQSYTNFIRAVRGRLITGADVREHLPVLRVGLPIN-QRFLVLSNNAELSY 73
QY 67 TAAIDVNNKYVAVYAGDQSYFLR-DAPRGAE--THFTGTRKSSLPFGSYXDLERYA 123
DB 74 TLADVTNAYVVGPRAGNSAVFHPHNDQDEALTHLFTDVONRYTAPAGVNDLRLQA 133
QY 124 GH-RDQIFLGIXQILQSYVAL--RXPQGSTKXQASILLIOWISEAARFPIIMEXRQ 179
DB 134 GMLRENTILNGPLEEALISALVYVSGTQPLTLARSFICIMISEARFQYIEGERT 193
QY 180 XINSGASFLPDXYMLETSNGQSGTQVQSTQVFNNEPRLAIXXNFVTLNTRXYIA 239
DB 194 RIRNRSAPDPSPVITLNSWGRSLTAIQSNQAFASPIQLQRNGSKFVYDVSLILP 250
QY 240 SLAINLFCVCGEPSSSDVRWMPVTPRYIADVTCASBPYRIVGKXQAVYVDRDDDF 299
DB 254 IIALWYRCAPPESSQ--FSLLRPVVPFNADVCMDEDEQLV-----Q 295
QY 300 DSNQIQMPSKSNNDPNQMLTKRDXITISNGSLTYG-----Y 339
DB 296 SGEFLK-----KFGS--TVK--ISCAASGTPANIGMMKAPGGLKMGKINVT 343
QY 340 TR-CYV-----MFDCAINRENT-----MOTKNGTILNPK 372
DB 344 TGGSTYADDPKREPAISLETATHTQHINNLNHSASATFCARRFGFAYGQCLTVS 403
QY 373 SNLVAAASGIGTTLVQTLVYTLQGLAGNDTPREVTIYGRFLCMESXNGSWAVE 432
DB 404 ASI--SSSGGGGS-----GGGSGGG-----GSDIQMOSPSLSLAS 438
QY 433 -----TKSSQ--XNXXV-ALVXGDSIR 453

DB 439 LGEKVSLTCRASODIQLNLTWLSQHPDGTIX 469
RESULT 12
US-07-901-707-1
Sequence 1: Application US/07901707
Sequence 2: 575546
Sequence 3: 575546
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
Composition and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS: O'Toole, Gerstein, Murray &
ADDRESSEE: Michael J.
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 537546and, 57546 E.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: 271229/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 984-5750
TELEFAX: (312) 346-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-901-707-1
Query Match 14.4%; Score 377.5; DB 1; Length 267;
Best Local Similarity 38.8%; Pred. No. 3.4e-34;
Matches 99; Conservative 41; Mismatches 104; Indels 11; Gaps 7;
DB 9 THQTTGAEYFRFTLLDNYVSSGS-FSNEIFLL-RGSTIVSDAQRVYVETLNGKDXK 66
13 TGAATVQSYTNFIRAVRGRLITGADVREHLPVLRVGLPIN-QRFLVLSNNAELSY 70
QY 67 TAAIDVNNKYVAVYAGDQSYFLR-DAPRGAE--THFTGTRKSSLPFGSYXDLERYA 123
DB 72 TLADVTNAYVVGPRAGNSAVFHPHNDQDEALTHLFTDVONRYTAPAGVNDLRLQA 130
QY 124 GH-RDQIFLGIXQILQSYVAL--RXPQGSTKXQASILLIOWISEAARFPIIMEXRQ 179
DB 131 GMLRENTILNGPLEEALISALVYVSGTQPLTLARSFICIMISEARFQYIEGERT 190
QY 180 XINSGASFLPDXYMLETSNGQSGTQVQSTQVFNNEPRLAIXXNFVTLNTRXYIA 239
DB 191 RIRNRSAPDPSPVITLNSWGRSLTAIQSNQAFASPIQLQRNGSKFVYDVSLILP 250
QY 240 SLAINLFCVCGEPSS 254

Thu Dec 11 16:09:42 2003

us-09-601-667c-1.fai

Page 7

Db 251 IIALMYRCAPPSS 265

```

RESULT 13
US-07-988-430-1
Sequence 1: Application US/07988430
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
      Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS: C/Toole, Gerstein, Murray &
      ADDRESSES: Bicknell
      ADDRESS: Two First National Plaza, 20 South Clark
      CITY: Chicago
      STATE: Illinois
      COUNTRY: USA
      ZIP: 60603
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19920819
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and Greeta B.
REGISTRATION NUMBER: 35302
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-988-430-1
Query Match
Best Local Similarity 14.4%; Score 377.5; DB 1; Length 267;
Matches 99; Conservative 41; Mismatches 104; Indels 11; Gaps 7;
```

```

QY 180 XINSGKSLPDYXMLETSNGCOASTQVSTDSYFNNKRLAIXGNFYTLKXRVIA 239
DB 191 RIRYNBRADPSVYTLNLSNGLSTALQSNQCFASIDQNRNSKRSYVIDSILIP 250
QY 240 SHAIMLFVCGERPSS 254
DB 251 IIALMYRCAPPSS 265
```

```

RESULT 14
US-08-218-303-16
Sequence 16: Application US/08218303
GENERAL INFORMATION:
APPLICANT: Kara, Bhupendra V.
APPLICANT: Hockney, Robert C.
APPLICANT: Pilton, John E.
TITLE OF INVENTION: FERMENTATION PROCESS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
      ADDRESSES: Cushman, Dardy & Cushman
      ADDRESS: 615 D Street, N.W.
      CITY: Washington
      STATE: Washington
      COUNTRY: U.S.A.
      ZIP: 20036-5601
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,303
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/841,533
FILING DATE: 26-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kowals, Paul N.
REGISTRATION NUMBER: 16,773
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3100
TELEFAX: 6742321944
TELEX: 6212221944
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-218-303-16
Query Match
Best Local Similarity 14.4%; Score 377.5; DB 1; Length 267;
Matches 99; Conservative 41; Mismatches 104; Indels 11; Gaps 7;
```

```

QY 9 THQTKAYEYRPTLLADYVSSGS-FSNEIPL-ROSTIPVSQRFVYVLTNQGKDX 66
DB 13 TKGATVOSTYNTFRAYRGRITLGDVVRHEIPLNRYGSLPIN--QRFIVLSNHAELSV 70
QY 67 TLAIDVTXKYVAYVQAGDSYFLR-DAPRGAE--THLFTGTRXSLSPYGSYDLERYA 123
DB 71 TLLADVTNAYVGVYRANSAVFPHDQDEPAKATHLFTDVQNRVYTFAGSYDRLQLA 130
QY 124 GH-RDQIFPLGIXQLQSYVAL--EXPQGSTXQARSILILQMTSEARPNPILMXHQ 179
DB 131 GNLERNIELGNGPLEBAISALVYSTGTQOLPFLARSFILQMTSEARFPYIEGEMT 190
```

```

QY 180 XINSGKSLPDYXMLETSNGCOASTQVSTDSYFNNKRLAIXGNFYTLKXRVIA 239
QY 191 RIRYNBRADPSVYTLNLSNGLSTALQSNQCFASIDQNRNSKRSYVIDSILIP 250
DB 240 SHAIMLFVCGERPSS 254
QY 251 IIALMYRCAPPSS 265
DB 191 RIRYNBRADPSVYTLNLSNGLSTALQSNQCFASIDQNRNSKRSYVIDSILIP 250
```

Thu Dec 11 16:09:42 2003

us-09-601-667c-1.ra1

QY 240 SLAIMEFYCGERPS 254
DB 251 IIALWYRCAPPS 265

RESULT 15
US-08-425-336-1
; Sequence 1, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroli, Stephen F.
; APPLICANT: Studlika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF INVENTIONS: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; INVENTION ID NO.: 1:
; INVENTION CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-1

Query Match 14.4%; Score 377.5; DB 1; Length 267;
Best Local Similarity 38.8%; Pred.-No. 3.4e-34;
Matches 99; Conservative 41; Mismatches 104; Indels 11; Gaps 7;

QY 9 THOTKXKRFETLEADVSSG--FSNRIPI--ROSTPIYDQRPVHEITWGXDSX 66
DB 13 TAGATVQSTNFINAVRERILTGADVREHILPILNVALEPIN--GRFIVLSNHAELSV 70
QY 67 TAAIVNNXYVAYQAGDSYFLR--DAERGA--THEFTGTXSLSPEFGSYXDERA 123
DB 71 TLADVTNAVYVYRAGNSAFYFHPDNOEDALITHFTDVQRYTFAPFGYDRLQLA 130
QY 124 GH-RQIPLGIXQLQSGVAL--KRPQSTEXQASISIIILQMISEARFPIIWRXQ 179
DB 131 GNLKREITELNGPLSEHISLILYITSGTQFTLANSFTICQWISNARFPIIISGKRT 190

QY 180 XINSKXSPFDXWLEETWQGOCTVOHSTQVFNKRLAIKXGFTYIANKXVIA 239
DB 191 RIKYRNKADPSTVITLNSWKRSLTAIOESNGAFSPIDLRNNSKRSYIVVSLIP 250
QY 240 SLAIMEFYCGERPS 254
DB 251 IIALWYRCAPPS 265

Search completed: December 11, 2003, 14:11:30
Job time : 19.4536 secs

Fri Dec 11 16:09:50 2003

us-09-601-667c-3.rpr

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:19 / Search time 8.20622 seconds
(without alignment)

3093.817 Million cell updates/sec

Title: US-09-601-667c-3

Sequence: 1 DDVTCASBPVTRIVGXKM.....RRIIVPATGKPNQWMLPVX 264

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96166622 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1
2: p1r2
3: p1r3
4: p1r4

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1290	97.2	264	2	PD0019	mistletoe lectin I
2	1279.5	96.4	265	2	JM0090	lectin-I B chain -
3	849.5	64.0	576	1	RLCSD	ricin B precursor
4	822	61.9	263	2	S06330	ricin E - catalor b
5	726.5	54.7	564	1	RLCAG	agglutinin precursor
6	717	54.0	528	1	RLCSA	agglutinin precursor
7	703	53.0	562	2	S16022	abrin-a precursor
8	702	52.9	562	2	S16022	abrin-b precursor
9	702	52.9	562	2	S16022	abrin-d precursor
10	492	37.4	328	2	S24334	agglutinin I, pectin
11	125.5	9.5	377	2	UC7834	endo-beta-1,2-xylosylase
12	118.5	8.9	477	1	US0588	endo-beta-1,2-xylosylase A - Strip
13	115.5	8.7	383	2	T34603	protease RPI - R
14	104	7.8	525	2	A45053	glucanase A - Strip
15	101	7.6	548	2	A39094	protease RPI - R
16	93.5	7.0	475	2	T35697	arabinofuranosidase
17	88.5	6.7	451	2	T34988	probable lipoprotein
18	86.5	6.5	1067	2	T28653	hypothetical prote
19	85.5	6.4	1067	2	T28653	hypothetical prote
20	85	6.4	464	2	AB1866	WP-40 repeat prote
21	84.5	6.4	464	2	T35943	probable hydrolytic
22	84.5	6.4	464	2	T35943	probable hydrolytic
23	82	6.2	1711	2	AB1823	hypothetical prote
24	81.5	6.1	160	2	UC7822	hypothetical prote
25	79.5	6.0	1693	2	S76086	beta transglutinin
26	79	6.0	295	2	H83452	probable short-chain
27	79	6.0	61	2	S49901	coat protein gp1 -
28	79	6.0	875	2	I40862	iota toxin compone
29	78.5	5.9	229	2	C43330	gene 7 protein - p

30	78.5	5.9	231	2	E90810	flagellar biosynth
31	78.5	5.9	231	2	A86670	hypothetical prote
32	78.5	5.9	542	2	A49114	protein-tyrosine k
33	78.5	5.9	1683	2	AF2071	MD-40 repeat prote
34	78	5.9	563	2	A88515	polypeptide N-acet
35	78	5.9	612	2	T42243	probable polypepti
36	77.5	5.8	231	2	H64850	flagellar hook for
37	77.5	5.8	386	2	AB1996	hypothetical prote
38	77.5	5.8	386	2	AB1996	hypothetical prote
39	77.5	5.7	197	2	S23242	hypothetical prote
40	76	5.7	2214	1	A48548	surface-layer glyc
41	75.5	5.7	593	2	S16225	endo-1,4-beta-xyla
42	75.5	5.7	1231	1	A48490	DIP2 protein - yea
43	75.5	5.7	943	2	S59317	hypothetical prote
44	75	5.7	1197	2	D82696	
45	75	5.7				

ALIGNMENTS

RESULT 1
PD0019
mistletoe lectin I B chain - Viscum album (fragment)
C/Species: Viscum album
C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
C/Accession: PD0019
R/Beschreibung, S./Klausenpaar, R./Mikhailov, A./Stoeva, S./Betz, C./Voelter, Blochem. Biophys. Res. Commun. 247, 367-372, 1998
A/File: Primary structure and molecular modeling of mistletoe lectin I from Viscum album (PD0019).
A/Reference number: PD0019, NCBI:8908123, PMID:964213
A/Molecule: PD0019, protein
A/Residues: 1764<RSC>
C/Superfamily: ricin, rRNA N-glycosidase homology

Query Match 97.2%, Score 1290, DB 2, Length 264;
Best Local Similarity 92.4%, Pred. No. 1.9e-117;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY	1	DDVTCASBPVTRIVGXKMVDVDDPDHGNQIQMPKSNNDPNQMLTKEGXTRIS 60	
DB	1	DDVTCASBPVTRIVGXKMVDVDDPDHGNQIQMPKSNNDPNQMLTKEGXTRIS 60	
QY	61	MSGLTGYGTAAVYTWIEPCNTPYREATIMQWNTINPRSNVYAASSIGTTL 120	
DB	61	MSGLTGYGTAAVYTWIEPCNTPYREATIMQWNTINPRSNVYAASSIGTTL 120	
QY	121	VQTLDTYGQGMAGNTPAPRVITIGRDCWESNKGWYECSSGXKQXALVGD 180	
DB	121	VQTLDTYGQGMAGNTPAPRVITIGRDCWESNKGWYECSSGXKQXALVGD 180	
QY	181	GSIRPNQNDQCTYGSDSVTVINIVSCSXGXQWAFVTEATLTKXXXXVDAQ 240	
DB	181	GSIRPNQNDQCTYGSDSVTVINIVSCSXGXQWAFVTEATLTKXXXXVDAQ 240	
QY	241	NRKRPITVYATGKPNQWMLPV 263	
DB	241	NRKRPITVYATGKPNQWMLPV 263	

RESULT 2
JM0090
lectin-I B chain - European mistletoe
N/Alternate names: MLI
C/Species: Viscum album (European mistletoe)
C/Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000
C/Accession: JM0090
R/Beschreibung, S./Klausenpaar, R./Mikhailov, A./Stoeva, S./Betz, C./Voelter, Blochem. Biophys. Res. Commun. 247, 367-372, 1998
A/File: Complete amino acid sequence of the B chain of mistletoe lectin I.
A/Reference number: JM0090, NCBI:98289575, PMID:9618256
A/Accession: JM0090

A: Molecule type: protein
A: Residues: 1-265 (SOL)
C: Superfamily: ricin, rRNA N-glycosylase homology
C: Keyword: glycoprotein
F: 61, 96, 116 Binding site: carbohydrate (asn) (covalt) #status experimental

Query Match 36.4%; Score 1279.5; DB 2; Length 265;
B: Similarity 92.0%; Freq. No. 2e-116
Matches 243; Conservative 0; Miscellaneous 20; Indels 1; Gaps 1;

Qy 1 DPTQSSAPSEFVRLVGRKGMKVDVDDPDHNGQIQIQAMSKSKNDNDQWLTKEDTIPS 60
Db 1 DPTQSSAPSEFVRLVGRKGMKVDVDDPDHNGQIQIQAMSKSKNDNDQWLTKEDTIPS 60
Qy 61 NSGCLTYVGTAGVYVIMPCVTVKAEATIMQWKNSTFINRNSNLVLAASGCKGTYLT 120
Db 61 NSGCLTYVGTAGVYVIMPCVTVKAEATIMQWKNSTFINRNSNLVLAASGCKGTYLT 120
Qy 121 VQTDLYTACGATAGNPTARETITNGPDLCSNGSGSWTFCSCQGNQXWALYED 160
Db 121 VQTDLYTACGATAGNPTARETITNGPDLCSNGSGSWTFCSCQGNQXWALYED 160
Qy 161 GSIRKXNODQCLTGRSESVTVNIVTSXKXGXQWPFNEKALIMLCKXXXXVDVQA 240
Db 161 GSIRKXNODQCLTGRSESVTVNIVTSXKXGXQWPFNEKALIMLCKXXXXVDVQA 240
Qy 241 NPKLRITITVPTIGRQNM-LEP 263
Db 241 NPKLRITITVPTIGRQNM-LEP 263

RESULT 3

RLCSD
ricin D precursor - castor bean
N: Contains: rRNA N-glycosylase (EC 3.2.2.22).
C: Species: Ricinus communis (castor bean)
C: Accession: J03493 #sequence 1-137; Dec-1993 #exact change 16-Jul-1999
C: Accession: J03493 #sequence 1-137; Mar-97 #accession 1-137; Mar-97
R: Halling, K. C.; Halling, J. C.; Murray, E. E.; Jadin, B. F.; Holscher, L. L.; Weaver, R. F.
Nucleic Acids Res. 11, 8019-8033, 1985
A: Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A: Reference number: J24041; MID: 86067214; PMID: 2999712
A: Accession: J24041
A: Molecule type: DNA
A: Residues: 1-576 (HLA)
R: Cross-references: DBJ:J031179; MID: g21082; PIDN: CA26593.1; PID: g21083
R: Title: Biochem. 148, 2685-2700, 1985
R: Title: Biochem. 148, 2685-2700, 1985
A: Reference number: J24614; MID: 85179479; PMID: 3838723
A: Accession: J24614
A: Molecule type: mRNA
A: Residues: 12-75, 'D', 77-550, 'R', 552-576 (HLA)
A: Cross-references: GB: X02388; PIDN: g21077; PIDN: CA26230.1; PID: g21078
R: Yoshitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
A: Title: Isolation and sequences of peptic peptides, and the complete sequence of the c

A:Reference number: A24010
 A:Accession: A24010
 A:Molecule type: Protein
 A:Residues: 315-383, 'P8', '386-576' <AAB>
 R:Funatsu, G.; Kimura, M.; Funatsu, M.
 Agric. Biol. Chem. 43, 2221-2224, 1979
 A>Title: Primary structure of Ala chain of ricin D.
 A:Reference number: A03374
 A:Accession: A03374
 A:Molecule type: Protein
 A:Residues: 315-325, 'N'
 R:Funatsu, G.; Kimura, M.; Funatsu, M.
 Agric. Biol. Chem. 43, 2221-2224, 1979
 A:Note: this paper, one of a series, summarizes the experimental details for the de
 R:Ready, M.P.; Kim, Y.; Robertus, J.D.
 Proteins 10, 270-278, 1991
 A>Title: Site-directed mutagenesis of ricin A-chain and implications for the mechan
 A:Reference number: A48237, PMID:9152006; PMID:1891893
 A:Accession: A48237, PMID:9152006; PMID:1891893
 A:Contents: annotation: active site
 R:Kutsumi, E.; Robertus, J.D.
 A:Title: Structure of ricin B-chain at 2.5 angstroms.
 A:Reference number: A48238, PMID:9152005; PMID:1891892
 A:Accession: A48238, PMID:9152005; PMID:1891892
 A:Contents: annotation: X-ray crystallography, 2.5 angstroms
 R:Kutsumi, E.; Collins, B.O.; Robertus, J.D.
 Proteins 10, 251-259, 1991
 A>Title: Structure of ricin A-chain at 2.5 angstroms.
 A:Reference number: A48239, PMID:9152004; PMID:1891891
 A:Accession: A48239, PMID:9152004; PMID:1891891
 A:Contents: annotation: X-ray crystallography, 2.5 angstroms
 R:Kutsumi, E.; Collins, B.O.; Robertus, J.D.
 Comment: The A chain inhibits protein synthesis. It inactivates the 60S ribosomal
 into the cell of the A chain. B chains are also responsible for cell agglutination
 C:Comment: This protein is cytotoxic and very poisonous to animals.
 C:Superfamily: ricin, rRNA N-glycosidase homology
 C:Keywords: duplication; glycoprotein; glycosylase; hydrolase; lectin; RNA binding;
 F:1-36/Domains: signal sequence #status experimental <SIG>
 F:1-36-302/Product: ricin D chain A #status experimental <ACH>
 F:1-36-359/Domains: rRNA N-glycosidase homology <RNG>
 F:1-31-315/Product: ricin A chain B #status experimental <ACH>
 F:1-31-315-315/Product: ricin A chain B #status experimental <ACH>
 F:415-409-449/binding site: carbohydrate (Asn) (covalent) #status experimental
 F:115-15-223-244/binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:212/Active site: Glu #status experimental
 F:215/Active site: Arg #status predicted
 F:294-318,324-353,377-394,465-478,504-521/Disulfide bonds: #status experimental
 F:336,349,350/binding site: N-acetylglucosamine (Asp, Glu, Asn) #status experimental
 F:348-359/binding site: N-acetylglucosamine (Asp, Asn) #status experimental
 F:348,359/binding site: N-acetylglucosamine (Asp, Asn) #status experimental
 Query Match 64.0%, Score 84.9 E: DB 1: Length 576;
 Best local similarity 60.0%, Pctid 2.4e-74; T: Matches 157; Conservative 29; Mismatches 72; Indels 1;
 DB 5 CSASPTVAIVGXGKAVDVRDFDGNQGLQWMSKSNDDNDLWTKEDXRTISNQC 64
 DB 318 QNDPEPVATVGRNGLCVDVGRFRHNGALQWPCPSNDNDLTLTIRBNTISNQC 127
 DB 65 LITGVYQAVYVIMFDYQVAVREATITWIKNGTILIRSNVILAASSGIKETTLTVQL 124
 DB 378 LITGVYQAVYVIMFDYQVAVREATITWIKNGTILIRSNVILAASSGILKTLTVQL 437
 DB 125 DTLGGQVLAAGNDPAREPVITVGRDLQWENKNGSWYWRCSQXKQXWALVYGCSTI 184
 DB 438 IYVSGQWLFNTNPFVTVIGLGLGICLQNGVWYEDCCSEKQD-QWALVADGSHI 496
 DB 185 PRKQNDQCLTYGRSGVSTVNTVNSQXSWXQWYFTNEXALINLKKXXXVDYQANKEI 244
 DB 497 PQKNDQCLTSDNIRLVKWLISGASQWMPKNDQTLNLVSGVLVDRAPDPL 556
 DB 245 RRTIYVATKGRQWVAV 253
 DB 557 KQILYVATKGRQWVAV 575
 RESULT 4

RESULT 4

506330 ricin B - castor bean (fragment)
N:Contains: chain B; rRNA N-glycosidase [EC 3.2.2.22] (chain A)
C/Spectra: Ricinus communis (castor bean)
C/Dates: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Aug-1999
R/Ident: B.F. 506330, JCS381
P/Ident: B.F. 506330, JCS381
Plant Mol. Biol. 1999, 267-295, 1997
A>Title: Characterization of a cDNA encoding ricin B, a hybrid ricin-Ricinus communis agglutinin
A.Reference number: S06330
A.Accession: 506330
A.Molecule type: protein
A.Status: not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-263 <LND>
R/Anki: T Ricinus Communis
Biochim. Biophys. Acta 911, 191-200, 1997
A>Title: The complete amino acid sequence of the B-chain of ricin B isolated from small
A.Reference number: JCS381; MID:87101186; PMID:3801493
A.Accession: JCS381
A.Molecule type: protein
A.Residues: 1-69, 'PS', 72-209, 'A', 211-241, 243-250, 'V', 252-263 <AA>
A.Experimental source: seed
A.Superfamily: ricin; rRNA N-glycosidase homology
C/Ident: Ricinus communis
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
F/17-59, 60-100, 103-111, 148-181, 185-197, 200-207, 209-210, 212-213, 215-216, 218-219, 221-222, 224-225, 227-228, 230-231, 233-234, 236-237, 239-240, 242-243, 245-246, 248-249, 251-252, 254-255, 257-258, 260-261, 263-264, 266-267, 269-270, 272-273, 275-276, 278-279, 281-282, 284-285, 287-288, 290-291, 293-294, 296-297, 299-300, 302-303, 305-306, 308-309, 311-312, 314-315, 317-318, 320-321, 323-324, 326-327, 329-330, 332-333, 335-336, 338-339, 341-342, 344-345, 347-348, 350-351, 353-354, 356-357, 359-360, 362-363, 365-366, 368-369, 371-372, 374-375, 377-378, 380-381, 383-384, 386-387, 389-390, 392-393, 395-396, 398-399, 401-402, 404-405, 407-408, 410-411, 413-414, 416-417, 419-420, 422-423, 425-426, 428-429, 431-432, 434-435, 437-438, 440-441, 443-444, 446-447, 449-450, 452-453, 455-456, 458-459, 461-462, 464-465, 467-468, 470-471, 473-474, 476-477, 479-480, 482-483, 485-486, 488-489, 491-492, 494-495, 497-498, 500-501, 503-504, 506-507, 509-510, 512-513, 515-516, 518-519, 521-522, 524-525, 527-528, 530-531, 533-534, 536-537, 539-540, 542-543, 545-546, 548-549, 551-552, 554-555, 557-558, 560-561, 563-564, 566-567, 569-570, 572-573, 575-576, 578-579, 581-582, 584-585, 587-588, 590-591, 593-594, 596-597, 599-600, 602-603, 605-606, 608-609, 611-612, 614-615, 617-618, 620-621, 623-624, 626-627, 629-630, 632-633, 635-636, 638-639, 641-642, 644-645, 647-648, 650-651, 653-654, 656-657, 659-660, 662-663, 665-666, 668-669, 671-672, 674-675, 677-678, 680-681, 683-684, 686-687, 689-690, 692-693, 695-696, 698-699, 701-702, 704-705, 707-708, 710-711, 713-714, 716-717, 719-720, 722-723, 725-726, 728-729, 731-732, 734-735, 737-738, 740-741, 743-744, 746-747, 749-750, 752-753, 755-756, 758-759, 761-762, 764-765, 767-768, 770-771, 773-774, 776-777, 779-780, 782-783, 785-786, 788-789, 791-792, 794-795, 797-798, 800-801, 803-804, 806-807, 809-810, 812-813, 815-816, 818-819, 821-822, 824-825, 827-828, 830-831, 833-834, 836-837, 839-840, 842-843, 845-846, 848-849, 851-852, 854-855, 857-858, 860-861, 863-864, 866-867, 869-870, 872-873, 875-876, 878-879, 881-882, 884-885, 887-888, 890-891, 893-894, 896-897, 899-900, 902-903, 905-906, 908-909, 911-912, 914-915, 917-918, 920-921, 923-924, 926-927, 929-930, 932-933, 935-936, 938-939, 941-942, 944-945, 947-948, 950-951, 953-954, 956-957, 959-960, 962-963, 965-966, 968-969, 971-972, 974-975, 977-978, 980-981, 983-984, 986-987, 989-990, 992-993, 995-996, 998-999, 1000-1001, 1003-1004, 1006-1007, 1009-1010, 1012-1013, 1015-1016, 1018-1019, 1021-1022, 1024-1025, 1027-1028, 1030-1031, 1033-1034, 1036-1037, 1039-1040, 1042-1043, 1045-1046, 1048-1049, 1051-1052, 1054-1055, 1057-1058, 1060-1061, 1063-1064, 1066-1067, 1069-1070, 1072-1073, 1075-1076, 1078-1079, 1081-1082, 1084-1085, 1087-1088, 1090-1091, 1093-1094, 1096-1097, 1099-1100, 1102-1103, 1105-1106, 1108-1109, 1111-1112, 1114-1115, 1117-1118, 1120-1121, 1123-1124, 1126-1127, 1129-1130, 1132-1133, 1135-1136, 1138-1139, 1141-1142, 1144-1145, 1147-1148, 1150-1151, 1153-1154, 1156-1157, 1159-1160, 1162-1163, 1165-1166, 1168-1169, 1171-1172, 1174-1175, 1177-1178, 1180-1181, 1183-1184, 1186-1187, 1189-1190, 1192-1193, 1195-1196, 1198-1199, 1201-1202, 1204-1205, 1207-1208, 1210-1211, 1213-1214, 1216-1217, 1219-1220, 1222-1223, 1225-1226, 1228-1229, 1231-1232, 1233-1234, 1236-1237, 1239-1240, 1242-1243, 1245-1246, 1248-1249, 1251-1252, 1254-1255, 1257-1258, 1260-1261, 1263-1264, 1266-1267, 1269-1270, 1272-1273, 1275-1276, 1278-1279, 1281-1282, 1284-1285, 1287-1288, 1290-1291, 1293-1294, 1296-1297, 1299-1300, 1302-1303, 1305-1306, 1308

[illegible]

[illegible]

```

Qy      124 LDYLTGGCGMANSNDYARRETYTFYFDLCESKXSNXWCEWCEASQADQVADALHJGSI 163
Db      389 REKMDQGMKRNKSNLSPFTYSLSISDLSKQKSNXWCEWCEASQADQVADALHJGSI 163
Qy      124 184 NKKMDQGMKRNKSNLSPFTYSLSISDLSKQKSNXWCEWCEASQADQVADALHJGSI 163
Db      448 ASYQVNNMNLCLSKHCKSGITLLMGCSNMGASQWVWPKQDGSITSLYDDMWDMVQGSDF 507
Qy      244 LRRITIVPATGKNGMWL 261
Db      508 LKQILMLPYTKNGKNGMWL 525

RESULT 7
SI6022
abrin-c precursor - Indian licorice
N:contains: rRNA N-glycosylase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C:Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #ext-1999
C:Accession: SI6022
R:Mod: K.R.; Lord, J.M.; MurtyGzarak, E.O.; Starak, M.
R:Mod: 1.0; BiochemAbz; 1997; 932
A:Reference number: SI6022; WUID:9165957; PMID:2050149
A:Accession: SI6022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-562 <MOD>
A:Cross-references: EMBL:X55667; NID:g16094; FIDN:CAJ9302.1; PID:g16095
C:Comment: Abtin consists of an A chain, which is linked by an interchain disulfide bond, which is essential for the A chain to bind to the B chain. rRNA N-glycosylase homology
C:Keywords: duplication; glycoprotein; glycosylase; hydrolase; lectin; pyroglyutamidase
F:35-285/Product: abrin-c chain A #status predicted <ACH>
F:41-280/Domains: rRNA N-glycosylase homology <RMS>
F:225-552/Product: abrin-c chain B #status predicted <BCH>
F:317-359,360-400,403-441,448-483,487-526,529-562/Region: 40, residues repeats
F:353/Motifs: 131; pyroglytamidase catalytic site; Glycyl (Glu, Asn) #status predicted
F:108-201;Active site: Glu,Asn #status predicted
F:124,287,327,395,435,436/Binding site: carbohydrate (Aan) (covalent) #status predicted
F:281-303,320-331,363-380,451-464,499-507/Disulfide bonds: #status predicted
F:332,346/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted
F:534,555/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted

Query Match 53.0%; Score 703; DB 2; Length 562;
Blast local similarity 53.3%; Filter NO 3, 64 50;
Matches 134; Conservative 39; Mismatches 83; Indels 2; Gaps 2;

Qy      5 CSAS-ETRYVIGXKQVVRVDRDPDNOQIOLMSEKSNNDQWLTXKDXTRNSGS 63
Db      303 CSRRREYRIGSDGDCVDDVDYDHNHNRILMKHCKDSELENDWLTXSDKTRINSKG 362
Qy      64 CLTGYTAGYAVNLEQDNRAVEKTLTQWIKNGTILNPSNLIPLAASQIGKTLTYQT 123
Db      363 CLTGTGAPVNVVHIDGCSHVAENITLNLNDSNLIINPSHVALESSNGQTLTYQT 422
Qy      124 LDYLTGGCGMANSNDYARRETYTFYFDLCESKXSNXWCEWCEASQADQVADALHJGSI 183
Db      423 NEYLKQGMWTKNNTSPFYSISGSLCLMCAQGSVWMLADCNKKRQ-QVALYDLSI 481
Qy      184 RPKMDQGMKRNKSNLSPFTYSLSISDLSKQKSNXWCEWCEASQADQVADALHJGSI 243
Db      482 RSYQVNNMNLCLSKHCKSGITLLMGCSNMGASQWVWPKQDGSITSLYDDMWDMVQGSDF 541
Qy      244 LRRITIVPATGKNGMWL 261
Db      542 LKQILMLPYTKNGKNGMWL 525

RSJ2430

```

N:Contains: rRNA N-glycosylase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C:Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
C:Accession: S32430; UCL1399
R:PubMed: 156393
J: Mol. Biol. 229, 263-267, 1993
T: C.; Lin, J.Y.
A:Title: Primary structure of three distinct isobrin determined by cDNA sequencing.
A:Reference number: S32429; PMID:9332799; PMID:8421333
A:Accession: S32430
A:Molecule type: rRNA
A:Residues: 1-527 <HUN>
A:Cross-references: GB:M98345; NID:9166296; PID:AAA32625.1; PID:g166297
R:Kimura, M.; Sumitawa, T.; Punaleu, G.
Biochem. Biotechnol. Biochem. 57, 166-169, 1993
A:Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A:Reference number: UCL1398; PMID:93169023; PMID:7763422
A:Molecule type: rRNA
A:Accession: S32430
A:Residues: 260-261 /D/ 283-290, 'N', 292-349, 'EQ', 352-377, 'N', 379-425, 'W', 427, 'D', 429-430
A:Experimental source: seed
C:Superfamily: ricin; rRNA N-glycosylase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosylase; hydrolase; lectin; F
F.1-250/Product: abrin-b chain A #status predicted <ACH>
F.7-245/Domains: rRNA N-glycosylase homology <RNG>
F.260-527/Product: abrin-b chain B #status experimental <BCH>
F.292-324,335-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F.110,360,406,428/Binding site: substrate (Tyr, Tyr, Gln, Asn) #status predicted
F.163,166/Active site: Glu, Arg #status predicted
F.246-268,285-304,328-345,416-429,455-477/Diulfide bonds: #status predicted
F.287,311/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F.499,520/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 52.9%; Score 702; DB 2; Length 527;
Best Local Similarity 51.9%; Pred. No. 4,2e-60;
Matches 134; Conservative 39; Mismatches 83; Indels 2; Gaps 2;

QY	5	CSAS-EPTVTVRKGKGVVDVDDPHQGNQQLMPEKSNNDPQQLMTIKEDTTRNSG	63
DB	268	GSKRSEPTVRLGKNGKGVVDVDDPHQGNQQLMPEKSNNDPQQLMTIKEDTTRNSG	327
QY	64	CLTVYVTVAGVYVMTFPCONTAVREARTNQTIXKGTTRNSG	123
DB	328	CLTTEGAPAGVYVMTFPCONTAVREARTNQTIXKGTTRNSG	387
QY	124	LDVTLGGVMAAGNDAPREVTYVGFRLQMSKXGVSFVETCSXGXKXQVWTFEXAIIINIKKXXXDVAAQAFK	243
DB	388	NEVLMRQGRGNTSPFTVSIIGSYDLQMGQSNWALACDNKKEQ-QNALVTDGSI	446
QY	184	RPQNDQCLTVGRDVSFVTVINIVSCSXGXKXQVWTFEXAIIINIKKXXXDVAAQAFK	243
DB	447	KSVQVNNCLTSKHKQSPFLVACSGNMAQALFNDGSIYNALHDMVWVYSGDS	506
QY	244	LRRIITVATGKGNQML	261
DB	507	LKEITLHPYKGNQML	524

RESULT 9
S32431
A:Title: precursor - Indian licorice (fragment)
N:Contains: rRNA N-glycosylase (EC 3.2.2.22)
C:Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
C:Accession: S32431; UCL1399
R:PubMed: 156393
J: Mol. Biol. 229, 263-267, 1993
T: C.; Lin, J.Y.
A:Title: Primary structure of three distinct isobrin determined by cDNA sequencing.
A:Reference number: S32429; PMID:9332799; PMID:8421333
A:Accession: S32431
A:Molecule type: rRNA
A:Residues: 1-528 <HUN>

A:Cross-references: GB:M98346
R:Hung, C.; Lee, M.; Lee, T.; Lin, J.Y.
submitted to the EMBL Data Library, March 1993
A:Reference number: S34408
A:Accession: S34408
A:Molecule type: rRNA
A:Residues: 1-169, 'C', 171-320, 'V', 322-528 <HUN>
A:Cross-references: GB:M98346; NID:9166296; PID:AAA32625.1; PID:g166297
R:Kimura, M.; Sumitawa, T.; Punaleu, G.
Biochem. Biotechnol. Biochem. 57, 166-169, 1993
A:Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A:Reference number: UCL1398; PMID:93169023; PMID:7763422
A:Molecule type: rRNA
A:Accession: S32430
A:Residues: 260-261 /D/ 283-290, 'N', 292-349, 'EQ', 352-377, 'N', 379-425, 'W', 427, 'D', 429-430
A:Experimental source: seed
C:Superfamily: ricin; rRNA N-glycosylase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosylase; hydrolase; lectin; F
F.1-250/Product: abrin-b chain A #status predicted <ACH>
F.7-245/Domains: rRNA N-glycosylase homology <RNG>
F.260-527/Product: abrin-b chain B #status experimental <BCH>
F.292-324,335-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F.110,360,406,428/Binding site: substrate (Tyr, Tyr, Gln, Asn) #status predicted
F.163,166/Active site: Glu, Arg #status predicted
F.246-268,285-304,328-345,416-429,455-477/Diulfide bonds: #status predicted
F.287,311/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F.499,520/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 52.9%; Score 702; DB 2; Length 528;
Best Local Similarity 51.9%; Pred. No. 4,2e-60;
Matches 134; Conservative 40; Mismatches 82; Indels 2; Gaps 2;

QY	5	CSAS-EPTVTVRKGKGVVDVDDPHQGNQQLMPEKSNNDPQQLMTIKEDTTRNSG	63
DB	268	GSKRSEPTVRLGKNGKGVVDVDDPHQGNQQLMPEKSNNDPQQLMTIKEDTTRNSG	327
QY	64	CLTVYVTVAGVYVMTFPCONTAVREARTNQTIXKGTTRNSG	123
DB	328	CLTTEGAPAGVYVMTFPCONTAVREARTNQTIXKGTTRNSG	387
QY	124	LDVTLGGVMAAGNDAPREVTYVGFRLQMSKXGVSFVETCSXGXKXQVWTFEXAIIINIKKXXXDVAAQAFK	243
DB	388	NEVLMRQGRGNTSPFTVSIIGSYDLQMGQSNWALACDNKKEQ-QNALVTDGSI	447
QY	184	RPQNDQCLTVGRDVSFVTVINIVSCSXGXKXQVWTFEXAIIINIKKXXXDVAAQAFK	243
DB	447	KSVQVNNCLTSKHKQSPFLVACSGNMAQALFNDGSIYNALHDMVWVYSGDS	507
QY	244	LRRIITVATGKGNQML	261
DB	507	LKEITLHPYKGNQML	525

RESULT 10
S62627
A:Title: precursor - European elder
N:Contains: rRNA N-glycosylase (EC 3.2.2.22)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C:Accession: S62627; S62619
R:Van Damme, E.; J.W.; Baire, A.; Rouge, P.; Van Leuven, F.; Peumans, W.J.
Biochem. Biotechnol. Biochem. 57, 166-169, 1993
A:Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A:Reference number: S62619; PMID:9620296; PMID:861119
A:Accession: S62627
A:Molecule type: rRNA
A:Residues: 1-570 <VAN>
A:Cross-references: EMBL:U27122; NID:9141772; PID:AA49158.1; PID:g141773
R:Kimura, M.; Sumitawa, T.; Punaleu, G.
Biochem. Biotechnol. Biochem. 57, 166-169, 1993
A:Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A:Reference number: UCL1398; PMID:93169023; PMID:7763422
A:Molecule type: rRNA
A:Accession: S32430
A:Residues: 260-261 /D/ 283-290, 'N', 292-349, 'EQ', 352-377, 'N', 379-425, 'W', 427, 'D', 429-430
A:Experimental source: seed
C:Superfamily: ricin; rRNA N-glycosylase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosylase; hydrolase; lectin; F
F.1-250/Product: abrin-b chain A #status predicted <ACH>
F.7-245/Domains: rRNA N-glycosylase homology <RNG>
F.260-527/Product: abrin-b chain B #status experimental <BCH>
F.292-324,335-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F.110,360,406,428/Binding site: substrate (Tyr, Tyr, Gln, Asn) #status predicted
F.163,166/Active site: Glu, Arg #status predicted
F.246-268,285-304,328-345,416-429,455-477/Diulfide bonds: #status predicted
F.287,311/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F.499,520/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 37.4%; Score 496; DB 2; Length 570;
Best Local Similarity 42.9%; Pred. No. 4,2e-40;

	Matches	111; Conservative	30; Mismatches	106; Indels	12; Gaps	6
QY	5	CSASPPFVRLVARKGXVDVADDDPFHQNQIQLTWPKSNDNPQQLMTIKEDYITRNSASC	64			
Db	316	GSVAVFTRISASNDGLCDVRYQYHIDGNFVOLF--GQNCQQLMTFFIDGTFRMLGKC	373			
QY	65	LTVYTAGVYVMPCTAVREATIQIINKXGIIIPNSVILAASSGIKQTLVAVTL	124			
Db	374	L-----TRASSSTGQVCTVPPATKRWVSIDGTTINPSALVTPAQAASBTLSTENR	422			
QY	125	DYLLDGLGAGMDPAREVTVPEPDLQWESKXG3--VHTVTS3QXQXKXVILVGGG3	182			
Db	429	IHAQGMVTV--DVEGLTPIVYKQGLCARNGKPNFVDECVLNRQV--EMLVIGGT	486			
QY	163	IRKPNDDQLXGDEPQSVYVIVYSCSXKXQXWVFNEXKLNLKXXXXXVQVQNP	242			
Db	487	IRANSNSLCVTSDEHSGLYLLKCE--GSQNGRVFVNVGTINSPALMLMDVARDV	545			
QY	243	KLRILIIYPAIKGNQML	261			
Db	546	SIRKILIIYPPGNQVMI	564			

```

RESULT 11
UC7535
Chromosome (EC 3.2.1.14) 25 - Streptomyces thermoviolaceus
Chromosome (EC 3.2.1.14) 25 - Streptomyces thermoviolaceus
C.Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #ext_change 30-Jun-2001
UC7535
Rijnsdijk, H., Okamoto, T., Hatano, N., Miyamoto, K., Vatanaba, T., Mitsuuchi, M., Inoue,
A. et al. Family 11 chitinases from Streptomyces thermoviolaceus
#Reference number: UC7535; PMID:21036907; PMID:11193414
#Reference number: UC7535; PMID:21036907; PMID:11193414

```

A:Cross-references: DDBJ:AB016942
A:Experimental source: strain OPC-50
C:Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin degradation.
C:Carbohydrate-binding domain that is important in the efficient hydrolysis of insoluble chitin.
C:Genetics:
A:Gene: chl35
K:Keywords: g-lycosidase; hydrolase

[illegible]

RESULT 12
 JS0589
 endo-1,4-beta-xylosanase (EC 3.2.1.8) A precursor - Streptomyces lividans
 C:accession:JS0589
 C:species:Streptomyces lividans
 C:release:10-Mar-1994
 C:change:revision 22-Nov-1996 #extn change 26-Feb-1999
 C:release:JS0589; PS0338
 R:Rothbreck, F., Roy, C., Yasuchi, M., Morziosi, R., Kluepfel, D.
 Amino acid sequence of the three genes encoding xylosanase in Streptomyces lividans
 A:reference number: JS0589; PMID:9207743; PMID:1743521
 A:accession:JS0589

A:Molecule type: DNA
A:Residues: 1-477 <SHA>
A:Cross-references: GB:IM6451
A:Accession: PS0238
A:Molecule type: Protein
A:Residues: 42-92 <SP2>
C:Genetics:
A:Gene: XlnA
A:Function: XlnA catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Similarity: Streptomyces endo-1,4-beta-xyylanase A, Streptomyces endo-1,4-beta-xylosidase, Streptomyces endo-1,4-beta-xylosidase des
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide deg
F:1-41/Domain: signal sequence #status predicted <S10>
F:42-47/Product: endo-1,4-beta-xyylanase A #status experimental <AM>
F:74-341/Domain: Streptomyces endo-1,4-beta-xyylanase A homology <SX>
F:169-271/Active site: GU #status predicted

```

Query Match      8.1%; Score 118.5; DB 1; Length 477;
Best Local Similarity 29.1%; Pred. No. 0.0013;
Matches 39; Conservative 19; Mismatches 63; Indels 13; Gaps 6;

Cy 7 AASP-----TTRVYKSGKAVVYRDPDFDGNQIQAPSSNRNDPGLTKRDKATFSN 61
Db 346 SSSPDPAGGQKIRNGV--SRCLDVPASSTSDGGLQIMCHSGT--NCGMVAATDAGELVY 402
Cy 62 G-SCTITVYGVGVTGVPFQNTAIREATVIGKTKXGNTINRSMVLA--SSGKRTT 118
Db 403 GKRLDAPATNSKQVQYCGNGENQK--WRNLSGSSVGVSGLSLANGNGTANLT 460

Cy 119 LTVQTDLYTLGQW 132
Db 461 IQLVYCSNGSNQWR 474

```

T34603
 xylanase_A - *Streptomyces coelicolor* (fragment)
 C:Species: *Streptomyces coelicolor*
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 28-Jul-2000
 C:Accession: T34603
 R:Worby, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1998

A:Accession: F334603
A:Status: preliminary; translated from GS/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1,383 <NR>
A:Cross-references: EMBL:AL021529; EIDN:CAA16468.1; GSPDB:GN00070; SCQEDB:SC10A5
A:Experimental source: strain AD(2)
C:Genetics:
C:Gene: xmd; SCQEDB:SC10A5.35c
C:Suprafamily: Streptomyces endo-1,4-beta-xylinase A; Streptomyces endo-1,4-beta-xylinase A homolog <XN1
E:1,247;Domain: Streptomyces endo-1,4-beta-xylinase A homolog <XN1
Query Match 8.7%; Score 115.5; DB 2; Length 383;
Best Local Similarity 82.1%; Pred. No. 0.0029;
Matches 39; Conservative 18; Mismatches 64; Indels 13; Gaps 6;

Db	232	SSBPADAGQIKGV-SERCLIVDPASTDQULQMHCHST-NQQAATDQAGELAVY	308
Qy	62	G-SCLITVYGRGVYVMEFQCTNAREATVQIWKXGIIINPSNLVLA--SSGIGKFTT	118
Dy	309	GDKCLDPAATGNSKVIQIICSGNSDMK--NRANSDSVGVQSSCLDQVGNQITNGLT	366
Qy	119	LTVQTLDPYLCGSK 132	
Dy	367	IDLPTCSNGSNQNR 380	

A45053
 proteinase RPI - *Ratobacter faecitabidus*
 C:Species: *Ratobacter faecitabidus*
 C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 22-Oct-1999
 C:Accession: A45053
 R:Shimoi, H.; Iinuma, Y.; Ohta, T.; Tadenuma, M.
 J. Biol. Chem. 267: 25189-25195, 1992
 A:Title: Molecular structure of *Ratobacter faecitabidus* protease I. A yeast-lytic serine
 A:Reference number: A45053; MUID:93094226; PMID:1339445
 A:Accession: A45053
 A:Status: preliminary
 A:Molecule type: DNA, protein
 A:Residues: 1525 <SH3>
 A:Cross-references: GB:D10753; PIDN:BA01585.1; PID:dl002060; PID:g912440
 A:Experimental source: YJM-50
 A:Note: sequence extracted from NCBI backbone (NCBIN:120149, NCBI:P:120151)

Query Match 7.8%; Score 104; DB 2; length 525;
 Best Local Similarity 30.2%; Pred. No. 0.0377; 45; indels 12; Gaps 5;
 Matches 32; Conservative 17; Mismatches 45;

QY 2 DVTCSAREPTVRIYGEKXKVDVDDDPDQNGIQMPSKSNPDQMTIKEDTIRSN 61
 DB 399 DVT-----TSYVGQYNNCIVDPSDPTDQKQIQMNCNGIN--AQKSEHPDGTIRIN 450
 QY 62 GSCL-ITVGYT-AGYVWIPDQNTAVREAITWQIMXNGTINPRSN 105
 DB 451 GKCDLRWAMTNGTEVQLMNCNGH--NQRTLNAGDLYVHAN 494

RESULT 15

A39094
 glucan endo-1,3-beta-glucosidase (EC 3.2.1.-) precursor - *Oerskovia xanthineolytica*
 C:Species: *Oerskovia xanthineolytica*
 C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 22-Oct-1999
 C:Accession: A39094
 R:Shen, S.H.; Chretien, P.; Bastien, L.; Siliaty, S.N.
 J. Biol. Chem. 266, 1058-1063, 1991
 A:Title: Primary sequence of the glucanase gene from *Oerskovia xanthineolytica*. Expressi
 A:Reference number: A39094; MUID:91093212; PMID:1985933
 A:Accession: A39094
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1548 <SH3>
 A:Cross-references: GB:M60826; GB:M8734; NID:g150444; PIDN:AA25520.1; PID:g150445
 C:Keywords: glycosidase; hydrolase

Query Match 7.6%; Score 101; DB 2; length 548;
 Best Local Similarity 30.8%; Pred. No. 0.075;
 Matches 37; Conservative 13; Mismatches 54; Indels 16; Gaps 5;

QY 22 VPDYDDPHDNGIQMPSKSNPDQMTIKEDTIRSNGL-ITVGYTGYTMIF 79
 DB 434 LVPWADPTDNGVQL--ATCSGMAQQTGCTGTVRAKCDLVASGADGTAWII 491
 QY 80 DQNTAVREAITWQIM--XNGTINPRSNLYAASGSI--KGTLLVQTLDTLTGGW 132
 DB 492 TCN-----GTGAQKTYDSATRALNPDGKCKIDAGGALPDQGVQLWTCNGTERQW 546

Search completed: December 11, 2003, 13:55:40
 Job time : 10.2062 secs

FT	VARIANT	231	231	
FT <td>VARIANT</td> <td>231<td>NL -> S OR T.</td><td></td></td>	VARIANT	231 <td>NL -> S OR T.</td> <td></td>	NL -> S OR T.	
FT <td>VARIANT</td> <td>233</td> <td>NL -> KGE.</td> <td></td>	VARIANT	233	NL -> KGE.	
FT <td>VARIANT</td> <td>232</td> <td>GLAM -> SLAM.</td> <td></td>	VARIANT	232	GLAM -> SLAM.	
SEQ <td>SEQUENCE</td> <td>264 AA;</td> <td>7DDDD326CCFFESA4 CRCE4;</td> <td></td>	SEQUENCE	264 AA;	7DDDD326CCFFESA4 CRCE4;	
Query Match				
Best Local Similarity		97.2%;	Score 1290;	DB 1;
Matches 243;		Conservative	0;	Mismatches 20;
			Indels	0;
			Gaps	0
Qy	1	DPTGSSASEPTAIVAEKXKXVADDDPHFDNDGICLWPKSSNNPQMDITKIDKTRIS	60	
Db	1	DPTGSSASEPTAIVAEKXKXVADDDPHFDNDGICLWPKSSNNPQMDITKIDKTRIS	60	
Qy	61	NSGCLTIVGTAGVAYVIMFDQNTAVRENTWQIMKNGTINPRSNVLAAASGKSTLTLL	120	
Db	61	NSGCLTIVGTAGVAYVIMFDQNTAVRENTWQIMKNGTINPRSNVLAAASGKSTLTLL	120	
Qy	121	VQTDLTLYAGQMLAGNDTAPAEVITYTFRDLCMESXASVWETCTKSQNNXKMLAYGD	180	
Db	121	VQTDLTLYAGQMLAGNDTAPAEVITYTFRDLCMESXASVWETCTKSQNNXKMLAYGD	180	
Qy	181	GSIPKRNQDGLTSSRQSVSTYINIVSGGASSGQWTFINSGALINLKNGLAMVQYA	240	
Db	181	GSIPKRNQDGLTSSRQSVSTYINIVSGGASSGQWTFINSGALINLKNGLAMVQYA	240	
Qy	241	NPLRLRIIIVPATKKNQMWLPV	263	
Db	241	NPLRLRIIIVPATKKNQMWLPV	263	

RP	SEQUENCE OF 315-576.
RQ	
RA	"Nucleotide sequence of cloned cDNA coding for preprovincin.";
RB	Eur. J. Biochem. 188:265-270(1985).
RC	(4)
RD	SEQUENCE OF 36-302.
RE	Toshitake S., Funatsu G., Funatsu M.;
RF	biochemical characterization of peptic peptides, and the complete
RG	amino acid sequence of the mature protein.
RH	Agric. Biol. Chem. 42:1267-1274(1978).
RI	(5)
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	
RH	
RI	
RJ	
RK	
RL	
RM	
RN	
RO	
RP	
RQ	
RA	
RB	
RC	
RD	
RE	
RF	
RG	

RA Funatsu G., Kimura M., Funatsu M.,
RA "Primary structure of Ala chain of ricin D.",
RA Agric. Biol. Chem. 43:2221-2224(1979).
RN [6]
RN CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
RN MEDLINE=90352221, PubMed=5583957.
RA Montfort M., Villafraña J.E., Monzingo A.F., Ernst S.R., Katzin B.,
RA Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.,
RA "The three-dimensional structure of ricin at 2.8 A.",
RA J. Biol. Chem. 262:5398-5403(1987).
RN [7]
RN AGRIC. BIOL. CHEM. 54:157-162(1990).
RN REVIEW.
RP MEDLINE=21480123, PubMed=11595634,
RA Olness S., Kozlov J.V.,
RA "Ricin.",
RA Toxicon 39:1723-1728(2001).
RN [8]
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RN MEDLINE=87165983, PubMed=5583957.
RA Montfort M., Villafraña J.E., Monzingo A.F., Ernst S.R., Katzin B.,
RA Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.,
RA "The three-dimensional structure of ricin at 2.8 A.",
RA J. Biol. Chem. 262:5398-5403(1987).
RN [9]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RN MEDLINE=91352004, PubMed=1891181,
RA Katzin B., Collins E.O., Robertus J.D.,
RA "Structure of ricin A-chain at 2.5 A.",
RA Proteins 10:251-259(1991).
RN [10]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
RN MEDLINE=91352005, PubMed=1891882,
RA Rutenber E., Robertus J.D.,
RA "Structure of ricin B-chain at 2.5-A resolution.",
RA Proteins 10:260-269(1991).
RN [11]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
RN MEDLINE=95082002, PubMed=7904130,
RA Westrich S.A., Tucker A.D., Macherer D.R., Detschire D.J.,
RA "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.",
RA J. Mol. Biol. 244:410-422(1994).
RN [12]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
RN MEDLINE=96374222, PubMed=780513,
RA Day P.J., Ernst S.R., Parkhal A.E., Monzingo A.F., Pascal J.M.,
RA Molnar-Svánh M.C., Robertus J.D.,
RA "Structure and activity of an active site substitution of ricin A
RA chain.
RA Biochemistry 35:11098-11103(1996).
RN [13]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RN MEDLINE=97240280, PubMed=9068280,
RA Van X., Hollis T., Svánh M., Day P., Monzingo A.F., Milne G.W.,
RA Robertus J.D.,
RA "Structure-based identification of a ricin inhibitor.",
RA J. Mol. Biol. 266:1043-1049(1997).
RN [14]
RN PROTEIN GENESIS
RN MEDLINE=91165613, PubMed=1287677,
RA Kün Y., Robertus J.D.,
RA "Analysis of several key active site residues of ricin A chain by
RA mutagenesis and X-ray crystallography.",
RA Protein Eng. 5:775-779(1992).
RN [15]
RN FUNCTION: Ricin is highly toxic to animal cells and to a less
RN extent to plant cells. The A chain is responsible for inhibiting
RN protein synthesis through the catalytic inactivation of 60S
RN ribosomal subunits. It acts as a glycosylase that removes
RN specific adenine residue from an exposed loop of 16S ribosomal
RN subunit. The modified ribosomes are unable to support protein
RN synthesis. The A chain can inactivate a few thousand ribosomes
RN per minute, thus inactivating them faster than the cell can make
RN new ones. A single A-chain molecule can therefore kill an animal

CC	cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity). It binds to beta-D-galactopyranoside moieties.
CC	-1- ERGASTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC	-1- SUBUNIT: Disulfide-linked dimer of A and B chains.
CC	-1- DOMAIN: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).
CC	-1- PIVR: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
CC	-1- IMMUNITY: IN THE N-TERMINAL SECTION, BELONGS TO THE FIBRONECTIN-INDUCING PROTEIN FAMILY. TYPE 2 RIF SUSCEPTIBILITY.
CC	-1- SIMILARITY: CONTAINS 2 EIGH B-TYPE LECTIN DOMAINS.
CC	-1- WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1), RIF.2 AND REF.3).
CC	-1- DATABASE: NMR-Protein Spotlight;
CC	NOTE: Issue 31 of February 2003;
CC	WWW= http://www.ebi.ac.uk/spotlight/articles/split03.html ".
CC	-----
CC	EMBL; X03179; CAA26939.1; -
CC	EMBL; X52908; CAA37095.1; -
CC	EMBL; X02388; CAA26230.1; -
CC	EMBL; A12892; CAA01058.1; -
CC	PIR; A24041; RECD.
CC	PDB; 2A41; 31-JUN-94.
CC	PDB; 2A42; 31-JUN-94.
CC	PDB; 11F7; 14-JAN-98.
CC	PDB; 11F8; 14-JAN-98.
CC	PDB; 11F9; 31-OCT-93.
CC	PDB; 11F7; 14-JAN-98.
CC	PDB; 11F8; 14-JAN-98.
CC	PDB; 11F9; 31-OCT-93.
CC	PDB; 10E7; 16-JUN-97.
CC	PDB; 10E8; 16-JUN-97.
CC	PDB; 10E9; 02-SEP-98.
CC	PDB; 10E8; 02-SEP-98.
CC	PDB; 11E4; 16-JUN-02.
CC	PDB; 11E9; 16-JUN-02.
CC	GlycoSuiteDB; P02879; -
CC	InterPro; IPR007172; Ricin_B_lectin.
CC	InterPro; IPR001574; RIF.
CC	Pfam; PF00652; Ricin_B_lectin. 6.
CC	Pfam; PF00151; RIF. 1.
CC	SMART; PF00396; SMARTICIN.
CC	PROSITE; PS00251; Ricin_B_lectin. 2.
CC	PROSITE; PS00251; SHIG_A_RICIN. 1.
CC	KM Plant defense; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;
CC	GW Glycoprotein; Lectin; Signal; 3D-structure.
CC	FT SIGNAL 1 35
CC	FT CHAIN 36 302
CC	FT PEPTIDE 303 314
CC	FT CHAIN 315 576
CC	FT DOMAIN 321 448
CC	FT DOMAIN 321 448
CC	FT REPEAT 331 373
CC	FT REPEAT 374 414
CC	FT REPEAT 417 449
CC	FT REPEAT 462 497
CC	FT REPEAT 501 540
CC	FT REPEAT 543 570
CC	FT ACT SITE 212 212
CC	FT DISULFID 294 318
CC	FT DISULFID 334 353
CC	INTERCHAIN.

```

FT     DT DISULFID    377      394
PT     FT DISULFID    465      478
DT     DT DISULFID    504      521
FT     FT CARBOHYD    45
PT     FT CARBOHYD    271      271
FT     PT CARBOHYD    409      409
FT     FT CARBOHYD    449      449
FT     FT CONFLICT    76       76
FT     FT CONFLICT    551      551
FT     FT STRAND      43       47
PT     FT TURN        49       50

Query March 64.6% Score 849.5 DB 1; Length 576;
Best local similarity 60.6%; Pred.No. 1,9e-76;
Matches 157; Conservative 29; Mismatches 72; Indels 1; Gaps 1

OY      5 CSASPEPVATVGRKGVADVDDDFHDGQQLTLPESKNNDPVLMTIKRDKTTIRNSNC 64
Db      318 CDMPEFVTIVRRGLACVDADRERHNGAALTLMPCKNTDAQTDLMLTKRDITIRNSKC 177
OY      65 LITTVTAAYGYVMIPCTNATEATINQIWKNGIIINRSNLVPLASSGIKTITFWOTL 124
Db      378 LTGGSPICAGANGUDAPRESEVITYGPFLCMENSKSVTECKXSOKXOXWALYGQSIR 184
OY      125 DYLIGGSPIAGANGUDAPRESEVITYGPFLCMENSKSVTECKXSOKXOXWALYGQSIR 184
Db      438 IYAVSCGWPMFNINOFPFTITVALGLCLANSOSCVITECSSEBAKO-QMALYSASGISR 495
OY      185 PRONODCUTLKARSVSFTVINIVSCKSXGXQRVFETEXALLIMKKXXXXDVAKNPRL 244
Db      497 PGMNDCMCLSDSNISLEIFEVKLSSIGPASGSRWFERNKDGTILNIISGLVIDVASPSRL 556
OY      245 RRTIIVPAECGNOMATLV 263
Db      557 KQTIIVPLADPNQIWLP 575

RESULT 3
AGGL_RICCO STANDARD; PROT; 564 AA.
ID AGGL_RICCO
RC 00E1J50;
RC 00E1J50-1988 (rel. 06, Created)
DT 01-JAN-1988 (rel. 06, Last sequence update)
DE 28-FEB-2003 (rel. 41, Containment update)
OE Agglutinin precursor (ICA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain)].
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; eucaryotes; core eudicots; Rosidae; Spermatophyta; Magnoliophyta; euclidyales; core eudicots; Kosidae; eurosids I; Malvaginales; Sapindaceae; Ricinus.
CC NCBI_xlatd=3988;
CX
SEQUENCE FROM N.A.
MEDLINE=6059449; PubMed=2999130;
RA Roberts L.M., Lamb F.I., Paplin D.J.C., Lord J.N.;
RT "The primary sequence of Ricinus communis agglutinin. Comparison with ricin."
RU J. Biol. Chem. 260:15682-15686(1985).
RN [2]
RP SEQUENCE OF 303-564.
RC
RC MEDLINE=6059449; PubMed=2999130;
RA Roberts L.M., Lamb F.I., Paplin D.J.C., Lord J.N.;
RT "The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-seed castor bean seeds."
RU Biochim. Biophys. Acta 872:277-285(1986).
RN [3]
RP SEQUENCE OF 303-337.
RC
RC MEDLINE=6018723; PubMed=6768555;
RA Lin T.T.-S., Li S.S.-L.;
RT "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis."

```

RL Eur. J. Biochem. 105:453-459(1980).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the EMBL, the SRS, the DDBJ, the EBI, the NCBI, the NIDDK, the
 CC the European Bioinformatics Institute and the EMBL. Contributions on its
 CC use by non-profit institutions are not removed, usage by and for commercial
 CC entities requires a license agreement (See <http://www.embnet.org/licenses/embnet.html>)
 CC or send an email to license@ebi.ac.uk.
 CC -----
 DR EMBL: M12089; AAA3869.1; -
 DR EMBL: S40368; AAB2584.1; -
 DR FIC: A24261; RLCBAG.
 DR HSR: P02879; IIR6.
 DR GYCSULCDB: P08750; -
 DR GYCSULCDB: P08750; Ricin_B_lectin.
 DR Interpro: IPR001574; RIP.
 DR Pfam: P00652; Ricin_B_lectin. 6.
 DR PRINTS: P00396; SHIGARICIN.
 DR SMART: SMO0458; RICIN. 2.
 DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE: PS00275; SHIGA_RICIN. 1.
 KM Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KM Glycoprotein; Lectin; Signal.
 KM CHAIN.
 FT PROPEP 231 302 AGADUTININ, A CHAIN.
 FT CHAIN 303 564 AGADUTININ B CHAIN.
 FT DOMAIN 309 563 RICIN B-TYPE LECTIN 1.
 FT DOMAIN 319 361 RICIN B-TYPE LECTIN 2.
 FT REPEAT 362 402 1-ALPHA.
 FT REPEAT 405 437 1-BETA.
 FT REPEAT 450 485 1-GAMMA.
 FT REPEAT 489 528 2-ALPHA.
 FT REPEAT 531 558 2-BETA.
 FT ACETIDE 200 200 BY SIMILARITY.
 FT ACETIDE 306 306 BY SIMILARITY.
 FT DISULFID 322 322 INTRACHAIN (BY SIMILARITY).
 FT DISULFID 365 365 BY SIMILARITY.
 FT DISULFID 453 466 BY SIMILARITY.
 FT DISULFID 492 509 BY SIMILARITY.
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 331 331 F -> T (IN REF. 2).
 FT CONFLICT 352 352 N -> D (IN REF. 2).
 FT CONFLICT 362 362 R -> G (IN REF. 2).
 FT CONFLICT 404 404 F -> V (IN REF. 2).
 FT CONFLICT 552 552 F -> V (IN REF. 2).
 SQ SEQUENCE 564 AA; 62851 MW; D4552A72609759 CMC4;
 Query Match 54.7%; Score 726.5; DB 1; Length 564;
 Best Local Similarity 53.3%; Pred. No. 2.7e-64;
 Matches 138; Conservative 36; Mismatches 84; Indels 1; Gaps 1;
 Oy 5 CSASEFTVIRKXKXVYDDDDHGNQIQLPKSKNDPQVLTIRKEDTIRNSNC 64
 Db 306 CMPSEFTVIRKXKXVYDDDDHGNQIQLPKSKNDPQVLTIRKEDTIRNSNC 365
 Oy 65 LITVYTAGVYVPCNTAARATQIKXGKIVINRSVYLAASGIGKTTITVOTL 124
 Db 366 LITVYTAGVYVPCNTAARATQIKXGKIVINRSVYLAASGIGKTTITVOTL 425
 Oy 125 DYLQGLMAGNDTAREVITVYGFDDLCSEKSKXSVWVTCXSOXQXVYVGGSGIR 184

Db 426 IYASQGMIPNNTPQVITVIGLCKMLQNSGKVLSDCTSEKAO-QVALYKDSIR 484
 Oy 185 PRONQDGLTQVGDVSTVNTVNSCXKXGQWFTNEXAILMXXXXXVDAQMPKL 244
 Db 485 PQVRNDCLTIDANKIKTVKILSCPSASQKWFNRDGLTLVNLGVLDVRSDDSL 544
 Oy 245 RRIITVATGKQVQMLPV 263
 Db 545 KQITVHPRGKINLQMLPL 563
 RESUT 4
 ID ABRA_ABRP STANDARD; PRT; 528 AA.
 AC P11340; P28589;
 DT 01-JUN-1989 (Rel. 11, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Abria-a precursor [Contains: Abria-a A chain (RNA N-glycosidase)
 DE (EC 3.2.2.22); Abria-a B chain].
 OS Abria-a precursor (Indian licorice) (Crab's eye)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Rosales; Fabaceae; Leguminosae; core eudicots; Rosidae;
 OC Nodulicorpus (Fabaceae); Fabaceae; Leguminosae; Abriae; Abriae.
 CX NBI_TaxID=3816.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9133798; PubMed=8421313;
 RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
 RT "Primary structure of three distinct isoabrians determined by cDNA
 RT sequencing. Conservation and significance."
 RT J. Mol. Biol. 229:263-267(1993).
 RN [2]
 RP SEQUENCE OF 1-251.
 RX MEDLINE=9133798; PubMed=8421313;
 RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
 RT "Primary structure of three distinct isoabrians determined by cDNA
 RT sequencing. Conservation and significance."
 RT J. Mol. Biol. 229:263-267(1993).
 RN [3]
 RP SEQUENCE OF 1-251 FROM N.A.
 RX MEDLINE=9133798; PubMed=8421313;
 RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
 RT "Primary structure of three distinct isoabrians determined by cDNA
 RT sequencing. Conservation and significance."
 RT J. Mol. Biol. 229:263-267(1993).
 RN [4]
 RP SEQUENCE OF 1-251 FROM N.A.
 RX MEDLINE=9133798; PubMed=8421313;
 RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
 RT "Primary structure of three distinct isoabrians determined by cDNA
 RT sequencing. Conservation and significance."
 RT J. Mol. Biol. 229:263-267(1993).
 RN [5]
 RP SEQUENCE OF 262-528.
 RX MEDLINE=92371656; PubMed=1505674;
 RA Chen Y.-L., Chow L.-P., Tsegats A., Lin J.-Y.;
 RT "The complete primary structure of abria-a B chain."
 RT FEBS Lett. 309:115-118(1992).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).
 RX MEDLINE=9533188; PubMed=7608990;
 RA Hahne T.H., Lin T.-H., Lin T.-H., Chen Y.-L., Lin J.-Y.;
 RT "Crystal structure of abria-a B chain (2.14 A)."
 RT Nature 380:381-385(1995).
 CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
 CC ABRIA-A IS MORE TOXIC THAN RICIN.
 CC -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
 CC FACILITATES THE BINDING OF ABRIA-A TO THE CELL MEMBRANE THAT
 CC PRECEDES ENDOCYTOSIS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.


```

Db      269  GSRREPEFARIGRGKMGCVVYDVGHNQNNIIIMKCGJREEMQMLTKSDKLTRENK 328
QY      64  CLTGYGTAGYVYIMFDCAVNAFEALIMQIVANGTIIIPNSVLYAASSGKCTTIVQT 123
Db      329  CLFTYGAGSFTVIMIDGICINAAKATVIMIDNGTIIIPNSVLYAASSGKCTTIVQT 388
QY      124  LPTLYAGGGLANDTAPAEVYITVYGRLLDQNSKXGSVWAEVTKSSQGXQXNNAVCGQST 183
Db      389  NEYLMRQGRATGNNTSPPTVTSISGYSDLLCMQAGSNWMAWLDSDNKEDQ-DNALVTGSI 447
QY      184  RFRQNDQCLTYSAGSVYVINYVNCSSXKXSRWFVFNFXALINTLXXXXXVYAQNEK 243
Db      448  RSVQNTNCLTISKRGKQWELTMDLGCSSNMASSGAVFANDGSITSLIDVMDVYGSIDS 507
QY      244  LRRIITVFNKQKQWEL 261
Db      508  LKQILMPVTVYKQWEL 525

RESULT 5
AERC_AERP  STANDARD  PRT, 562 AA.
ID  AERC_AERP
PC  P28510;
DT  01-DEC-1992 (Rel. 24, Created)
DT  01-DEC-1992 (Rel. 24, Last sequence update)
DT  01-DEC-2003 (Rel. 24, Last annotation update)
DE  Abirh-2003 (Abirh) [Comment: Abirh-c A chain (tRNA N-glycosidase)
DE  (RC 3 2, 222); Abirh-c B chain)
OS  Abura preacitoria (Indian licorice) (Crab's eye).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eusticoid I; Fabales; Fabaceae; Papilionoideae; Aburae; Abura.
OC  NCBI_TaxID=3816;
EN  [1]
PR  SEQUENCE FROM N.A.
RS  R5859-1;
RC  R5859-1; R5857, PubMed2050149;
RT  Wood K.A., Ford J.M., Wawrzyniak E.J., Piatek M.;
RT  "Preproabrin: genomic cloning, characterization and the expression of
RT  the A-chain in Escherichia coli."
RL  Eur. J. Biochem. 198-723-732(1991).
CC  -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC  SYNTHESIS THROUGH THE CYTOKINETIC INACTIVATION OF 60S RIBOSOMAL
CC  SUBUNITS BY REMOVING ADENINE FROM POSITIONS 4,124 AND 5. THE
CC  B CHAIN IS A GULONIC ACID-CONTAINING PEPTIDE 4,124 RESIDUES LONG. THE
CC  B CHAIN IS A GULONIC ACID-CONTAINING PEPTIDE THAT PREPARES ENDOTOXINIS.
CC  -1- CATALYTIC ACTIVITY: endonuclease activity.
CC  -1- specific adenosine on the 28S rRNA.
CC  -1- SHUNTIN: DISRUPTED-LINKED DIMER OF A AND B CHAINS.
CC  -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC  CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC  -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
CC  INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC  -1- SIMILARITY: CONTAINS 2 RICH B-type lectin domains.
CC  THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL consortium.
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.1ab-sib.ch/announce/
CC  or send an email to license@sib-sib.ch).
CC  R5857, CA132902.1; --
CC  R5858, P11140.1A8R.
CC  R5859, P11140.1A8R.
DR  Interpro: IPRO001772; RICH_B_lectin.
DR  Interpro: IPRO001574; RIP.
DR  Pfam: PF006153; RICH_B_lectin; 6.
DR  Pfam: PF001614; RIP; 1.
DR  PRINTS: PR003966; SHIGACIN.
DR  SMART: SMO03968; RICHIN.2.

```

[illegible]

```

RT sequencing. Conservation and significance."
J. Mol. Biol. 229:263-267 (1993).
[2]
SEQUENCE OF 260-527.
RC TISSUE=Seed; PubMed=7763422;
RX MEDLINE=3169023; PubMed=7763422;
RN "Hultin R., Samadpour T., Funatsu G.;
RT "The complete amino acid sequence of the B-chains of abrin-a and
RT abrin-b toxic proteins from Rhus precatensis."
RT Biochim. Biophys. Acta 571:165-169 (1993).
CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,124 OF 28 S RNA.
CC ABRIN-A IS MORE TOXIC THAN RICIN.
CC -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
CC PRECEDES ENDOCYTOSIS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S RNA.
CC -1- DOMAIN: THE B CHAIN IS A MONOMER. EACH DOMAIN
CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC This Swiss-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M98345; AAA32625.1; -
DR PIR, S32430; S32430.
DR HSSP, P11140; 1ABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.
DR Pfam, PF00652; Ricin_B_lectin; 6.
DR SMART, SM00458; RICIN2.
DR SMART, SM00631; R1; 1.ABPR.
DR SMART, SM00631; R2; 1.BBPR.
DR SMART, SM00631; R3; 1.CBPR.
DR SMART, SM00631; R4; 1.DBPR.
DR SMART, SM00631; R5; 1.EBPR.
DR SMART, SM00631; R6; 1.FBPR.
DR SMART, SM00631; R7; 1.GBPR.
DR SMART, SM00631; R8; 1.HBPR.
DR SMART, SM00631; R9; 1.IBPR.
DR SMART, SM00631; R10; 1.JBPR.
DR SMART, SM00631; R11; 1.KBPR.
DR SMART, SM00631; R12; 1.LBPR.
DR SMART, SM00631; R13; 1.MBPR.
DR SMART, SM00631; R14; 1.NBPR.
DR SMART, SM00631; R15; 1.OBPR.
DR SMART, SM00631; R16; 1.PBPR.
DR SMART, SM00631; R17; 1.QBPR.
DR SMART, SM00631; R18; 1.RBPR.
DR SMART, SM00631; R19; 1.SBPR.
DR SMART, SM00631; R20; 1.TBPR.
DR SMART, SM00631; R21; 1.UBPR.
DR SMART, SM00631; R22; 1.VBPR.
DR SMART, SM00631; R23; 1.WBPR.
DR SMART, SM00631; R24; 1.XBPR.
DR SMART, SM00631; R25; 1.YBPR.
DR SMART, SM00631; R26; 1.ZBPR.
DR SMART, SM00631; R27; 1.ABPR.
DR SMART, SM00631; R28; 1.BBPR.
DR SMART, SM00631; R29; 1.CBPR.
DR SMART, SM00631; R30; 1.DBPR.
DR SMART, SM00631; R31; 1.EBPR.
DR SMART, SM00631; R32; 1.FBPR.
DR SMART, SM00631; R33; 1.GBPR.
DR SMART, SM00631; R34; 1.HBPR.
DR SMART, SM00631; R35; 1.IBPR.
DR SMART, SM00631; R36; 1.JBPR.
DR SMART, SM00631; R37; 1.KBPR.
DR SMART, SM00631; R38; 1.LBPR.
DR SMART, SM00631; R39; 1.MBPR.
DR SMART, SM00631; R40; 1.NBPR.
DR SMART, SM00631; R41; 1.OBPR.
DR SMART, SM00631; R42; 1.PBPR.
DR SMART, SM00631; R43; 1.QBPR.
DR SMART, SM00631; R44; 1.RBPR.
DR SMART, SM00631; R45; 1.SBPR.
DR SMART, SM00631; R46; 1.TBPR.
DR SMART, SM00631; R47; 1.UBPR.
DR SMART, SM00631; R48; 1.VBPR.
DR SMART, SM00631; R49; 1.WBPR.
DR SMART, SM00631; R50; 1.XBPR.
DR SMART, SM00631; R51; 1.YBPR.
DR SMART, SM00631; R52; 1.ZBPR.
DR SMART, SM00631; R53; 1.ABPR.
DR SMART, SM00631; R54; 1.BBPR.
DR SMART, SM00631; R55; 1.CBPR.
DR SMART, SM00631; R56; 1.DBPR.
DR SMART, SM00631; R57; 1.EBPR.
DR SMART, SM00631; R58; 1.FBPR.
DR SMART, SM00631; R59; 1.GBPR.
DR SMART, SM00631; R60; 1.HBPR.
DR SMART, SM00631; R61; 1.IBPR.
DR SMART, SM00631; R62; 1.JBPR.
DR SMART, SM00631; R63; 1.KBPR.
DR SMART, SM00631; R64; 1.LBPR.
DR SMART, SM00631; R65; 1.MBPR.
DR SMART, SM00631; R66; 1.NBPR.
DR SMART, SM00631; R67; 1.OBPR.
DR SMART, SM00631; R68; 1.PBPR.
DR SMART, SM00631; R69; 1.QBPR.
DR SMART, SM00631; R70; 1.RBPR.
DR SMART, SM00631; R71; 1.SBPR.
DR SMART, SM00631; R72; 1.TBPR.
DR SMART, SM00631; R73; 1.UBPR.
DR SMART, SM00631; R74; 1.VBPR.
DR SMART, SM00631; R75; 1.WBPR.
DR SMART, SM00631; R76; 1.XBPR.
DR SMART, SM00631; R77; 1.YBPR.
DR SMART, SM00631; R78; 1.ZBPR.
DR SMART, SM00631; R79; 1.ABPR.
DR SMART, SM00631; R80; 1.BBPR.
DR SMART, SM00631; R81; 1.CBPR.
DR SMART, SM00631; R82; 1.DBPR.
DR SMART, SM00631; R83; 1.EBPR.
DR SMART, SM00631; R84; 1.FBPR.
DR SMART, SM00631; R85; 1.GBPR.
DR SMART, SM00631; R86; 1.HBPR.
DR SMART, SM00631; R87; 1.IBPR.
DR SMART, SM00631; R88; 1.JBPR.
DR SMART, SM00631; R89; 1.KBPR.
DR SMART, SM00631; R90; 1.LBPR.
DR SMART, SM00631; R91; 1.MBPR.
DR SMART, SM00631; R92; 1.NBPR.
DR SMART, SM00631; R93; 1.OBPR.
DR SMART, SM00631; R94; 1.PBPR.
DR SMART, SM00631; R95; 1.QBPR.
DR SMART, SM00631; R96; 1.RBPR.
DR SMART, SM00631; R97; 1.SBPR.
DR SMART, SM00631; R98; 1.TBPR.
DR SMART, SM00631; R99; 1.UBPR.
DR SMART, SM00631; R100; 1.VBPR.
DR SMART, SM00631; R101; 1.WBPR.
DR SMART, SM00631; R102; 1.XBPR.
DR SMART, SM00631; R103; 1.YBPR.
DR SMART, SM00631; R104; 1.ZBPR.
DR SMART, SM00631; R105; 1.ABPR.
DR SMART, SM00631; R106; 1.BBPR.
DR SMART, SM00631; R107; 1.CBPR.
DR SMART, SM00631; R108; 1.DBPR.
DR SMART, SM00631; R109; 1.EBPR.
DR SMART, SM00631; R110; 1.FBPR.
DR SMART, SM00631; R111; 1.GBPR.
DR SMART, SM00631; R112; 1.HBPR.
DR SMART, SM00631; R113; 1.IBPR.
DR SMART, SM00631; R114; 1.JBPR.
DR SMART, SM00631; R115; 1.KBPR.
DR SMART, SM00631; R116; 1.LBPR.
DR SMART, SM00631; R117; 1.MBPR.
DR SMART, SM00631; R118; 1.NBPR.
DR SMART, SM00631; R119; 1.OBPR.
DR SMART, SM00631; R120; 1.PBPR.
DR SMART, SM00631; R121; 1.QBPR.
DR SMART, SM00631; R122; 1.RBPR.
DR SMART, SM00631; R123; 1.SBPR.
DR SMART, SM00631; R124; 1.TBPR.
DR SMART, SM00631; R125; 1.UBPR.
DR SMART, SM00631; R126; 1.VBPR.
DR SMART, SM00631; R127; 1.WBPR.
DR SMART, SM00631; R128; 1.XBPR.
DR SMART, SM00631; R129; 1.YBPR.
DR SMART, SM00631; R130; 1.ZBPR.
DR SMART, SM00631; R131; 1.ABPR.
DR SMART, SM00631; R132; 1.BBPR.
DR SMART, SM00631; R133; 1.CBPR.
DR SMART, SM00631; R134; 1.DBPR.
DR SMART, SM00631; R135; 1.EBPR.
DR SMART, SM00631; R136; 1.FBPR.
DR SMART, SM00631; R137; 1.GBPR.
DR SMART, SM00631; R138; 1.HBPR.
DR SMART, SM00631; R139; 1.IBPR.
DR SMART, SM00631; R140; 1.JBPR.
DR SMART, SM00631; R141; 1.KBPR.
DR SMART, SM00631; R142; 1.LBPR.
DR SMART, SM00631; R143; 1.MBPR.
DR SMART, SM00631; R144; 1.NBPR.
DR SMART, SM00631; R145; 1.OBPR.
DR SMART, SM00631; R146; 1.PBPR.
DR SMART, SM00631; R147; 1.QBPR.
DR SMART, SM00631; R148; 1.RBPR.
DR SMART, SM00631; R149; 1.SBPR.
DR SMART, SM00631; R150; 1.TBPR.
DR SMART, SM00631; R151; 1.UBPR.
DR SMART, SM00631; R152; 1.VBPR.
DR SMART, SM00631; R153; 1.WBPR.
DR SMART, SM00631; R154; 1.XBPR.
DR SMART, SM00631; R155; 1.YBPR.
DR SMART, SM00631; R156; 1.ZBPR.
DR SMART, SM00631; R157; 1.ABPR.
DR SMART, SM00631; R158; 1.BBPR.
DR SMART, SM00631; R159; 1.CBPR.
DR SMART, SM00631; R160; 1.DBPR.
DR SMART, SM00631; R161; 1.EBPR.
DR SMART, SM00631; R162; 1.FBPR.
DR SMART, SM00631; R163; 1.GBPR.
DR SMART, SM00631; R164; 1.HBPR.
DR SMART, SM00631; R165; 1.IBPR.
DR SMART, SM00631; R166; 1.JBPR.
DR SMART, SM00631; R167; 1.KBPR.
DR SMART, SM00631; R168; 1.LBPR.
DR SMART, SM00631; R169; 1.MBPR.
DR SMART, SM00631; R170; 1.NBPR.
DR SMART, SM00631; R171; 1.OBPR.
DR SMART, SM00631; R172; 1.PBPR.
DR SMART, SM00631; R173; 1.QBPR.
DR SMART, SM00631; R174; 1.RBPR.
DR SMART, SM00631; R175; 1.SBPR.
DR SMART, SM00631; R176; 1.TBPR.
DR SMART, SM00631; R177; 1.UBPR.
DR SMART, SM00631; R178; 1.VBPR.
DR SMART, SM00631; R179; 1.WBPR.
DR SMART, SM00631; R180; 1.XBPR.
DR SMART, SM00631; R181; 1.YBPR.
DR SMART, SM00631; R182; 1.ZBPR.
DR SMART, SM00631; R183; 1.ABPR.
DR SMART, SM00631; R184; 1.BBPR.
DR SMART, SM00631; R185; 1.CBPR.
DR SMART, SM00631; R186; 1.DBPR.
DR SMART, SM00631; R187; 1.EBPR.
DR SMART, SM00631; R188; 1.FBPR.
DR SMART, SM00631; R189; 1.GBPR.
DR SMART, SM00631; R190; 1.HBPR.
DR SMART, SM00631; R191; 1.IBPR.
DR SMART, SM00631; R192; 1.JBPR.
DR SMART, SM00631; R193; 1.KBPR.
DR SMART, SM00631; R194; 1.LBPR.
DR SMART, SM00631; R195; 1.MBPR.
DR SMART, SM00631; R196; 1.NBPR.
DR SMART, SM00631; R197; 1.OBPR.
DR SMART, SM00631; R198; 1.PBPR.
DR SMART, SM00631; R199; 1.QBPR.
DR SMART, SM00631; R200; 1.RBPR.
DR SMART, SM00631; R201; 1.SBPR.
DR SMART, SM00631; R202; 1.TBPR.
DR SMART, SM00631; R203; 1.UBPR.
DR SMART, SM00631; R204; 1.VBPR.
DR SMART, SM00631; R205; 1.WBPR.
DR SMART, SM00631; R206; 1.XBPR.
DR SMART, SM00631; R207; 1.YBPR.
DR SMART, SM00631; R208; 1.ZBPR.
DR SMART, SM00631; R209; 1.ABPR.
DR SMART, SM00631; R210; 1.BBPR.
DR SMART, SM00631; R211; 1.CBPR.
DR SMART, SM00631; R212; 1.DBPR.
DR SMART, SM00631; R213; 1.EBPR.
DR SMART, SM00631; R214; 1.FBPR.
DR SMART, SM00631; R215; 1.GBPR.
DR SMART, SM00631; R216; 1.HBPR.
DR SMART, SM00631; R217; 1.IBPR.
DR SMART, SM00631; R218; 1.JBPR.
DR SMART, SM00631; R219; 1.KBPR.
DR SMART, SM00631; R220; 1.LBPR.
DR SMART, SM00631; R221; 1.MBPR.
DR SMART, SM00631; R222; 1.NBPR.
DR SMART, SM00631; R223; 1.OBPR.
DR SMART, SM00631; R224; 1.PBPR.
DR SMART, SM00631; R225; 1.QBPR.
DR SMART, SM00631; R226; 1.RBPR.
DR SMART, SM00631; R227; 1.SBPR.
DR SMART, SM00631; R228; 1.TBPR.
DR SMART, SM00631; R229; 1.UBPR.
DR SMART, SM00631; R230; 1.VBPR.
DR SMART, SM00631; R231; 1.WBPR.
DR SMART, SM00631; R232; 1.XBPR.
DR SMART, SM00631; R233; 1.YBPR.
DR SMART, SM00631; R234; 1.ZBPR.
DR SMART, SM00631; R235; 1.ABPR.
DR SMART, SM00631; R236; 1.BBPR.
DR SMART, SM00631; R237; 1.CBPR.
DR SMART, SM00631; R238; 1.DBPR.
DR SMART, SM00631; R239; 1.EBPR.
DR SMART, SM00631; R240; 1.FBPR.
DR SMART, SM00631; R241; 1.GBPR.
DR SMART, SM00631; R242; 1.HBPR.
DR SMART, SM00631; R243; 1.IBPR.
DR SMART, SM00631; R244; 1.JBPR.
DR SMART, SM00631; R245; 1.KBPR.
DR SMART, SM00631; R246; 1.LBPR.
DR SMART, SM00631; R247; 1.MBPR.
DR SMART, SM00631; R248; 1.NBPR.
DR SMART, SM00631; R249; 1.OBPR.
DR SMART, SM00631; R250; 1.PBPR.
DR SMART, SM00631; R251; 1.QBPR.
DR SMART, SM00631; R252; 1.RBPR.
DR SMART, SM00631; R253; 1.SBPR.
DR SMART, SM00631; R254; 1.TBPR.
DR SMART, SM00631; R255; 1.UBPR.
DR SMART, SM00631; R256; 1.VBPR.
DR SMART, SM00631; R257; 1.WBPR.
DR SMART, SM00631; R258; 1.XBPR.
DR SMART, SM00631; R259; 1.YBPR.
DR SMART, SM00631; R260; 1.ZBPR.
DR SMART, SM00631; R261; 1.ABPR.
DR SMART, SM00631; R262; 1.BBPR.
DR SMART, SM00631; R263; 1.CBPR.
DR SMART, SM00631; R264; 1.DBPR.
DR SMART, SM00631; R265; 1.EBPR.
DR SMART, SM00631; R266; 1.FBPR.
DR SMART, SM00631; R267; 1.GBPR.
DR SMART, SM00631; R268; 1.HBPR.
DR SMART, SM00631; R269; 1.IBPR.
DR SMART, SM00631; R270; 1.JBPR.
DR SMART, SM00631; R271; 1.KBPR.
DR SMART, SM00631; R272; 1.LBPR.
DR SMART, SM00631; R273; 1.MBPR.
DR SMART, SM00631; R274; 1.NBPR.
DR SMART, SM00631; R275; 1.OBPR.
DR SMART, SM00631; R276; 1.PBPR.
DR SMART, SM00631; R277; 1.QBPR.
DR SMART, SM00631; R278; 1.RBPR.
DR SMART, SM00631; R279; 1.SBPR.
DR SMART, SM00631; R280; 1.TBPR.
DR SMART, SM00631; R281; 1.UBPR.
DR SMART, SM00631; R282; 1.VBPR.
DR SMART, SM00631; R283; 1.WBPR.
DR SMART, SM00631; R284; 1.XBPR.
DR SMART, SM00631; R285; 1.YBPR.
DR SMART, SM00631; R286; 1.ZBPR.
DR SMART, SM00631; R287; 1.ABPR.
DR SMART, SM00631; R288; 1.BBPR.
DR SMART, SM00631; R289; 1.CBPR.
DR SMART, SM00631; R290; 1.DBPR.
DR SMART, SM00631; R291; 1.EBPR.
DR SMART, SM00631; R292; 1.FBPR.
DR SMART, SM00631; R293; 1.GBPR.
DR SMART, SM00631; R294; 1.HBPR.
DR SMART, SM00631; R295; 1.IBPR.
DR SMART, SM00631; R296; 1.JBPR.
DR SMART, SM00631; R297; 1.KBPR.
DR SMART, SM00631; R298; 1.LBPR.
DR SMART, SM00631; R299; 1.MBPR.
DR SMART, SM00631; R300; 1.NBPR.
DR SMART, SM00631; R301; 1.OBPR.
DR SMART, SM00631; R302; 1.PBPR.
DR SMART, SM00631; R303; 1.QBPR.
DR SMART, SM00631; R304; 1.RBPR.
DR SMART, SM00631; R305; 1.SBPR.
DR SMART, SM00631; R306; 1.TBPR.
DR SMART, SM00631; R307; 1.UBPR.
DR SMART, SM00631; R308; 1.VBPR.
DR SMART, SM00631; R309; 1.WBPR.
DR SMART, SM00631; R310; 1.XBPR.
DR SMART, SM00631; R311; 1.YBPR.
DR SMART, SM00631; R312; 1.ZBPR.
DR SMART, SM00631; R313; 1.ABPR.
DR SMART, SM00631; R314; 1.BBPR.
DR SMART, SM00631; R315; 1.CBPR.
DR SMART, SM00631; R316; 1.DBPR.
DR SMART, SM00631; R317; 1.EBPR.
DR SMART, SM00631; R318; 1.FBPR.
DR SMART, SM00631; R319; 1.GBPR.
DR SMART, SM00631; R320; 1.HBPR.
DR SMART, SM00631; R321; 1.IBPR.
DR SMART, SM00631; R322; 1.JBPR.
DR SMART, SM00631; R323; 1.KBPR.
DR SMART, SM00631; R324; 1.LBPR.
DR SMART, SM00631; R325; 1.MBPR.
DR SMART, SM00631; R326; 1.NBPR.
DR SMART, SM00631; R327; 1.OBPR.
DR SMART, SM00631; R328; 1.PBPR.
DR SMART, SM00631; R329; 1.QBPR.
DR SMART, SM00631; R330; 1.RBPR.
DR SMART, SM00631; R331; 1.SBPR.
DR SMART, SM00631; R332; 1.TBPR.
DR SMART, SM00631; R333; 1.UBPR.
DR SMART, SM00631; R334; 1.VBPR.
DR SMART, SM00631; R335; 1.WBPR.
DR SMART, SM00631; R336; 1.XBPR.
DR SMART, SM00631; R337; 1.YBPR.
DR SMART, SM00631; R338; 1.ZBPR.
DR SMART, SM00631; R339; 1.ABPR.
DR SMART, SM00631; R340; 1.BBPR.
DR SMART, SM00631; R341; 1.CBPR.
DR SMART, SM00631; R342; 1.DBPR.
DR SMART, SM00631; R343; 1.EBPR.
DR SMART, SM00631; R344; 1.FBPR.
DR SMART, SM00631; R345; 1.GBPR.
DR SMART, SM00631; R346; 1.HBPR.
DR SMART, SM00631; R347; 1.IBPR.
DR SMART, SM00631; R348; 1.JBPR.
DR SMART, SM00631; R349; 1.KBPR.
DR SMART, SM00631; R350; 1.LBPR.
DR SMART, SM00631; R351; 1.MBPR.
DR SMART, SM00631; R352; 1.NBPR.
DR SMART, SM00631; R353; 1.OBPR.
DR SMART, SM00631; R354; 1.PBPR.
DR SMART, SM00631; R355; 1.QBPR.
DR SMART, SM00631; R356; 1.RBPR.
DR SMART, SM00631; R357; 1.SBPR.
DR SMART, SM00631; R358; 1.TBPR.
DR SMART, SM00631; R359; 1.UBPR.
DR SMART, SM00631; R360; 1.VBPR.
DR SMART, SM00631; R361; 1.WBPR.
DR SMART, SM00631; R362; 1.XBPR.
DR SMART, SM00631; R363; 1.YBPR.
DR SMART, SM00631; R364; 1.ZBPR.
DR SMART, SM00631; R365; 1.ABPR.
DR SMART, SM00631; R366; 1.BBPR.
DR SMART, SM00631; R367; 1.CBPR.
DR SMART, SM00631; R368; 1.DBPR.
DR SMART, SM00631; R369; 1.EBPR.
DR SMART, SM00631; R370; 1.FBPR.
DR SMART, SM00631; R371; 1.GBPR.
DR SMART, SM00631; R372; 1.HBPR.
DR SMART, SM00631; R373; 1.IBPR.
DR SMART, SM00631; R374; 1.JBPR.
DR SMART, SM00631; R375; 1.KBPR.
DR SMART, SM00631; R376; 1.LBPR.
DR SMART, SM00631; R377; 1.MBPR.
DR SMART, SM00631; R378; 1.NBPR.
DR SMART, SM00631; R379; 1.OBPR.
DR SMART, SM00631; R380; 1.PBPR.
DR SMART, SM00631; R381; 1.QBPR.
DR SMART, SM00631; R382; 1.RBPR.
DR SMART, SM00631; R383; 1.SBPR.
DR SMART, SM00631; R384; 1.TBPR.
DR SMART, SM00631; R385; 1.UBPR.
DR SMART, SM00631; R386; 1.VBPR.
DR SMART, SM00631; R387; 1.WBPR.
DR SMART, SM00631; R388; 1.XBPR.
DR SMART, SM00631; R389; 1.YBPR.
DR SMART, SM00631; R390; 1.ZBPR.
DR SMART, SM00631; R391; 1.ABPR.
DR SMART, SM00631; R392; 1.BBPR.
DR SMART, SM00631; R393; 1.CBPR.
DR SMART, SM00631; R394; 1.DBPR.
DR SMART, SM00631; R395; 1.EBPR.
DR SMART, SM00631; R396; 1.FBPR.
DR SMART, SM00631; R397; 1.GBPR.
DR SMART, SM00631; R398; 1.HBPR.
DR SMART, SM00631; R399; 1.IBPR.
DR SMART, SM00631; R400; 1.JBPR.
DR SMART, SM00631; R401; 1.KBPR.
DR SMART, SM00631; R402; 1.LBPR.
DR SMART, SM00631; R403; 1.MBPR.
DR SMART, SM00631; R404; 1.NBPR.
DR SMART, SM00631; R405; 1.OBPR.
DR SMART, SM00631; R406; 1.PBPR.
DR SMART, SM00631; R407; 1.QBPR.
DR SMART, SM00631; R408; 1.RBPR.
DR SMART, SM00631; R409; 1.SBPR.
DR SMART, SM00631; R410; 1.TBPR.
DR SMART, SM00631; R411; 1.UBPR.
DR SMART, SM00631; R412; 1.VBPR.
DR SMART, SM00631; R413; 1.WBPR.
DR SMART, SM00631; R414; 1.XBPR.
DR SMART, SM00631; R415; 1.YBPR.
DR SMART, SM00631; R416; 1.ZBPR.
DR SMART, SM00631; R417; 1.ABPR.
DR SMART, SM00631; R418; 1.BBPR.
DR SMART, SM00631; R419; 1.CBPR.
DR SMART, SM00631; R420; 1.DBPR.
DR SMART, SM00631; R421; 1.EBPR.
DR SMART, SM00631; R422; 1.FBPR.
DR SMART, SM00631; R423; 1.GBPR.
DR SMART, SM00631; R424; 1.HBPR.
DR SMART, SM00631; R425; 1.IBPR.
DR SMART, SM00631; R426; 1.JBPR.
DR SMART, SM00631; R427; 1.KBPR.
DR SMART, SM00631; R428; 1.LBPR.
DR SMART, SM00631; R429; 1.MBPR.
DR SMART, SM00631; R430; 1.NBPR.
DR SMART, SM00631; R431; 1.OBPR.
DR SMART, SM00631; R432; 1.PBPR.
DR SMART, SM00631; R433; 1.QBPR.
DR SMART, SM00631; R434; 1.RBPR.
DR SMART, SM00631; R435; 1.SBPR.
DR SMART, SM00631; R436; 1.TBPR.
DR SMART, SM00631; R437; 1.UBPR.
DR SMART, SM00631; R438; 1.VBPR.
DR SMART, SM00631; R439; 1.WBPR.
DR SMART, SM00631; R440; 1.XBPR.
DR SMART, SM00631; R441; 1.YBPR.
DR SMART, SM00631; R442; 1.ZBPR.
DR SMART, SM00631; R443; 1.ABPR.
DR SMART, SM00631; R444; 1.BBPR.
DR SMART, SM00631; R445; 1.CBPR.
DR SMART, SM00631; R446; 1.DBPR.
DR SMART, SM00631; R447; 1.EBPR.
DR SMART, SM00631; R448; 1.FBPR.
DR SMART, SM00631; R449; 1.GBPR.
DR SMART, SM00631; R450; 1.HBPR.
DR SMART, SM00631; R451; 1.IBPR.
DR SMART, SM00631; R452; 1.JBPR.
DR SMART, SM00631; R453; 1.KBPR.
DR SMART, SM00631; R454; 1.LBPR.
DR SMART, SM00631; R455; 1.MBPR.
DR SMART, SM00631; R456; 1.NBPR.
DR SMART, SM00631; R457; 1.OBPR.
DR SMART, SM00631; R458; 1.PBPR.
DR SMART, SM00631; R459; 1.QBPR.
DR SMART, SM00631; R460; 1.RBPR.
DR SMART, SM00631; R461; 1.SBPR.
DR SMART, SM00631; R462; 1.TBPR.
DR SMART, SM00631; R463; 1.UBPR.
DR SMART, SM00631; R464; 1.VBPR.
DR SMART, SM00631; R465; 1.WBPR.
DR SMART, SM00631; R466; 1.XBPR.
DR SMART, SM00631; R467; 1.YBPR.
DR SMART, SM00631; R468; 1.ZBPR.
DR SMART, SM00631; R469; 1.ABPR.
DR SMART, SM00631; R470; 1.BBPR.
DR SMART, SM00631; R471; 1.CBPR.
DR SMART, SM00631; R472; 1.DBPR.
DR SMART, SM00631; R473; 1.EBPR.
DR SMART, SM00631; R474; 1.FBPR.
DR SMART, SM00631; R475; 1.GBPR.
DR SMART, SM00631; R476; 1.HBPR.
DR SMART, SM00631; R477; 1.IBPR.
DR SMART, SM00631; R478; 1.JBPR.
DR SMART, SM00631; R479; 1.KBPR.
DR SMART, SM00631; R480; 1.LBPR.
DR SMART, SM00631; R481; 1.MBPR.
DR SMART, SM00631; R482; 1.NBPR.
DR SMART, SM00631; R483; 1.OBPR.
DR SMART, SM00631; R484; 1.PBPR.
DR SMART, SM00631; R485; 1.QBPR.
DR SMART, SM00631; R486; 1.RBPR.
DR SMART, SM00631; R487; 1.SBPR.
DR SMART, SM00631; R488; 1.TBPR.
DR SMART, SM00631; R489; 1.UBPR.
DR SMART, SM00631; R490; 1.VBPR.
DR SMART, SM00631; R491; 1.WBPR.
DR SMART, SM00631; R492; 1.XBPR.
DR SMART, SM00631; R493; 1.YBPR.
DR SMART, SM00631; R494; 1.ZBPR.
DR SMART, SM00631; R495; 1.ABPR.
DR SMART, SM00631; R496; 1.BBPR.
DR SMART, SM00631; R497; 1.CBPR.
DR SMART, SM00631; R498; 1.DBPR.
DR SMART, SM00631; R499; 1.EBPR.
DR SMART, SM00631; R500; 1.FBPR.
DR SMART, SM00631; R501; 1.GBPR.
DR SMART, SM00631; R502; 1.HBPR.
DR SMART, SM00631; R503; 1.IBPR.
DR SMART, SM00631; R504; 1.JBPR.
DR SMART, SM00631; R505; 1.KBPR.
DR SMART, SM00631; R506; 1.LBPR.
DR SMART, SM00631; R507; 1.MBPR.
DR SMART, SM00631; R508; 1.NBPR.
DR SMART, SM00631; R509; 1.OBPR.
DR SMART, SM00631; R510; 1.PBPR.
DR SMART, SM00631; R511; 1.QBPR.
DR SMART, SM00631; R512; 1.RBPR.
DR SMART, SM00631; R513; 1.SBPR.
DR SMART, SM00631; R514; 1.TBPR.
DR SMART, SM00631; R515; 1.UBPR.
DR SMART, SM00631; R516; 1.VBPR.
DR SMART, SM00631; R517; 1.WBPR.
DR SMART, SM00631; R518; 1.XBPR.
DR SMART, SM00631; R519; 1.YBPR.
DR SMART, SM00631; R520; 1.ZBPR.
DR SMART, SM00631; R521; 1.ABPR.
DR SMART, SM00631; R522; 1.BBPR.
DR SMART, SM00631; R523; 1.CBPR.
DR SMART, SM00631; R524; 1.DBPR.
DR SMART, SM00631; R525; 1.EBPR.
DR SMART, SM00631; R526; 1.FBPR.
DR SMART, SM00631; R527; 1.GBPR.
DR SMART, SM00631; R528;
```

CC	SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNIT BY REMOVING ADENINE FROM POSITION 4,124 OF 28S RNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PROBESSES ENDOCYTOSIS.
CC	-1- CATALYTIC ACTIVITY: Endopolymerolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC	-1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC	-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.
CC	-1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC	This Swiss-Pro entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).
CC	-- -- -- -- --
DR	EMBL: Y41299, J03839, F71511. -
DR	IRP: P00007722. Ricin_B_lectin.
DR	Interpro: IPR001574; RIP.
DR	Pfam: PF00652; Ricin_B_lectin. 6.
DR	Pfam: PF00161; RIP.1.
DR	PRINTS: PR00396; SHIGARICIN.
DR	SMART: SMO0459; RICIN; 2.
DR	PROSITE: PS0075; SHIGA_RICIN. 1.
DR	FLORESITE: RS00231; RICIN_B_LECTIN; 2.
KR	Plant defense: Ribicin B lectin synthetis inhibitor; Toxin; Repeat;
KX	Giant defense: Ribicin B lectin synthetis inhibitor; Toxin; Repeat;
FT	SIGNAL 1 25
FT	CHAIN 26 297
FT	NIGRIN B A CHAIN.
FT	CHAIN 298 563
FT	NIGRIN B B CHAIN.
FT	DOMAIN 305 431
FT	RICIN B-TYPE LECTIN 1.
FT	DOMAIN 434 559
FT	RICIN B-TYPE LECTIN 2.
FT	REPEAT 316 356
FT	1-ALPHA.
FT	REPEAT 357 397
FT	1-BETA.
FT	REPEAT 398 438
FT	1-ALPHA.
FT	REPEAT 445 482
FT	2-ALPHA.
FT	REPEAT 526 554
FT	2-BETA.
FT	REPEAT 554 582
FT	2-GAMMA.
FT	ACT SITE 188 188
FT	DISULFID 274 302
FT	BY SIMILARITY.
FT	INTERCHAIN (BY SIMILARITY).
FT	DISULFID 310 338
FT	BY SIMILARITY.
FT	DISULFID 360 377
FT	BY SIMILARITY.
FT	CASABOYD 448 463
FT	N-LINKED (GLCNAAC.)
FT	CASABOYD 421 436
FT	N-LINKED (GLCNAAC.)
FT	CASABOYD 368 383
FT	N-LINKED (GLCNAAC.)
FT	CASABOYD 376 376
FT	N-LINKED (GLCNAAC.)
FT	CASABOYD 483 483
FT	N-LINKED (GLCNAAC.)
FT	CASABOYD 537 537
FT	N-LINKED (GLCNAAC.)
FT	CASABOYD 39 39
FT	K > V (IN REF. 2).
FT	CONFLICT
SO	SEQUENCE 563 AA; 62300 MW; F50CEBCE4621BF14 CRGCA4;
	Query Match 37.38; Score 494.5; DB.1 Length 563;
	Best Local Similarity 39.4%; Proc No. 2.5e-41;
	Matches 104; Conservative 40; Mismatches 113; Indels 7; Gaps 5
D5	1 DDVTCASAEETVR-IIVGRGXQKQVDYDDDFHGHQNIQLMPSKSNDRPVQATLTIRDXDTIR 59
D6	298 GSECTCTLSFTSMNVIRPGDCADVANSVDTSTFLDLFGFCIOR-NQRMTFFSDSRIR 355
Oy	60 HNSGCTCTTGRTSMNVIRPGCNAPAGTGTQIQWKKSGTIIPRNYSMLIASSGIKOTLL 119
D8	356 HWCKCTGNTANGSVTVIFVFNCSIAEKLAKWEVDPIGDSINBSGLWTAPLARSPTLL 415
Oy	120 TWQTLDYTLTGQGLMGADAPREVTTVFQFDLCQENSN-XGSIVWETCASQSQXQXVMVL 177
DB	416 LLEBNITVAASGVATVINNRKVIVASIVYIKWKQLQSNBNGNWEDDEKTSLLQC-QML 474

```

OY      178 YDDSDSIFRPNQDQCCLTNGDSVSIVINIVISCSXXXKXRFVFNENALINKKKXXXXXV 237
Db      475 YDDDTIRNARSRLCVTTNVNSXXDLIIITLKQGLF-SGFVFNISGDAIYNRSRWMDV 533
OY      238 AQAAPKLRIILIPATSGNQMA 261
Db      534 RANVSLRELIIRAFNRQDM 557

-----
OY      RESULT 8
ID      XYNA_STRL1
AC      P26514; E96464; STANDARD; FRT; 477 AA.
DE      01-AUG-1992 (Rel. 23, Created)
DF      03-MAY-2000 (Rel. 39, Last sequence update)
DI      15-SEP-2003 (Rel. 45, Last annotation update)
DR      Kunitz, J., Miller, A. precursor (BC 3.2.1.6) (Xylanase A)
DN      beta-D-xylan xylohydrolase A).
OS      Streptomyces lividans.
OC      Bacteria; Actinobacterii; Actinomycetales;
CC      Streptomycetaceae; Streptococcaceae; Streptomyces.
CX      NCBI_TaxID=1916;
NM      [1]
NN      SEQUENCE FROM N.A., AND SEQUENCE OF 42-92.
RX      STRAIN=66_1126; PubMed=174351;
RA      Kluepfel D.; Roy C.; Yaguchi M.; Morosoli R.; Kluepfel D.;
RP      "Genomics of three gene specifying xylanases in Streptomyces
RT      lividans.";
RL      Gene 107:75-82(1991).
RN      (2)
RR      REVISIONS TO 20 AND 140-141.
RS      STRAIN=66 / 1326;
RA      Shareck F.;
RB      Submitted (JUL-1996) to the EMBL/Genbank/DDCG databases.
RX      X-343 CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 42-340.
ME      MERLIN=94342323; PubMed=665693;
RA      Derewenda U.; Swenson L.; Green R.; Wei Y.Y.; Morosoli R.; Shareck F.;
RT      "Crystal structure, at 2.6-A resolution, of the Streptomyces lividans
RL      xylanase A, a member of the F family of beta-1,4-D-glycoses.";
RJ      J. Biol. Chem. 269:20811-20814(1994).
CC      -1- FUNCTION: Contributes to hydrolytic hemifiliplose, the major
CC      component of plant cell-walls. Substrate xylan seem to act
CC      sequentially on the substrate to yield xylobiose and xylotriose
CC      oligomers.
CC      -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC      linkages in xylans.
CC      -1- PATHWAY: Xylan degradation.
CC      -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY F (FAMILY 10 OF GLYCOSTYL
CC      HYDROLASES).
CC      -1- SIMILARITY: Contains I ylein B-type lectin domain.
CC      -----
CC      THIS SWISS-PROT entry is a copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL databank. The
CC      European Bioinformatics Institute. There are no restrictions on its use.
CC      CC use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/about/cvse/
CC      or send an email to licenses@isb-sib.ch).
CC      -----
DB      EMBL; AE64551; AAC26525.1; -.
DB      EMBL; U50289; S0AX25.
DB      EMBL; LE0V; 25-MAY-01.
DB      EMBL; IE0W; 25-MAY-01.
DB      EMBL; IKML; 19-JUN-02.
DB      EMBL; IKMW; 19-JUN-02.
DB      EMBL; IMC9; 11-SEP-02.
DB      Interpro; IPRO01000; Glyco_hydr_10.

```

```
DR Interpro: IPR000772; Ricin B lectin.
DR Pfam: PF00331; Glyco_Hydro_10; 1.
DR Pfam: PF00652; Ricin B lectin; 3.
DR PRINTS: PR00134; GUMHYDROLASE10.
DR SMART: SM00653; Glyco_10; 1.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE: PS00231; RICIN B LECTIN; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
KW 3D-structure.
FT SIGNAL. 1 41
FT CHAIN 42 477 ENDO-1,4-BETA-XYLANASE A.
FT DOMAIN 361 477 RICIN B-TYPE LECTIN.
FT ACT_SITE 169 169 PROTON DONOR.
FT ACT_SITE 277 277 NUCLEOPHILS.
SQ SEQUENCE 477 AA; 51162 MW; E14AFB37BDC68CC CRC64;

Query Match
Best Local Similarity 29.18%; Pred. No. 000363;
Matches 39; Conservative 19; Mismatches 63; Indels 13; Gaps 6;

QY 7 ASER-----TWIATGKXKXVYVNDPDPHNGNIOIPEKSNMPPNOLMTIKKXITRSM 61
Db 346 SSBPAPDGGQIKVWG-SGRCLADVPDASTSDGTLQIMDCSGT--NOMALATAGALRY 402
QY 62 G-SCLTGYGTAGVYVMTFPCNTAVREATIWIQXKGIINPNSLVLA--SSGIKQT 118
Db 403 GRCILDAGTNSKVOIYSCWGDNR--WRINSDSVGVGSLCLAVNGTANGTL 460
QY 119 LVVQTLDTTLQCGW 132
Db 461 IOLYTGNSGNSQNR 474

RESULT 9
SPL_RARFA STANDARD; PRT; 525 AA.
AC 005308;
DT 01-FEB-1995 (Rel. 31, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
OS Parabacter faecitabidus
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Parabacteraceae; Parabacter.
NCBI_TaxId=13243;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 212-222; 224-238 AND 240-244.
RC STRAIN-YLM-50;
RX MEDLINE=9309426; PubMed=133945;
RA Shimoi H., Iimura Y., Oota T., Tadenuma M.;
RT Molecular structure of Parabacter faecitabidus protease I. A yeast-
RT lytic serine protease having mannose-binding activity.";
RL J Biol. Chem. 267:25189-25193 (1992).
RN [2]
RP SEQUENCE OF 212-247.
RX MEDLINE=9233666; PubMed=1776983;
RA Shimoi H., Tadenuma M.;
RT "Characterization of Parabacter faecitabidus protease I, a
RT yeast-lytic serine protease having mannose-binding activity.";
RL J. Biochem. 110:608-613 (1991).
RN [3]
RP FUNCTION: MAJOR SERINE PROTEASE EXHIBITING LYTIC ACTIVITY TOWARD
RP LIVING YEAST CELLS. SIMILAR TO ELASTASE IN ITS SUBSTRATE
RP SPECIFICITY AND HAS A LECTIN-LIKE AFFINITY FOR MANNOSE.
RP PARABACTER LOCATED IN THE MANNIT SUBSTRATE FOR PFI.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2A.
CC -1- SIMILARITY: BELONGS TO RICIN B-TYPE LECTIN DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2A.
CC -1- SIMILARITY: BELONGS TO RICIN B-TYPE LECTIN DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
```

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

```
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

```
DR EMBL: D10753; AA05053.
DR EMBL: A45053; AA05053.
DR EMBL: F00178; F00178.
DR EMBL: F00178; F00178.
DR Interpro: IPR004216; AL protease.
DR Interpro: IPR001315; Endopeptidase.
DR Interpro: IPR000772; Ricin B lectin.
DR Interpro: IPR001254; Ser protease_Try.
DR Pfam: PF02983; AL protease; 1.
DR Pfam: PF00652; Ricin B lectin; 3.
DR PRINTS: PR00861; ALYITCPTASE.
DR SMART: SM00459; RYPSIN_HIS; 1.
DR PROSITE: PS00134; TRYPsin_HIS; 1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
DR PROSITE: PS00231; RICIN B LECTIN; 1.
DR Xylan degradation; Serine protease; Mannose-binding; Signal; Zymogen;
KW Lectin.
FT SIGNAL. 1 32
FT PROPER 33 211 POTENTIAL.
FT CHAIN 212 525 SERINE PROTEASE I.
FT DOMAIN 396 525 RICIN B-TYPE LECTIN.
FT DOMAIN 401 525 ESSENTIAL FOR THE LYTIC ACTIVITY, BUT NOT
FT DISULFID 223 239 BY SIMILARITY.
FT DISULFID 310 320 BY SIMILARITY.
FT DISULFID 346 346 BY SIMILARITY.
FT DISULFID 412 412 BY SIMILARITY.
FT DISULFID 443 443 BY SIMILARITY.
FT DISULFID 496 514 BY SIMILARITY.
FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 270 270 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 525 AA; 55654 MW; DA2BCF7330EBB61 CRC64;

Query Match
Best Local Similarity 30.28%; Pred. No. 0.01; Length 525;
Matches 32; Conservative 17; Mismatches 45; Indels 12; Gaps 5;

QY 2 DYCNSAPSPVIVIGKXKXVYVNDPDPHNGNIOIPEKSNMPPNOLMTIKKXITRSM 61
Db 451 GRCILDAGTNSKVOIYSCWGDNR--WRINSDSVGVGSLCLAVNGTANGTL 494
QY 399 DVT-----TSYGVQGNICIDVNSDPTDQGVNNGNIN--AQVGFPHDGLRLIN 450
```


CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
 CC in 1,3-beta-D-glucans.
 CC -1- SUBCELLULAR LOCATION: Periplasmic (by similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY 64 OF GLYCOSYL HYDROLASES.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D21668; RA04892.1;
 CC DR HESP; P02879; 2A1.
 CC DR InterPro; IPR000772; Ricin B lectin.
 CC DR Pfam; P00652; Ricin B lectin; 3.
 CC DR SMART; SM00458; RICIN; 1.
 CC DR PROSITE; PS0231; Ricin B lectin; 1.
 CC KW Hydroxylase; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.
 CC FT SIGNAL 1 36 POTENTIAL.
 CC FT CHAIN 37 548 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE.
 CC FT DOMAIN 422 548 RICIN B-TYPE LECTIN.
 CC SEQUENCE 548 AA; 58164 MW; ED6354315750596 CRC64;
 CC -----
 CC Query Match 7.6%; Score 101; DB 1; Length 548;
 CC Best Local Similarity 30.8%; Pred. No. 0.021;
 CC Matches 37; Conservative 13; Mismatches 54; Indels 16; Gaps 5;
 CC -----
 CC Db 434 LDVPMADPTDITNOVL-ATCGNAAQQTGRTGDTFALGKLDVARSGTADGNVWIT 491
 CC QY 80 DONTAVRENTIWIIV---XNGTIPRNSVLAASGI---KGTTLVQTLDTYLAGQW 132
 CC DB 492 TCN-----GTGAQKVTDSATKALRNFGSKGLDQGAFLDQKQVQLMTCTNQTBAQW 546
 CC -----
 CC RESULT 11
 CC E13B OERXA STANDARD; PRT; 548 AA.
 CC AC P2222;
 CC DT 01-AUG-1991 (Rel. 19, Created)
 CC DT 01-AUG-1991 (Rel. 19, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-
 CC glucan endoglucanase) ((1->3)-beta-glucanase).
 CC DE Desoxya xanthinobactera Actinobacteridae; Actinomycetales;
 CC DE Desoxya xanthinobactera Actinobacteridae; Actinomycetales;
 CC CC Micrococciaceae; Promicromonosporaceae; Cellulosimicrobium.
 CC CC NCBI_Taxid=4710;
 CC RN [1]
 CC RP SEQUENCE FROM N.A. AND SEQUENCE OF 37-63.
 CC RA MEDLINE-91093212; PubMed-1985933;
 CC RA Shen S.-H., Chretien P., Baettlen L., Siliaty S.N.,
 CC RT "Primary sequence of the glucanase gene from Oerskovia
 CC xanthinobactera: Expression and purification of the enzyme from
 CC Escherichia coli." J. Biol. Chem. 268:1058-1063 (1991).
 CC RT J. Biol. Chem. 268:1058-1063 (1991).
 CC CC -1- INVOLVED IN THE DEFENSE AGAINST FUNGAL PATHOGENS.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
 CC in 1,3-beta-D-glucans.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: BELONGS TO FAMILY 64 OF GLYCOSYL HYDROLASES.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M60826; AA25520.1;
 CC DR EPR; A39094; A39094.
 CC DR HESP; P02879; 2A1.
 CC DR InterPro; IPR000772; Ricin B lectin.
 CC DR Pfam; P00652; Ricin B lectin; 3.
 CC DR SMART; SM00458; RICIN; 1.
 CC DR PROSITE; PS0231; Ricin B lectin; 1.
 CC KW Hydroxylase; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.
 CC FT SIGNAL 1 36 POTENTIAL.
 CC FT CHAIN 37 548 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE.
 CC FT DOMAIN 422 548 RICIN B-TYPE LECTIN.
 CC FT DOMAIN 430 430 UNABLE TO LYSE VIABLE CELLS.
 CC FT DOMAIN 472 548 ESSENTIAL FOR THE LYTIC ACTIVITY, BUT NOT
 CC FT SEQUENCE 548 AA; 58088 MW; 412554AA24C04B CRC64;
 CC -----
 CC Query Match 7.6%; Score 101; DB 1; Length 548;
 CC Best Local Similarity 30.8%; Pred. No. 0.021;
 CC Matches 37; Conservative 13; Mismatches 54; Indels 16; Gaps 5;
 CC -----
 CC Db 434 LDVPMADPTDITNOVL-ATCGNAAQQTGRTGDTFALGKLDVARSGTADGNVWIT 491
 CC QY 80 DONTAVRENTIWIIV---XNGTIPRNSVLAASGI---KGTTLVQTLDTYLAGQW 132
 CC DB 492 TCN-----GTGAQKVTDSATKALRNFGSKGLDQGAFLDQKQVQLMTCTNQTBAQW 546
 CC -----
 CC RESULT 12
 CC ABBE STRECO STANDARD; PRT; 475 AA.
 CC AC O6461;
 CC DT 15-DEC-1998 (Rel. 37, Created)
 CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).
 CC GN ABBE OR SC05932 OR SC7H.02.
 CC OS Streptomyces coelicolor.
 CC CC Bacteria; Actinobacteridae; Actinomycetales;
 CC CC Streptomyces; Streptomyces; Streptomyces.
 CC CC NCBI_Taxid=1902;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RA MEDLINE-2196410; PubMed-1200953;
 CC RA Bentley S.D., Chater K.F., Csereto-Farraga A.-W., Challis G.L.,
 CC RA Thomson N.R., James K.D., Harris D.S., Quail M.A., Kleser H.,
 CC RA Harper D., Bateman A., Brown S., Chanda G., Chen C.W., Collins M.,
 CC RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 CC RA Huang C.-H., Kleser T., Latke L., Murphy L., Oliver K., O'Neill S.,
 CC RA Rabinowitsch S., Rajandream M.A., Rutherford S., Rutter C., Taylor K.,
 CC RA Seeger K., Saunders D., Sharp S., Segura K., Singer G., Taylor K.,
 CC RA Wanger I., Metcalf A., Woodward A., Barrett B.G., Parkhill J.,
 CC RA "Complete genome sequence of the model actinomycete Streptomyces
 CC coelicolor (312)." Nature 417:141-147 (2002).
 CC RT Nature 417:141-147 (2002).
 CC CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-
 CC arabinofuranoside residues in alpha-L-arabinosides.
 CC -1- PATHWAY: xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: A091125; CANA6189.1; --

DR PIR: P03697; 1567; Glyco hydro 62.
 DR Interpro: IPR005193; Glyco hydro 62.
 DR Interpro: IPR00772; Ricin B lectin.
 DR Pfam: PF03664; Glyco hydro 62; 1.
 DR Pfam: PF00652; Ricin B lectin; 3.
 DR SMART: SM00458; RICIN, 1.
 DR PROSITE: PS50231; RICIN B LECTIN; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
 KM Complete proteome.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 475 ALPHA-L-ARABINOFURANOSIDASE.
 FT DOMAIN 39 166 RICIN B-TYPE LECTIN.
 FT SEQUENCE 475 AA; 50045 MW; 476707F833C60D CRC64;
 Query Match 7.0%; Score 93.5; DB 1; Length 475;
 Best Local Similarity 27.3%; Pred. No. 0.1; Mismatches 66; Indels 9; Gaps 6;
 Matches 35; Conservative 18; Mismatches 66; Indels 9; Gaps 6;

QY 22 VDVRDDDFDNGNQLMPKSKNDPQQLTKRDXITRNSG-SCITTYGYTA--GYVMI 78
 DB 52 LDVLGSGDDGALLQLYDCMGST--NQMTSTDTGRLTYGDKLDPGHAATPRTVQI 109
 QY 79 FDCNTAVREATIQWIXNGTIINPNSLVL-ASASGI-KETITLVQTLDTYLGQGLAGN 136
 DB 110 WSGSGNQ--WRVSDGVIVGVSGLCLAKAKGTGNGAVQMTGNSGNGKXTGLT 167
 QY 137 DPAPEVT 144
 DB 168 GTPPTDT 175

RESULT 13
 ASPE STRLI STANDARD; FRT; 475 AA.
 ID ASPE STRLI
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).
 GN ASFP.
 OS Streptomyces lividans.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Streptomycinae; Streptomycetaceae; Streptomyces.
 OK NCBI_TaxID=1916;
 RN 111
 RM SEQUENCE FROM N.A.
 RC MEDLINE=97220326; PubMed=9148759.
 RX Vincent P. Sharick F. Dupont C. Morosoli P. Kuepfel D.;
 RA "New alpha-L-arabinofuranosidase produced by Streptomyces lividans:
 RT cloning and DNA sequence of the abds gene and characterisation of the
 RT enzyme";
 RL Biochem. J. 322:845-852(1997).
 RN 121
 RM REVIEWS.
 RC STRAIN=66 / 1326;
 RA Sharick P.; (1998) to the EMBL/GenBank/DBJ databases.
 RL FUNCTION: Has a specific role in synthesizing activity on
 CC XYLANS FROM GRAMINAE ACTS SYMBIOTICALLY WITH ARABINOSIDES AND
 CC IT LIBERATES ARABINOS AND, AFTER PROLONGED INCUBATION, THE
 CC PURIFIED ENZYME EXHIBITS SOME XYLANOLYTIC ACTIVITY AS WELL.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-
 CC arabinofuranoside residues in alpha-L-arabinosides.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.

-1- SIMILARITY: Contains 1 ricin B-type lectin domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

EMBL: M64551; AAC26524.1;
 DR Interpro: IPR005193; Glyco hydro 62.
 DR Interpro: IPR00772; Ricin B lectin.
 DR Pfam: PF03664; Glyco hydro 62; 1.
 DR Pfam: PF00652; Ricin B lectin; 3.
 DR SMART: SM00458; RICIN, 1.
 DR PROSITE: PS50231; RICIN B LECTIN; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin.
 KM Complete proteome.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 475 ALPHA-L-ARABINOFURANOSIDASE.
 FT DOMAIN 39 166 RICIN B-TYPE LECTIN.
 FT SEQUENCE 475 AA; 50045 MW; 476707F833C60D CRC64;
 Query Match 6.8%; Score 90.5; DB 1; Length 475;
 Best Local Similarity 27.3%; Pred. No. 0.2; Mismatches 66; Indels 9; Gaps 6;
 Matches 35; Conservative 18; Mismatches 66; Indels 9; Gaps 6;

QY 22 VDVRDDDFDNGNQLMPKSKNDPQQLTKRDXITRNSG-SCITTYGYTA--GYVMI 78
 DB 52 LDVLGSGDDGALLQLYDCMGST--NQMTSTDTGRLTYGDKLDPGHAATPRTVQI 109
 QY 79 FDCNTAVREATIQWIXNGTIINPNSLVL-ASASGI-KETITLVQTLDTYLGQGLAGN 136
 DB 110 WSGSGNQ--WRVSDGVIVGVSGLCLAKAKGTGNGAVQMTGNSGNGKXTGLT 167
 QY 137 DPAPEVT 144
 DB 168 GTPPTDT 175

RESULT 14
 Y163-STRY3 STANDARD; FRT; 1693 AA.
 ID Y163-STRY3
 DT 15-DEC-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical WD-repeat protein sl10163.
 GN Sl10163.
 OS Synecocystis sp. (strain PCC 6803).
 CC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
 OK NCBI_TaxID=1148;
 RN 111
 RM SEQUENCE FROM N.A.
 RC MEDLINE=96127529; PubMed=8590279;
 RX Sano T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 648 to 928 of the genome";
 RL DNA Res. 2:153-166(1995).
 RL -1- SIMILARITY: Contains 16 WD repeats.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

EMBL: D63999; BAI0064.1; --
 DR PIR: S76086; S76086.

AC OBLK01;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Lectin chain B isoform 3 (fragment).
OS Viscum album subsp. coloratum.
OC Burkariophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Streptophyta; Charophyta; Viscum.
OC NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21566752; PubMed=11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RL M01. Cells 12:215-220(2001).
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=21566752; PubMed=11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508919; AA046937.1; -;
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR SMART; SM00458; RICIN_2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 263 AA; 29071 MW; 399C4ADA860F061D CRC64;

Query Match 77.6%; Score 1029.5; DB 10; Length 263;
Best Local Similarity 74.5%; Pval No. 6e-99; Indels 1; Gaps 1;

Matches 196; Conservative 19; Mismatches 47; Indels 1; Gaps 1;

QY 1 DVTCSASEPTVAVGKXGVYVDDPDHGNQIQMPKSKNDPNQMTIKDXTIRS 60
DB 1 DDTCTPSEPTVAVGKXGVYVDDPDHGNQIQMPKSKNDPNQMTIKDXTIRS 60
QY 61 NSCLTGYGTAGVYVMIIPDCTVAREATITWQIKNGTIIIPSSNLVLAASSGIGTTL 120
DB 61 NSCLTGYGTAGVYVMIIPDCTVAREATITWQIKNGTIIIPSSNLVLAASSGIGTTL 120
QY 121 VQTVDTLTCQMLASGNTARREVTITGFDICMENSXSVETCTSHKQK FKLAKXD 179
DB 121 VQTVDTLTCQMLASGNTARREVTITGFDICMENSXSVETCTSHKQK FKLAKXD 179
QY 181 GSIRPKNDQCLTKGRSIVSVINIVSCSXGXQVWFTKEALINIKKXXXXVDAQ 240
DB 180 GSIRPKNDQCLTKGRSIVSVINIVSCSXGXQVWFTKEALINIKKXXXXVDAQ 239
QY 241 NPKRLRIIIPATGKRNQMLPY 263
DB 240 NPKRLRIIIPATGKRNQMLPY 262

RESULT 5

OBLK03
ID OBLK03 PRELIMINARY; PRT; 266 AA.
AC OBLK03;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Lectin chain B isoform 1 (fragment).
OS Viscum album subsp. coloratum.
OC Burkariophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Streptophyta; Charophyta; Viscum.
OC NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21566752; PubMed=11710524;

RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RL M01. Cells 12:215-220(2001).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=21566752; PubMed=11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508917; AA046935.1; -;
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 5.
DR SMART; SM00458; RICIN_2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 266 AA; 29537 MW; 4A51473C37B94C73 CRC64;

Query Match 71.5%; Score 949; DB 10; Length 266;
Best Local Similarity 64.5%; Pval No. 1e-99; Indels 4; Gaps 2;

QY 1 DVTCSASEPTVAVGKXGVYVDDPDHGNQIQMPKSKNDPNQMTIKDXTIRS 60
DB 1 DDTCTPSEPTVAVGKXGVYVDDPDHGNQIQMPKSKNDPNQMTIKDXTIRS 60
QY 61 NSCLTGYGTAGVYVMIIPDCTVAREATITWQIKNGTIIIPSSNLVLAASSGIGTTL 120
DB 61 NSCLTGYGTAGVYVMIIPDCTVAREATITWQIKNGTIIIPSSNLVLAASSGIGTTL 120
QY 118 TLVQVDTLTCQMLASGNTARREVTITGFDICMENSXSVETCTSHKQK FKLAKXD 177
DB 121 TFLVQVDTLTCQMLASGNTARREVTITGFDICMENSXSVETCTSHKQK FKLAKXD 179
QY 178 YGSGIRPKNDQCLTKGRSIVSVINIVSCSXGXQVWFTKEALINIKKXXXXV 237
DB 180 YGSGIRPKNDQCLTKGRSIVSVINIVSCSXGXQVWFTKEALINIKKXXXXV 239
QY 238 AQMPRLRIIIPATGKRNQMLPY 263
DB 240 AQMPRLRIIIPATGKRNQMLPY 265

RESULT 6

OBLK174
ID OBLK174 PRELIMINARY; PRT; 541 AA.
AC OBLK174;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Protein A chain (BC 3.2.2.22) (rRNA N-glycosylase) (fragment).
OS Ricinus communis (castor bean).
OC Burkariophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Streptophyta; Charophyta; Euphorbiaceae; Ricinus.
OC NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92338377; PubMed=163311;
RA Roberts L.M., Tregear D.M., Lord J.M.;
RT "Molecular cloning of ricin.";
RT Targeted Diast. Ther. 7:81-97(1992).
CC -1- CATALYTIC ACTIVITY: ENDOTHEROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADPOSING ON THE 28S RRNA
CC -1- SPECIFIC ADPOSING ON THE 28S RRNA
EMBL; F02079.1; AB22582.1; -;
DR HSRP; R02079.1; AB22582.1; -;
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001400; Smactocropln.
DR Pfam; PF00652; Ricin_B_lectin; 6.


```
Db 496 GSIRPHDRCLTSTNHSQSSIISSCSFSSSGRWFWFNDGTLNKLNLVNDVKG 555
Qy 240 ANPRLRRIIIPATKRNQWMLPV 263
556 SNPSLHQIILIPATKRNQWMLPV 579

RESULT 9
Q94BW3 PRELIMINARY; FRT; 580 AA.
ID Q94BW3
AC Q94BW3; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin III precursor
DS Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
  genes encoding cinnamomin proteins and study of their expression
  patterns." JIM-2001) to the EMBL/GenBank/DBJ databases.
RI Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY. ENDORHYDOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
  -1- SPECIFIC ADENOSINE ON THE 28S RRNA OF THE RIBOSOME-INACTIVATING
  PROTEIN FAMILY.
DR EMBL; AY039803; AAK82460.1; -.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
FM HYDROLASE; Signal; Toxin.
FM NON_TIR
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINTRAMOMIN III
SQ SEQUENCE 580 AA; 64421 MW; 940010P0I7FE558 CRC64;

Query Match 60.7%; Score 805; DB 10; Length 580;
Best Local Similarity 59.1%; Pred. No. 4,2e-75;
Matches 156; Conservative 32; Mismatches 74; Indels 2; Gaps 2;
```

```
AC Q9FV22; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DR 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (rRNA
  N-glycosylase) (fragment).
DS Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Xie L., Liu W.-Y., Wang E.-D.;
RT "Molecular cloning of cinnamomin A-, B-chain and the expression,
  purification, characterization and mutagenesis of the A-chain."
  Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY. ENDORHYDOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
  -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
DR EMBL; AF293448; AF293978.2; -.
DR HSRP; P02873; 2A1.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 5.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
FM HYDROLASE; Toxin.
FM NON_TIR
FT CHAIN 1 549
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINTRAMOMIN III
SQ SEQUENCE 549 AA; 60648 MW; 02607F8607C44B0 CRC64;

Query Match 58.1%; Score 771.5; DB 10; Length 549;
Best Local Similarity 56.6%; Pred. No 1.2e-71;
Matches 150; Conservative 31; Mismatches 81; Indels 3; Gaps 2;
```


Query Match 52.3%, Score 694.5; DB 10; Length 382;
 Best Local Similarity 51.8%; Pred. No. 7.9e-64;
 Matches 131; Conservative 37; Mismatches 84; Indels 1; Gaps 1;

QY 9 EFTYRIVGKXKXVVDVDDPHDNOIQWPSKSNNDPQWLTIKKXITRSNGLTIT 68
 DB 128 EFTYRIVGKXKXVVDVDDPHDNOIQWPSKSNNDPQWLTIKKXITRSNGLTIT 187
 QY 69 GYTAGVYVWIEDCNFAVEKTIYQWKNGTIIPRSNVLAASSGKGTITVOTL 128
 DB 188 GYDPGVYVWIDCTSNVPEKTYMEIMNGTIIIPKSLVLSASSMGKLTIVQNDY 247
 QY 129 GQWLAQNTAFPEVTIYGFRLCWESNKGSWVETCKSSQXQXWALYGDGSTR 188
 DB 248 RQWMTGNDTSPFTVITISGIDLCNEMHSMWMLADCKRKEQ-QWALYDGSIR 306
 QY 189 QDQCTKGRSDSVYINISGCSXSKXQWFTNEXALILKXXXXXVQANFTRIT 248
 DB 307 TNNCTISMDHKGSTIVLMGCSNEMASQWVFDGSGVSLYDPMVYKSDPBL 366
 QY 249 IYVATGKPNQW 261
 DB 367 IWEYTKRPNQW 379

RESULT 14
 QY 9 EFTYRIVGKXKXVVDVDDPHDNOIQWPSKSNNDPQWLTIKKXITRSNGLTIT 68
 DB 128 EFTYRIVGKXKXVVDVDDPHDNOIQWPSKSNNDPQWLTIKKXITRSNGLTIT 187
 QY 69 GYTAGVYVWIEDCNFAVEKTIYQWKNGTIIPRSNVLAASSGKGTITVOTL 128
 DB 188 GYDPGVYVWIDCTSNVPEKTYMEIMNGTIIIPKSLVLSASSMGKLTIVQNDY 247
 QY 129 GQWLAQNTAFPEVTIYGFRLCWESNKGSWVETCKSSQXQXWALYGDGSTR 188
 DB 248 RQWMTGNDTSPFTVITISGIDLCNEMHSMWMLADCKRKEQ-QWALYDGSIR 306
 QY 189 QDQCTKGRSDSVYINISGCSXSKXQWFTNEXALILKXXXXXVQANFTRIT 248
 DB 307 TNNCTISMDHKGSTIVLMGCSNEMASQWVFDGSGVSLYDPMVYKSDPBL 366
 QY 249 IYVATGKPNQW 261
 DB 367 IWEYTKRPNQW 379

PRELIMINARY; PRT; 547 AA.
 AC Q9MGE9; 110
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Preproagglutinin (EC 3.2.2.22) (rRNA N-glycosidase).
 GN AG.
 OS Abrus precatorius (indian licorice) (Crab's eye).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Rosales; Fabaceae; Papilionoideae; Abreae; Abrus.
 OC NCBI_TaxID=3816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20102702; PubMed=10636890;
 RA Liu C.L., Tsai C.C., Lin S.C., Wang L.I., Han C.I., Hwang M.J.,
 RA Lin J.Y.;
 RT "Primary Structure and Function Analysis of the Abrus precatorius
 RT Agglutinin A Chain by Site-directed Mutagenesis: Prolong of Amphiphilic
 RT alpha-Helix A Impairs Protein Synthesis Inhibitory Activity.";
 RL J. Biol. Chem. 275:1897-1901(2000).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL: AF090173; AF28309.1; .
 DR HSP; P1140; IABR.
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00652; Ricin_B_lectin; 6.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR SMART: SM00458; SHIGARICIN.
 DR PROSITE: PS00231; RICIN_B_Lectin; 2.
 DR PROSITE: PS00275; SHIG_RICIN; 1.
 DR Hydrolase; Toxin.
 SQ SEQUENCE 547 AA; 61248 MW; 355A32EC35A1BD CRC64;

Query Match 52.1%; Score 691; DB 10; Length 547;
 Best Local Similarity 51.8%; Pred. No. 2.9e-63;
 Matches 133; Conservative 35; Mismatches 87; Indels 2; Gaps 2;

QY 5 CSAS-EFTYRIVGKXKXVVDVDDPHDNOIQWPSKSNNDPQWLTIKKXITRSN 63
 DB 288 CSAS-EFTYRIVGKXKXVVDVDDPHDNOIQWPSKSNNDPQWLTIKKXITRSN 347

QY 64 CLTYGTAGVYVWIEDCNFAVEKTIYQWKNGTIIPRSNVLAASSGKGTITVOT 123
 DB 348 CLTYGTAGVYVWIEDCNFAVEKTIYQWKNGTIIPRSNVLAASSGKGTITVOT 407
 QY 124 LDYTAGQWLAQNTAFPEVTIYGFRLCWESNKGSWVETCKSSQXQXWALYGD 183
 DB 408 NDYRMRQSMRTNDTSPFTVITISGIDLCNEMHSMWMLADCKRKEQ-QWALY 466
 QY 184 RPNQNDQCTKGRSDSVYINISGCSXSKXQWFTNEXALILKXXXXXVQAN 243
 DB 467 RPNQNTNCLTCEHHQGANITVWGCNMAASQWVFDGSGVSLYDPMVYKSD 526
 QY 244 LRRIIYVATGKPNQW 260
 DB 527 LRRIIYVATGKPNQW 543

RESULT 15
 QY 64 CLTYGTAGVYVWIEDCNFAVEKTIYQWKNGTIIPRSNVLAASSGKGTITVOT 123
 DB 348 CLTYGTAGVYVWIEDCNFAVEKTIYQWKNGTIIPRSNVLAASSGKGTITVOT 407
 QY 124 LDYTAGQWLAQNTAFPEVTIYGFRLCWESNKGSWVETCKSSQXQXWALYGD 183
 DB 408 NDYRMRQSMRTNDTSPFTVITISGIDLCNEMHSMWMLADCKRKEQ-QWALY 466
 QY 184 RPNQNDQCTKGRSDSVYINISGCSXSKXQWFTNEXALILKXXXXXVQAN 243
 DB 467 RPNQNTNCLTCEHHQGANITVWGCNMAASQWVFDGSGVSLYDPMVYKSD 526
 QY 244 LRRIIYVATGKPNQW 260
 DB 527 LRRIIYVATGKPNQW 543

PRELIMINARY; PRT; 573 AA.
 AC Q9MGE9; 110
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Ribosome-inactivating protein IRAR (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
 GN LECTINAR.
 OS Iris hollandica (Dutch iris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
 OC NCBI_TaxID=35876;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van Damme E.J.M., Peumans W.J.;
 RT "Iris (Iris hollandica var. Professor Blaauw) plants express both type
 RT 1 and type 2 ribosome-inactivating proteins in bulb tissue.";
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL: AF28309.1; AF28309.1; .
 DR InterPro: IPR000772; RIP.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00652; Ricin_B_lectin; 6.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR SMART: SM00458; SHIGARICIN.
 DR PROSITE: PS00231; RICIN_B_Lectin; 2.
 DR PROSITE: PS00275; SHIG_RICIN; 1.
 DR Hydrolase; Toxin.
 SQ SEQUENCE 573 AA; 63759 MW; 144A3B9ACD4F5C CRC64;

Query Match 47.1%; Score 624.5; DB 10; Length 573;
 Best Local Similarity 47.5%; Pred. No. 2.6e-56;
 Matches 124; Conservative 38; Mismatches 96; Indels 3; Gaps 3;

QY 1 DDTYCSAEFTYRIVGKXKXVVDVDDPHDNOIQWPSKSNNDPQWLTIKKXITRS 60
 DB 311 EDTYCSAEFTYRIVGKXKXVVDVDDPHDNOIQWPSKSNNDPQWLTIKKXITRS 370
 QY 371 NGKCLIRAGNAGVWIDCTSNVPEKTYMEIMNGTIIIPKSLVLSASSMGKLT 429
 DB 121 VQGLYTAGQWLAQNTAFPEVTIYGFRLCWESNKGSWVETCKSSQXQXWALY 179
 QY 430 MOUNHASSQWMLSPNTRPRLPIGLNGLNGLNGLNGLNGLNGLNGLNGLNGL 488
 DB 180 DGSIRPNQNDQCTKGRSDSVYINISGCSXSKXQWFTNEXALILKXXXXXVQ 239
 QY 489 DGSIRPNQNDQCTKGRSDSVYINISGCSXSKXQWFTNEXALILKXXXXXVQ 546

Thu Dec 11 16:09:51 2003

us-09-601-667c-3.rpt

Page 8

Qy 240 ANPKLRRIIYPATGKPCPCW 250
Db 549 SDPSLQOIIINSTTANPCPCW 559

Search completed: December 11, 2003, 14:00:59
Job time : 21.3487 secs

Thu Dec 11 16:09:49 2003

us-09-601-667c-3.1ag

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 26.0864 Seconds

1606.345 Million Cell updates/sec

Title: US-09-601-667C-3

Perfect score: 1327

Sequence: 1 DVYTCASSEPTVRIYGRXNM.....RRIITYPATCKPMQWMLPVX 264

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Prod No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1291	97.3	264	AAV25987	Mistletoe lectin B
2	1291	97.3	264	AAV25988	Mistletoe lectin B
3	1291	97.3	264	AAV25989	Mistletoe lectin B
4	1291	97.3	264	AAV25990	Mistletoe lectin B
5	1290	97.2	264	AAV25991	Mistletoe lectin B
6	1290	97.2	264	AAV25992	Mistletoe lectin B
7	1290	97.2	264	AAV25993	Mistletoe lectin B
8	1290	97.2	264	AAV25994	Mistletoe lectin B
9	1289	97.1	264	AAV25995	Mistletoe lectin B

10	1289	97.1	265	20	AAV25995	Mistletoe lectin B
11	1286	96.9	264	20	AAV25978	Mistletoe lectin B
12	1286	96.9	264	20	AAV25979	Mistletoe lectin B
13	1286	96.9	264	20	AAV25978	Mistletoe lectin B
14	1286	96.9	533	20	AAV25970	Mistletoe lectin P
15	1286	96.9	533	20	AAV25970	Mistletoe lectin P
16	1286	96.9	533	20	AAV25976	Mistletoe lectin B
17	1277.5	96.3	533	20	AAV25976	Mistletoe lectin B
18	1277.5	96.3	533	20	AAV25979	Mistletoe lectin B
19	1277.5	96.3	533	20	AAV25979	Mistletoe lectin B
20	1277.5	96.3	532	20	AAV25982	Mistletoe lectin I
21	1287.5	95.5	263	19	AAW64652	Mistletoe lectin var
22	1287.5	95.5	264	18	AAW10023	Mistletoe ML B-cha
23	1287.5	95.5	264	20	AAW90126	Mistletoe lectin I
24	1287.5	95.5	267	19	AAW64660	Mistletoe lectin I
25	1287.5	95.5	564	18	AAW10021	Prepro mistletoe I
26	1287.5	95.5	564	20	AAW90127	Mistletoe lectin P
27	1183.5	93.9	267	19	AAW64667	Mistletoe lectin P
28	1080.5	79.9	263	19	AAW64667	Mistletoe lectin P
29	1080.5	79.9	263	19	AAW64667	Mistletoe lectin P
30	1080.5	79.9	263	19	AAW64667	Mistletoe lectin P
31	1080.5	79.9	263	19	AAW64667	Mistletoe lectin P
32	851.5	64.2	565	6	AAW0166	Sequence of prepro
33	851.5	64.2	565	22	AAW78900	Castor bean prepro
34	849.5	64.0	574	8	AAW78904	Modified castor be
35	849.5	64.0	574	8	AAW78904	Sequence of Ricinu
36	849.5	64.0	574	10	AAW94793	DNA sequence of r1
37	849.5	64.0	576	18	AAW25977	Castor bean r1
38	849.5	64.0	576	20	AAW25972	Castor bean r1
39	849.5	64.0	576	21	AAW25972	Castor bean r1
40	849.5	64.0	576	21	AAW25972	Castor bean r1
41	849.5	64.0	576	22	AAW25972	Castor bean r1
42	849.5	64.0	565	7	AAW60220	Prepro ricin D
43	849.5	63.6	262	10	AAW60220	Ricin B chain of ricin
44	849.5	63.6	262	10	AAW60220	Ricin B chain of ricin
45	833.5	62.8	576	8	AAW0326	Sequence of Ricinu

ALIGNMENTS

RESULT 1
AAV25987
AAV25987 standard; Protein: 264 AA.
AAV25987;
18-OCT-1999 (first entry)
Mistletoe lectin B2 protein fragment.
DE
XX
Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
KW
XX
lysozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW
XX
lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW
XX
cancer; cytotoxicity; antigen; isotom; lectin B2.
KW
XX
Vaccum album.
KW
XX
DE19804210-A1.
KW
XX
12-AUG-1999.
KW
XX
03-FEB-1999; 96DB-1004210.
KW
XX
03-FEB-1999; 96DB-1004210.
KW
XX
03-FEB-1999; 96DB-1004210.
KW
XX
(BIOG-) BIOSYN ARZENEINTEL GMBH.
KW
XX
Morris P, Stiefel T, Voelker W, Wolters P;
KW
XX
WPI: 1999-445335/38.
KW
XX
N-PDB; AA200111.
KW
XX

Thu Dec 11 16:09:49 2003

us-09-601-667c-3.rag

Page 2

PT		Preparation of mistletoe lectinins heterologous systems.
PR		Particularly for use as anticancer agents and immunostimulants
PX		Claim 9; Fig 9B; 78pp; German.
XX		This invention describes a novel mistletoe lectin (I) and its fragments which have antitumour and immunostimulatory activity. The A-chain (MA)
CC		mistletoe lectin binds to, and inactivates, the Z88 subunit of
CC		ribosome. Moreover, it stimulates the production of interleukin-1 and its
CC		immunoprotecting macrophages, so stimulate immunity (I) and its
CC		fragments are used to treat uncontrolled cell growth (particularly of the
CC		cancers) and if they lack cytotoxicity, to increase the strength of the
CC		immune response, particularly to a co-administered antigen
CC		(tumour-associated, bacterial or viral). The method allows production of
CC		mistletoe lectin, and its individual chains, in many different isoforms
CC		and on a large scale, at any time of the year. Recombinant products are
CC		free from toxins present in natural mistletoe extracts. This sequence
XX		represents a fragment of a mistletoe lectin B2 protein.
XX		Sequence 264 AA:
QY		Query Match 97.3%; Score 1291; DB 20; length 264;
Db		Best Local Similarity 92.4%; Pred. No. 2,55-136;
Matches	243;	Conservative 0; Mismatches 106; Indels 0; Gaps 0;
Qy	1	DVDTGASSEPTVRIVAKSGKAVDVDDDFDSDNOIQLPFSKSNDDPQQLMTREKDITRS 60
Db	1	EDVTGSASEPTVRIVAGSRGVADVDDDFDSNQIQLPFSKSNDDPQQLMTIKNDITRS 60
Oy	61	NSSCITTCGTCTCACTTAAACPGCATATREATTATQINKNNGTTINPSNHTLAASSGICETTLT 120
Db	61	NSSCITTCGTCTCACTTAAACPGCATATREATTATQINDGGTTINRSHSLVAASSGICKITLT 120
Qy	121	VQDLVYLTLGGGLMGADMDAPPEVTYGFRLDCMSKWSGWATCSQSOKQNXMALVGD 180
Db	121	VQDLVYLTLGGGLMGADMDAPPEVTYGFRLDCMSKWSQWVATCSQKQGMALVGD 180
Oy	181	GSTRKQNDQCILTKGRDVSSTVINNVSCSXSKXCRWFTEKXALINTLXXXXXDVAQA 240
Db	181	GSTRKQNDQCILTKGRSVDSTVINNVSCGSSGSSQNWFTENXALINTLSGLADVQA 240
Oy	241	NPLRRRIITYPATRGKDMWLVEY 263
Db	241	NPLRRRIITYPATRGKDMWLVEY 263
RESULT 2		
AATZ5988		AKI25988 standard; Protein; 264 AA.
AC		AAV25988;
DX		18-OCT-1999 (first entry)
DE		Mistletoe lectin B3 protein fragment.
KM		Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;
KM		ribozyme Z88 subunit; non-cytotoxic; T-cell activation; immune response;
KM		lymphokine macrophage uncontrolled cell growth; treatment;
KM		cancer; cytotoxicity; antigen; isoform; lectin B3.
OS		Viscum album.
PN		DE19804210-A1.
PD		12-NOV-1999.
KX		03-FEB-1998; 98DE-1004210.
KX		03-FEB-1998; 98DE-1004210.
FA		(BIOS-) BIOSYN ANZENMITTEL GmbH.

PI	Morris P., Stefefel T., Voelter W., Welters P.
DR	WP1: 1999-44535/58.
N-PSDB:	AAZ09112.
XX	
PT	Preparation of mistletoe lectins in heterologous systems,
XX	particularly for use as anticancer agents and immunostimulants
XX	Claim 9; Fig 10b; 76pg; German.
CC	This invention describes a novel mistletoe lectin (I) and its fragments
CC	which have antitumour and immunostimulatory activity. The A-chain (MA)
CC	of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC	ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC	lymphokine-producing macrophages, so stimulate immunity. (II) and its
CC	fragments are used to treat uncontrolled cell growth (particularly
CC	cancers) and if they lack cytotoxicity, to increase the strength of the
CC	immune response, particularly to a co-administered antigen
CC	(tumour-associated, bacterial or viral). The method allows production of
CC	and active lectins, and their fragments, at any time of the year. Recombinant products are
CC	free from toxins present in natural mistletoe extracts. This sequence
XX	represents a fragment of a mistletoe lectin B3 protein.
SQ	
XX	Sequence 264 AA;
Query Match	97.3%; Score 1291; DB 20; Length 264;
Best Local Similarity	92.4%; Pred. No. 2,56-136;
Matches 243;	Conservative 0; Mismatches 20; Indels 0; Gaps 0;
OY	1 DDTGTSASPEFTRVGRKXGVNDVRDHPDNQGLDPKSKNDPRLQTLTKDDTTRS 60
Db	1 DVTGSASEPRVRVGRNGRVDVDDDFHQNQLVPKSKNDPRLQTLTKDDTTRS 60
OY	61 NAGSCITTYGYGVAYVMLEFCNTAVREATIQIWKXGFTINPRSLVLAASSGIKCTLT 120
Db	61 NSGCITTYGYGVAYVMLEPCNTAVREATIQINDGGTIINPSRLVLAASSGIKCTLT 120
OY	121 VGTDLTTLGGMLAKNUTAREEVITGFEDLCHESTKSYATWETCKSOXKKXALMGD 180
Db	121 VGTDLTLLCGMLAKNDTAREETVTFEFDLCHESTSGSWETCKSOXKKXALMGD 180
OY	181 GSFRKNODQCLXPDSVSIVTVIVSCSXKXORVFNFENKXLIINKXXXXXVQA 240
Db	181 GSFRKNODQCLISRDVSIVTVIVSCSGASQSQRVFNEGAILNLKTGLAMLVQA 240
OY	241 NPKEERILITTPATSKNDWMLEPV 263
Db	241 NPKEERILITTPATSKNDWMLPV 263
RESULT 3	
ID	AAZ5994 standard; Protein; 265 AA.
XX	AAZ5994;
AC	AAZ5994;
XX	
DT	18-OCT-1999 (First entry)
XX	
XX	Mistletoe lectin B3 variant protein fragment.
KW	Mistlecote, lectin; antitumor; immunostimulant; A-chain; MA; immunity;
KW	ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW	lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW	cancer; cytotoxicity; antigen; isoform; lectin B3.
CS	Viscum album.
XX	
RN	DE19804210-A1.
XX	
XX	12-NOV-1999
XX	
XX	03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelker W, Walters P;
 XX MPI; 1999-44535/38.
 XX N-PSDB; AA209118.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 16b; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (MLA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX derived from toxins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a variant mistletoe lectin B3 protein.
 SO Sequence 265 AA;
 Query Match 97.3%; Score 1291; DB 20; Length 265;
 Best Local Similarity 92.4%; Pred. No. 2.5e-136;
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 DDTVCASBPYVAIVGKXKAVDVEDDFHDSNCIQLPFSKSNDDPQMLTTRKDYTRIS 60
 DB 1 DDTVCASBPYVAIVGKXKAVDVEDDFHDSNCIQLPFSKSNDDPQMLTTRKDYTRIS 60
 QY 61 NSGCLTGYTAGYVWIFDCNTAVRATIQWIKXGTTINPNSNVLAAASGIKETILT 120
 DB 61 NSGCLTGYTAGYVWIFDCNTAVRATIQWIKXGTTINPNSNVLAAASGIKETILT 120
 QY 121 VQTLDTLGGGMLAGNDTAPREVITYGFDDLOMESNGSWWETCSXQXKXMAALYGD 180
 DB 121 VQTLDTLGGGMLAGNDTAPREVITYGFDDLOMESNGSWWETCSXQXKXMAALYGD 180
 QY 181 GSIRPKXNDQCLTSGRDSVSTVINIVSCSXKXKQKRVNFTNEALINLXXXXXADYQA 240
 DB 181 GSIRPKXNDQCLTSGRDSVSTVINIVSCSXKXKQKRVNFTNEALINLXXXXXADYQA 240
 QY 241 NPKLRRIITYPATCKXNQWMLPV 263
 DB 241 NPKLRRIITYPATCKXNQWMLPV 263
 RESULT 4
 AA25993
 ID AA25993 standard; Protein; 265 AA.
 AC AA25993;
 XX 18-OCT-1999 (first entry)
 XX Mistletoe lectin B2 variant protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform; lectin B2.
 OS Viscum album.
 XX

EN DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX MPI; 1999-44535/38.
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelker W, Walters P;
 XX MPI; 1999-44535/38.
 XX N-PSDB; AA209117.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 15b; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (MLA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX derived from toxins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a variant mistletoe lectin B2 protein.
 SO Sequence 265 AA;
 Query Match 97.3%; Score 1291; DB 20; Length 265;
 Best Local Similarity 92.4%; Pred. No. 2.5e-136;
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 DDTVCASBPYVAIVGKXKAVDVEDDFHDSNCIQLPFSKSNDDPQMLTTRKDYTRIS 60
 DB 1 DDTVCASBPYVAIVGKXKAVDVEDDFHDSNCIQLPFSKSNDDPQMLTTRKDYTRIS 60
 QY 61 NSGCLTGYTAGYVWIFDCNTAVRATIQWIKXGTTINPNSNVLAAASGIKETILT 120
 DB 61 NSGCLTGYTAGYVWIFDCNTAVRATIQWIKXGTTINPNSNVLAAASGIKETILT 120
 QY 121 VQTLDTLGGGMLAGNDTAPREVITYGFDDLOMESNGSWWETCSXQXKXMAALYGD 180
 DB 121 VQTLDTLGGGMLAGNDTAPREVITYGFDDLOMESNGSWWETCSXQXKXMAALYGD 180
 QY 181 GSIRPKXNDQCLTSGRDSVSTVINIVSCSXKXKQKRVNFTNEALINLXXXXXADYQA 240
 DB 181 GSIRPKXNDQCLTSGRDSVSTVINIVSCSXKXKQKRVNFTNEALINLXXXXXADYQA 240
 QY 241 NPKLRRIITYPATCKXNQWMLPV 263
 DB 241 NPKLRRIITYPATCKXNQWMLPV 263
 RESULT 5
 AA25986
 ID AA25986 standard; Protein; 264 AA.
 AC AA25986;
 XX 18-OCT-1999 (first entry)
 XX Mistletoe lectin B1 protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX

Thu Dec 11 16:09:49 2003

us-09-601-667c-3.rag

Page 4

XX	lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX	caner; cytotoxicity; antigen; isoform; lectin B1.
XX	VAcum album.
XX	DE19604210-A1.
XX	12-AUG-1999.
XX	03-FEB-1998.
XX	98DE-1004210.
XX	03-FEB-1998.
XX	98DE-1004210.
XX	(BIO5-) B10SYN ARZNMITTEL GMBH.
XX	Morris P, Stiefel T, Voelter W, Welters P;
XX	WPI: 1999-445315/38.
XX	N-PSDB; AA029110.
XX	Preparation of mistletoe lectins in heterologous systems,
XX	particularly for use as anticancer agents and immunostimulants
XX	Claim 9; Fig 8B; 78pp; German.
XX	This invention describes a novel mistletoe lectin (I) and its fragments
XX	and a method for the use of these fragments. The fragments of the
XX	lectin are characterized by the fact that they are active against
XX	ribosomes. Non-cytotoxic forms of (I) activate T-cell and its
XX	lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX	fragments are used to treat uncontrolled cell growth (particularly
XX	cancers) and if they lack cytotoxicity, to increase the strength of the
XX	immune response, particularly to a co-administered antigen
XX	(tumour-associated, bacterial or viral). The method allows production of
XX	mistletoe lectin, and its individual chains, in many different isoforms
XX	and on a large scale, at any time of the year. Recombinant products are
XX	also produced. The fragments of the lectin are used, this sequence
XX	represents a fragment of a mistletoe lectin B1 protein.
XX	Sequence 264 AA:
XX	
XX	Query Match 97.2%; Score 1290; DB 20; Length 264;
XX	Best Local Similarity 92.4%; Pred. No. 3,2e-136;
XX	Matches 243; Conservativity 0; Mismatches 20; Indels 0; Gaps 0
XX	1 DDTGMSASPTATVREKXKXVYDDDDPHDNGDGLAFKSNUNPNDGTTKPTTIS 60
XX	1 DDTGMSASPTATVREKXKXVYDDDDPHDNGDGLAFKSNUNPNDGTTKPTTIS 60
XX	61 NGSCITVGTGAGVYVIMDDCNAREKLTWIMVNDGTLIPSSNIVLAASGIGITLT 120
XX	61 NGSCITVGTGAGVYVIMDDCNAREKLTWIMVNDGTLIPSSNIVLAASGIGITLT 120
XX	121 VQGLDPTLGGGLAAGNTPAEVTIVSGFRLCNESNKNSSVWETCKSSQNXKXALYED 180
XX	121 VQGLDPTLGGGLAAGNTPAEVTIVSGFRLCNESNKNSSVWETCKSSQNXKXALYED 180
XX	181 GSRRKNOOQCTKXGDSVETVYINRSGSCXXSXKXGWFWENKXALNLKXXXXVDPAQ 240
XX	181 GSRRKNOOQCTKXGDSVETVYINRSGSCXXSXKXGWFWENKXALNLKXXXXVDPAQ 240
XX	241 NPTKRRITITVPAKTRPQNMWLPV 263
XX	241 NPTKRRITITVPAKTRPQNMWLPV 263
XX	RESULT 5
XX	AAZ55990
XX	AAZ55990 standard; Protein; 264 AA.
XX	AAZ55990;
XX	18-OCT-1999 (first entry)

XX	Mistletoe lectin B5 protein fragment.
KX	Mistletoe lectin; antitumour; immunostimulant; A-chain; MAb; immunity;
KW	ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KM	lymphoid tissue; macrophage; tumour; growth; treatment;
KV	cancer; cytotoxicity; antigen; isoform; lectin B5.
OS	Viscum album.
PX	DEJ9804210-A1.
FX	12-AUG-1999.
FD	03-FEB-1998; 98DBE-1004210.
PF	03-FEB-1998; 98DBE-1004210.
KX	03-FEB-1998; 98DBE-1004210.
KX	(BIOS-) BIOSAN ARZNEIMITTEL GMBH.
PA	Morris P, Stiefel T, Voelter W, Welters P;
PT	WP1; 1999-445335/38.
DR	N-P50B; AA209114.
PP	Preparation of mistletoe lectins in heterologous systems,
PT	particularly for use as anticancer agents and immunostimulants
XX	Claim 9; Fig 12b; 78pp; German.
CC	This invention describes a novel mistletoe lectin (I) and its fragments
CC	CC which have antitumour and immunostimulatory activity. The A-chain (MA)
CC	of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC	ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
CC	lysophosphine-producing macrophages, so stimulate immunity. Particularly
CC	fragments of the A-chain are useful as adjuvants, particularly
CC	immune response, particularly to a co-administered antigen
CC	(tumour-associated, bacterial or viral). The method allows production of
CC	mistletoe lectin, and its individual chains, in many different isoforms
CC	and on a large scale, at any time of the year. Recombinant products are
CC	free from toxins present in natural mistletoe extracts. This sequence
CC	represents a fragment of a mistletoe lectin B5 protein.
XX	Sequence 264 AA:
SQ	Query Match 57.2%; Score 1290; DB 20; Length 264;
	Best Local Similarity 32.4%; Pred. No.3.2e-136;
	Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0
OY	1 DDVTCSASBEFTFARVKRKKGVADDDDFPDGNGIQLPSSSNMPQLMTIKEDTIRS 60
DB	1 DDTGSASBEFTFARVKRKKGVADDDDFPDGNGIQLPSSSNMPQLMTIKEDGIRIS 60
OY	61 NSGGCTATGTTCATGATGACDGNATKATNQTAKXTGITIPRSNVLAASSGKTITLT 120
DB	61 NSGGCTATGTTCATGATGACDGNATKATNQTAKXTGITIPRSNLVAASSGKITTLT 120
DB	61 NSGGCTATGTTCATGATGACDGNATKATNQTAKXTGITIPRSNLVAASSGKITTLT 120
OY	121 VQLDLYTAGGWLAKNDTPPEETTVYGRRLCMESXKSQVWEFCCKSQKNXXMALYGD 180
DB	121 VQLDLYTAGGWLAKNDTPPEETTVYGRRLCMESXKSQVWEFCDSQONSGKALYGD 180
OY	181 GSIRKPNQNDGLTXRSDSVSTINVSQSXXXSKQAWTFNEKAILMLFKXXKXDYDA 240
DB	181 GSIRKPNQNDGLTXRSDSVSTINVSQSXSQSGSWYFTNSCALINLNSLMATDVADR 240
OY	241 NPLTRRIIVPRTKRNQWMLVF 263
DB	241 NPLTRRIIVPRTKRNQWMLVF 263

ID AAY25996 standard; Protein; 265 AA.
 AC AAY25996;
 DN 18-OCT-1999 (first entry)
 XX Mistletoe lectin B5 variant protein fragment.
 DE Mistletoe lectin B5 variant protein fragment.
 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
 KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin B5.
 XX Viscum album.
 CS DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelter W, Walters P;
 XX WPI; 1999-44535/38.
 XX N-PSDB; AAZ09120.
 PT Preparation of mistletoe lectins in heterologous systems.
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 18B; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MHA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B5 protein.
 XX Sequence 265 AA;
 SQ
 Query Match 97.2%; Score 1290; DB 20; Length 265;
 Best Local Similarity 92.4%; Pred. No. 3,2e-136;
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 DDTVCASAEPTVRIYGRKXKAVDVEDDDPHDGNQIQLPSSKSNDDPNQMTIKKXTIIS 60
 DB 1 DDTVCASAEPTVRIYGRKXKAVDVEDDDPHDGNQIQLPSSKSNDDPNQMTIKKXTIIS 60
 QY 61 NSGCLTYTGAGYVNIIPDCNVAWEATIMQINXGTTINPNSNLYLAASGIGKTTT 120
 DB 61 NSGCLTYTGAGYVNIIPDCNVAWEATIMQINXGTTINPNSNLYLAASGIGKTTT 120
 QY 121 VQILDYTLGQMLAGNDTAPREYTIYGRDLCHSNGSGWVETLDSQNGKHALYSD 180
 DB 121 VQILDYTLGQMLAGNDTAPREYTIYGRDLCHSNGSGWVETLDSQNGKHALYSD 180
 QY 181 GSIRPKONODCLTXGRDSVSTVINIVSCSXKXQWVFTNEXALINLXXXXXXVQA 240
 DB 181 GSIRPKONODCLTXGRDSVSTVINIVSCSXKXQWVFTNEXALINLXXXXXXVQA 240
 QY 241 NPKLRITITTPATGRKNQWMLPV 263
 DB 241 NPKLRITITTPATGRKNQWMLPV 263

DB 241 NPKLRITITTPATGRKNQWMLPV 263
 RESULT 8
 ID AAY25992 standard; Protein; 265 AA.
 AC AAY25992;
 DN 18-OCT-1999 (first entry)
 XX Mistletoe lectin B1 variant protein fragment.
 DE Mistletoe lectin B1 variant protein fragment.
 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
 KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin B1.
 XX Viscum album.
 CS DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelter W, Walters P;
 XX WPI; 1999-44535/38.
 XX N-PSDB; AAZ09116.
 PT Preparation of mistletoe lectins in heterologous systems.
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 14B; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MHA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B1 protein.
 XX Sequence 265 AA;
 SQ
 Query Match 97.2%; Score 1290; DB 20; Length 265;
 Best Local Similarity 92.4%; Pred. No. 3,2e-136;
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 DDTVCASAEPTVRIYGRKXKAVDVEDDDPHDGNQIQLPSSKSNDDPNQMTIKKXTIIS 60
 DB 1 DDTVCASAEPTVRIYGRKXKAVDVEDDDPHDGNQIQLPSSKSNDDPNQMTIKKXTIIS 60
 QY 61 NSGCLTYTGAGYVNIIPDCNVAWEATIMQINXGTTINPNSNLYLAASGIGKTTT 120
 DB 61 NSGCLTYTGAGYVNIIPDCNVAWEATIMQINXGTTINPNSNLYLAASGIGKTTT 120
 QY 121 VQILDYTLGQMLAGNDTAPREYTIYGRDLCHSNGSGWVETLDSQNGKHALYSD 180
 DB 121 VQILDYTLGQMLAGNDTAPREYTIYGRDLCHSNGSGWVETLDSQNGKHALYSD 180
 QY 181 GSIRPKONODCLTXGRDSVSTVINIVSCSXKXQWVFTNEXALINLXXXXXXVQA 240
 DB 181 GSIRPKONODCLTXGRDSVSTVINIVSCSXKXQWVFTNEXALINLXXXXXXVQA 240

Db 181 GSIRKPNODCLTSGRDSVSTVINIVSCSGSGSQRMVFTNKGALINLKRGALADVAQA 240
QY 241 NPKLRRIIYPATGKPNQWMLPV 263
Db 241 NPKLRRIIYPATGKPNQWMLPV 263

RESULT 9

AAV25989 standard; Protein; 264 AA.

AAV25989;

18-OCT-1999 (first entry)

Mistletoe lectin B4 protein fragment.

Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity; ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response; cancer; cytotoxicity; antigen; isoform; lectin B4.

Viscum album.

DE19804210-A1.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

03-FEB-1998; 98DE-1004210.

(BIOG-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelter W, Welters P;

WPI; 1999-445335/38.

N-PSDB; AA205113.

Preparation of mistletoe lectins in heterologous systems, particularly for use as anticancer agents and immunostimulants

Claim 9; Fig 11B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments which have antitumor and immunostimulatory activity. The A-chain (MIA) of the mistletoe lectin binds to, and inactivates, the 28S subunit of ribosomes. Non-cytotoxic forms of (I) activate T-cell and lymphokine-producing macrophages, so stimulate immunity. (I) and its fragments are used to treat uncontrolled cell growth (particularly of cancers) and if they lack cytotoxicity, to increase the strength of the immune response, particularly to a co-administered antigen (tumour-associated, bacterial or viral). The method allows production of mistletoe lectin and its fragments in many different isoforms and on a large scale at any time of the year. Recombinant products are free from toxins present in natural mistletoe extracts. This sequence represents a fragment of a mistletoe lectin B4 protein.

Sequence 264 AA;

Query Match 97.1%; Score 1289; DB 20; Length 264;

Best Local Similarity 92.4%; Pred. No. 4,2e-136; Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 DDTTCASBPRTVIVGKXKXNDVDDPHDQNGQLAPSKSNDDPNQWMLTKEDGTIS 60
Db 1 DDTTCASBPRTVIVGKXKXNDVDDPHDQNGQLAPSKSNDDPNQWMLTKEDGTIS 60
QY 61 NSCLTIVGYAGYVMIKPCNTAVKATVQWKNSTINPNSNLTAAASGIGTIT 120
Db 61 NSCLTIVGYAGYVMIKPCNTAVKATVQWKNSTINPNSNLTAAASGIGTIT 120

QY 121 VQTLGYTLGGGKLAGNDTAPREVTIYGRPLCMESNKGSGVWETCKSGKQXWALYCD 180
Db 121 VQTLGYTLGGGKLAGNDTAPREVTIYGRPLCMESNKGSGVWETCKSGKQXWALYCD 180
QY 181 GSIRKPNODCLTSGRDSVSTVINIVSCSGSGSQRMVFTNKGALINLKRGALADVAQA 240
Db 181 GSIRKPNODCLTSGRDSVSTVINIVSCSGSGSQRMVFTNKGALINLKRGALADVAQA 240
QY 241 NPKLRRIIYPATGKPNQWMLPV 263
Db 241 NPKLRRIIYPATGKPNQWMLPV 263

RESULT 10

AAV25995 standard; Protein; 265 AA.

AAV25995;

18-OCT-1999 (first entry)

Mistletoe lectin B4 variant protein fragment.

Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity; ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response; cancer; cytotoxicity; antigen; isoform; lectin B4.

Viscum album.

DE19804210-A1.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

(BIOG-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelter W, Welters P;

WPI; 1999-445335/38.

N-PSDB; AA205113.

Preparation of mistletoe lectins in heterologous systems, particularly for use as anticancer agents and immunostimulants

Disclosure; Fig 17B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments which have antitumor and immunostimulatory activity. The A-chain (MIA) of the mistletoe lectin binds to, and inactivates, the 28S subunit of ribosomes. Non-cytotoxic forms of (I) activate T-cell and lymphokine-producing macrophages, so stimulate immunity. (I) and its fragments are used to treat uncontrolled cell growth (particularly of cancers) and if they lack cytotoxicity, to increase the strength of the immune response, particularly to a co-administered antigen (tumour-associated, bacterial or viral). The method allows production of mistletoe lectin and its individual chains, in many different isoforms and on a large scale, at any time of the year. Recombinant products are free from toxins present in natural mistletoe extracts. This sequence represents a fragment of a variant mistletoe lectin B4 protein.

Sequence 265 AA;

Query Match 97.1%; Score 1289; DB 20; Length 265;

Best Local Similarity 92.4%; Pred. No. 4,2e-136; Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 DDTTCASBPRTVIVGKXKXNDVDDPHDQNGQLAPSKSNDDPNQWMLTKEDGTIS 60
Db 1 DDTTCASBPRTVIVGKXKXNDVDDPHDQNGQLAPSKSNDDPNQWMLTKEDGTIS 60


```

DT 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B chain MLB consensus protein sequence 1.
DE
XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MAb; immunity;
KV ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KV lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; MLB; B-chain.
OS
XX Viscum album.
XX
XX Key Location/Qualifiers
FH Mistletoe 18
FT Mistletoe 18 /label= Asn, Ser
FT Mistletoe 21 /label= Cys, Arg
FT Mistletoe 56 /label= Gly, Asn
FT Mistletoe 95 /label= Gly, Asp
FT Mistletoe 157 /label= Gly, Gln
FT Mistletoe 166 /label= Val, Asp
FT Mistletoe 170 /label= Gln, Lys
FT Mistletoe 173 /label= Gly or none
FT Mistletoe 174 /label= Arg, Lys
FT Mistletoe 195 /label= Cys, Ser, Val
FT Mistletoe 212 /label= Ala, Gly
FT Mistletoe 214 /label= Ser, Gly
FT Mistletoe 215 /label= Gly, Ser
FT Mistletoe 224 /label= Gly, Tyr
FT Mistletoe 231 /label= Asn, Ser, Thr, Lys
FT Mistletoe 232 /label= Ser, Gly
FT Mistletoe 233 /label= Leu, Pro
FT Mistletoe 234 /label= Ala, Met
FT Mistletoe 235 /label= Met, Val
FT Mistletoe 264 /label= Pro, Phe
XX
XX DE19804210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX (BIOS-) BIOSYN ARKANEWITTEL GMBH.
XX
XX Morris P. Stiefel T. Voelker W. Weilers P.
XX
XX MPI, 1999-44535/38.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 3, Page 28; 78pp; German.

```

```

XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MLB)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response against bacterial or viral infections. The production of
CC mistletoe lectin and its individual chains in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a consensus sequence of the mistletoe lectin B chain (MLB)
XX described in the invention.
XX
XX Sequence 264 AA:
SQ
XX
XX Query Match 96.9%; Score 1286; DB 20; Length 264;
XX Best Local Similarity 100.0%; Pred. No. 96-116;
XX Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 DPTGASAPPTVIRVGRKXGVYVDDPHDQNOIOLWPKSNMPQWATPKXDTIRS 60
XX 1 DPTGASAPPTVIRVGRKXGVYVDDPHDQNOIOLWPKSNMPQWATPKXDTIRS 60
XX 61 NSGCLTYGYTGYGVYVIFDQNTAVREATIQIXXGTTIIPRSNLVLAASGKXTILT 120
XX 61 NSGCLTYGYTGYGVYVIFDQNTAVREATIQIXXGTTIIPRSNLVLAASGKXTILT 120
XX 121 VQTLDTYTLQGLMAKNDJAPREVTIYGFDDLCMESKGVVETGSSQNNXXALIGD 180
XX 121 VQTLDTYTLQGLMAKNDJAPREVTIYGFDDLCMESKGVVETGSSQNNXXALIGD 180
XX 122 VQTLDTYTLQGLMAKNDJAPREVTIYGFDDLCMESKGVVETGSSQNNXXALIGD 180
XX 122 VQTLDTYTLQGLMAKNDJAPREVTIYGFDDLCMESKGVVETGSSQNNXXALIGD 180
XX 181 GSIRKXNDQCLTXGRDSVGTIVIVSSXXSXQRFVFNEXALINLKKXXKXVQA 240
XX 181 GSIRKXNDQCLTXGRDSVGTIVIVSSXXSXQRFVFNEXALINLKKXXKXVQA 240
XX 241 NPLRRIITYPATGKNDQWMLPV 263
XX 241 NPLRRIITYPATGKNDQWMLPV 263
XX
XX RESULT 13
XX ID AAY25975
XX AC AAY25975;
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B chain MLB consensus protein sequence 2.
DE
XX
XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MAb; immunity;
KV ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KV lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; MLB; B-chain.
OS
XX Viscum album.
XX
XX Key Location/Qualifiers
FH Mistletoe 18
FT Mistletoe 18 /label= Asn, Ser
FT Mistletoe 21 /label= Cys, Arg
FT Mistletoe 56 /label= Gly, Asn
FT Mistletoe 95 /label= Gly, Asp
FT Mistletoe 157 /label= Gly, Gln
FT Mistletoe 166 /label= Val, Asp

```

FT Misc-difference 170 /label= Gln, Lys
FT Misc-difference 173 /label= Gly or none
FT Misc-difference 174 /label= Arg, Lys
FT Misc-difference 195 /label= Cys, Ser, Val
FT Misc-difference 211 /label= Ala, Gly
FT Misc-difference 212 /label= Gly, Ala
FT Misc-difference 214 /label= Ser, Gly
FT Misc-difference 215 /label= Gly, Ser
FT Misc-difference 224 /label= Gly, Tyr
FT Misc-difference 231 /label= Asn, Ser, Thr, Lys
FT Misc-difference 232 /label= Ser, Gly
FT Misc-difference 233 /label= Leu, Pro
FT Misc-difference 234 /label= Ala, Met
FT Misc-difference 235 /label= Met, Val
FT Misc-difference 264 /label= Pro, Phe
XX DE19804210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welters P;
XX MPI; 1999-44535/38.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 6, Page 31; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MLA)
XX of the mistletoe lectin binds to and activates T-cells. The B-chain
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and a large scale, at any time of the year. Recombinant products are
XX free from the presence in natural mistletoe extracts. This sequence
XX represents a consensus sequence of the mistletoe lectin B chain (MB3)
XX described in the invention.
XX
XX Sequence 264 AA:

Query Match 96.3%; Score 1286; DB 20; Length 264;
Best Local Similarity 100.0%; Pred. No. 9e-136;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 1 DDTVTSASPTVAVTIGEXKXKVDVDDPDHNGQIQLPKSKNNDPVOGLMTIKEDYTIHS 60
|||||

DB 1 DDTVTSASPTVAVTIGEXKXKVDVDDPDHNGQIQLPKSKNNDPVOGLMTIKEDYTIHS 60
QY 61 NSCLITVGYTAGVYVMIPOCTAVREATVQIWKXGTFIINPRSNVLVAASGIGKTTLT 120
DB 61 NSCLITVGYTAGVYVMIPOCTAVREATVQIWKXGTFIINPRSNVLVAASGIGKTTLT 120
QY 121 VQTDITVIGQCMVLAGNDTAREVTIVGFQDCMESNKGSTWETCXSQXQXWALYGD 180
DB 121 VQTDITVIGQCMVLAGNDTAREVTIVGFQDCMESNKGSTWETCXSQXQXWALYGD 180
QY 181 GSIRPKNODQCLTKGRDSVSTVINIVSCSXKXQGWFTWEXAIIINIKXXKXDPVQA 240
DB 181 GSIRPKNODQCLTKGRDSVSTVINIVSCSXKXQGWFTWEXAIIINIKXXKXDPVQA 240
QY 241 NPKLRRIIYPANGKRNQMLPV 263
DB 241 NPKLRRIIYPANGKRNQMLPV 263
PSCHT 14
ID AAY25970 standard; protein, 533 AA.
XX AAY25970;
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin protein consensus sequence 1.
XX
XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MLA; immunity;
XX ribosome 268 subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform.
XX
XX Viscum album.
XX
XX Key Location/Qualifiers
XX Misc-difference 15 /label= Asp, Gln
XX Misc-difference 63 /label= Gly, Gln
XX Misc-difference 66 /label= Ile, Val
XX Misc-difference 75 /label= Leu, Ala
XX Misc-difference 107 /label= Asp, Arg or none
XX Misc-difference 113 /label= Asn, Thr
XX Misc-difference 117 /label= Pro, Thr
XX Misc-difference 134 /label= Asp, Gln
XX Misc-difference 141 /label= Ser, Thr
XX Misc-difference 148 /label= Phe, Tyr
XX Misc-difference 152 /label= Thr, Ala
XX Misc-difference 177 /label= Ala, Tyr
XX Misc-difference 180 /label= Tyr, Asp
XX Misc-difference 185 /label= Ala, Gln
XX Misc-difference 191 /label= Val, Met
XX Misc-difference 219 /label= Ile, Phe
XX Misc-difference 224 /label= Pro, Ser
XX Misc-difference 225 /label= Pro, Thr
XX

CC	immune response, particularly to a co-administered antigen (tumor-associated, bacterial or viral). The method allows production of
CC	mistletoe lectin, and its individual chains. In many different products are
CC	and on a large scale, at any time of the year. The products are
CC	free from toxins present in natural plant extracts. This sequence
CC	represents the consensus sequence of the mistletoe lectin described in the
CC	specification.
CC	
CC	Sequence 533 AA:
CC	Query Match 96.9%; Score 1286; DB 20; Length 533;
CC	Best Local Similarity 100.0%; Posit. No. 2,4e-15;
CC	Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	
CC	1 DDTYTSASPPFRVVERGXKXVDVDDPHDGNQIQLPKSNDFPQMLTIRKXDTIRS 60
CC	DB DDTYTSASPPFRVVERGXKXVDVDDPHDGNQIQLPKSNDFPQMLTIRKXDTIRS 329
CC	
CC	61 NSGCLTYGTRGVYVMLFCQNTAARATQIWNXNGTINPESNLVLASSGIKQTLL 120
CC	DB NSGCLTYGTRGVYVMLFCQNTAARATQIWNXNGTINPESNLVLASSGIKQTLL 389
CC	330 NSGCLTYGTRGVYVMLFCQNTAARATQIWNXNGTINPESNLVLASSGIKQTLL 449
CC	QY VQILDYTLGGMLAAGNTIPREVTYFRQLQNESTXSVVETCSXGXOXNAXLXSD 180
CC	DB VQILDYTLGGMLAAGNTIPREVTYFRQLQNESTXSVVETCSXGXOXNAXLXSD 449
CC	QY 390 GSPRPNODQGLXKRSVSWIVIVSGXSSXXORVWPFNEXALINLKKXXXXVADA 240
CC	DB 450 GSPRPNODQGLXKRSVSWIVIVSGXSSXXORVWPFNEXALINLKKXXXXVADA 509
CC	QY 241 NPLRRRIIIPYTKGNQWMLPV 263
CC	DB 510 NPLRRRIIIPYTKGNQWMLPV 532
CC	
CC	RESULT 15
CC	ID AAY25973
CC	AA25973 standard; protein: 533 AA.
CC	
CC	AA25973:
CC	18-OCT-1999 (first entry)
CC	
CC	Mistletoe lectin protein consensus sequence 2.
CC	
CC	Mistletoe, lectin; antitumor; immunostimulant; A-chain; MDA; immunity;
CC	lysozyme 288 subunit; non-cytotoxic; T-cell activation; immune response;
CC	lymphokine-producing macrophages; uncontrolled cell growth; treatment;
CC	cancer; cytotoxicity; antigen; isoform.
CC	
CC	Viscum album.
CC	
CC	Key Location/Qualifiers
CC	FT MISC-difference 15 /label= Asp, Glu
CC	FT MISC-difference 62 /label= Gly, Gln
CC	FT MISC-difference 66 /label= Ile, Val
CC	FT MISC-difference 75 /label= Leu, Ala
CC	FT MISC-difference 107 /label= Asp, none
CC	FT MISC-difference 113 /label= Asn, Thr
CC	FT MISC-difference 117 /label= Pro, Thr
CC	FT MISC-difference 134 /label= Asp, Glu
CC	FT MISC-difference 141 /label= Ser, Thr
CC	FT MISC-difference 145 /label= Phe, Tyr

FT Misc-difference 152 /label= Thr, Ala
FT Misc-difference 177 /label= Ala, Tyr
FT Misc-difference 180 /label= Tyr, Asp
FT Misc-difference 183 /label= Ala, Glu
FT Misc-difference 191 /label= Val, Met
FT Misc-difference 219 /label= Ile, Phe
FT Misc-difference 224 /label= Phe, Ser
FT Misc-difference 225 /label= Pro, Thr
FT Misc-difference 232 /label= Thr, Ser
FT Misc-difference 236 /label= Asp, Ser
FT Misc-difference 283 /label= Asn, Ser
FT Misc-difference 290 /label= Cys, Arg
FT Misc-difference 325 /label= Gly, Asn
FT Misc-difference 364 /label= Gly, Asp
FT Misc-difference 427 /label= Gly, Gln
FT Misc-difference 439 /label= Val, Asp
FT Misc-difference 442 /label= Gln, Lys
FT Misc-difference 443 /label= Gly, none
FT Misc-difference 464 /label= Arg, Lys
FT Misc-difference 480 /label= Cys, Ser, Val
FT Misc-difference 481 /label= Ala, Gly
FT Misc-difference 483 /label= Gly, Ala
FT Misc-difference 484 /label= Ser, Gly
FT Misc-difference 493 /label= Gly, Ser
FT Misc-difference 500 /label= Gly, Tyr
FT Misc-difference 501 /label= Asn, Ser, Thr, Lys
FT Misc-difference 502 /label= Ser, Gly
FT Misc-difference 503 /label= Leu, Pro
FT Misc-difference 504 /label= Ala, Met
FT Misc-difference 533 /label= Met, Val
FT Misc-difference 533 /label= Pro, Phe
XX DE19804210-AL.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOG-) BIOSYN ARZNEIMITTEL GMBH.
XX

PI Morris P, Stiefel T, Voelter W, Welters P;
XX WPI; 1999-445335/38.
XX Preparation of mistletoe lectins in heterologous systems,
PI particularly for use as anticancer agents and immunostimulants
XX
XX Claim 4, Page 28-29; 78pp; German.
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a consensus sequence of the mistletoe lectin described in the
CC specification.
XX
SQ Sequence 533 AA;
Query Match 96.9%; Score 1286; DB 20; Length 533;
Best Local Similarity 100.0%; Pred. No. 2,4e-135;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 DDVTCASAEPTVRIYKXKXKXVDVDDDRHNDGICLPKSKNNDPQMLTKEDXTIRS 60
DB 276 DDVTCASAEPTVRIYKXKXKXVDVDDDRHNDGICLPKSKNNDPQMLTKEDXTIRS 329
CY 61 NSGCTTYGTVAGVYVMEPCNTAFREATTGQIMXNGTIIIPSNLVLAASGKKTIT 120
DB 330 NSGCTTYGTVAGVYVMEPCNTAFREATTGQIMXNGTIIIPSNLVLAASGKKTIT 389
CY 121 VQTLDYTLAQGLAGMDTAPPEVTYGFRLCOMESXKXSVWETCXSSQXNXXMALYGD 180
DB 390 VQTLDYTLAQGLAGMDTAPPEVTYGFRLCOMESXKXSVWETCXSSQXNXXMALYGD 449
CY 181 GSIRKQNDQCLTXGRDSVETVINYSCXKXKXQXRVNFTNEXAIIINLKKXXXQVAAQ 240
DB 490 GSIRKQNDQCLTXGRDSVETVINYSCXKXKXQXRVNFTNEXAIIINLKKXXXQVAAQ 509
CY 241 NPLKRRITIIYPATKRNQMWLPV 263
DB 510 NPLKRRITIIYPATKRNQMWLPV 532

Search completed: December 11, 2003, 14:07:41
Job time : 27.0864 secs

Thu Dec 11 16:09:49 2003

us-09-601-667c-3.rapb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 14:01:14 ; Search time 17.0129 seconds
(without alignments)

2896.029 Million call updates/sec

Title: US-09-601-667C-3
Perfect score: 1267
Sequence: 1 DVTCSASPTVRIVGRXKX.....RRITVPATGKDNQMLPYX 264

Scoring table: BLOSUM62
Gapcost 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: /cnm2_6/pdata/1/pubpa/US07_PUBCOMB.pep.*
- 2: /cnm2_6/pdata/1/pubpa/US06_NEW_PUB.pep.*
- 3: /cnm2_6/pdata/1/pubpa/US06_PUBCOMB.pep.*
- 4: /cnm2_6/pdata/1/pubpa/US06_PUBCOMB.pep.*
- 5: /cnm2_6/pdata/1/pubpa/US07_NEW_PUB.pep.*
- 6: /cnm2_6/pdata/1/pubpa/US07_PUBCOMB.pep.*
- 7: /cnm2_6/pdata/1/pubpa/US08_NEW_PUB.pep.*
- 8: /cnm2_6/pdata/1/pubpa/US08_PUBCOMB.pep.*
- 9: /cnm2_6/pdata/1/pubpa/US08_PUBCOMB.pep.*
- 10: /cnm2_6/pdata/1/pubpa/US08_PUBCOMB.pep.*
- 11: /cnm2_6/pdata/1/pubpa/US09_NEW_PUB.pep.*
- 12: /cnm2_6/pdata/1/pubpa/US09_PUBCOMB.pep.*
- 13: /cnm2_6/pdata/1/pubpa/US10_PUBCOMB.pep.*
- 14: /cnm2_6/pdata/1/pubpa/US10_PUBCOMB.pep.*
- 15: /cnm2_6/pdata/1/pubpa/US10_NEW_PUB.pep.*
- 16: /cnm2_6/pdata/1/pubpa/US60_NEW_PUB.pep.*
- 17: /cnm2_6/pdata/1/pubpa/US60_PUBCOMB.pep.*
- 18: /cnm2_6/pdata/1/pubpa/US60_PUBCOMB.pep.*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1267.5	95.5	263	9	US-09-347-064-10 Sequence 10, Appl1
2	1267.5	95.5	267	9	US-09-347-064-4 Sequence 4, Appl1
3	849.5	64.0	576	12	US-10-083-326A-1 Sequence 17, Appl1
4	849.5	64.0	576	12	US-10-127-077-17 Sequence 17, Appl1
5	182	11.2	144	13	US-10-156-761-14970 Sequence 14, Appl1
6	182	11.2	420	15	US-10-156-761-14970 Sequence 14, Appl1
7	136.5	10.3	658	15	US-10-156-761-8170 Sequence 8170, Ap
8	121.5	9.2	536	15	US-09-973-457-5 Sequence 5, Appl1
9	119.5	9.0	135	10	US-09-973-457-5 Sequence 5, Appl1
10	119.5	9.0	135	14	US-10-074-527-6 Sequence 10246, A
11	118.5	8.9	647	15	US-10-156-761-10246 Sequence 10246, A
12	117.5	8.9	480	9	US-09-770-621-5 Sequence 4, Appl1
13	117.5	8.9	492	9	US-09-770-621-4 Sequence 4, Appl1
14	117.5	8.9	492	9	US-09-770-621-7 Sequence 7, Appl1
15	117.5	8.9	492	12	US-10-286-993-4 Sequence 4, Appl1

16	115.5	8.7	491	9	US-09-770-621-8 Sequence 8, Appl1
17	104	7.8	41	15	US-10-137-077-18 Sequence 18, Appl1
18	104	7.8	45	15	US-10-137-077-19 Sequence 19, Appl1
19	98	7.4	41	15	US-10-137-077-20 Sequence 20, Appl1
20	86.5	6.5	340	15	US-10-128-714-8037 Sequence 8037, Ap
21	81	6.1	278	15	US-10-128-714-3037 Sequence 3037, Ap
22	79	6.0	295	9	US-09-815-742-1153 Sequence 1153, A
23	78	5.9	1781	14	US-10-094-749-293 Sequence 293, Ap
24	78	5.9	1781	14	US-10-094-749-293 Sequence 293, Ap
25	77	5.8	625	15	US-10-156-761-15008 Sequence 15008, A
26	76	5.7	434	9	US-09-770-621-6 Sequence 6, Appl1
27	75.5	5.7	356	10	US-09-976-059-8 Sequence 8, Appl1
28	75.5	5.7	770	9	US-09-815-056-11 Sequence 31, Appl1
29	73.5	5.5	138	12	US-10-292-896-102 Sequence 102, App
30	73.5	5.5	435	12	US-10-074-566-18 Sequence 18, Appl1
31	73.5	5.5	435	14	US-10-000-512-18 Sequence 12875, A
32	73.5	5.5	627	15	US-10-156-761-12875 Sequence 48, Appl1
33	73	5.5	510	12	US-10-190-115-48 Sequence 293, Ap
34	72	5.4	1614	12	US-10-094-749-293 Sequence 16, Appl1
35	72	5.4	1614	12	US-10-094-749-293 Sequence 16, Appl1
36	72	5.4	1032	11	US-10-120-801-16 Sequence 9, Appl1
37	71.5	5.4	401	12	US-10-009-823-9 Sequence 14, Appl1
38	71.5	5.4	788	11	US-09-733-643-14 Sequence 47, Appl1
39	71	5.4	638	12	US-10-345-680-47 Sequence 15004, A
40	71	5.4	955	15	US-10-156-761-15004 Sequence 9647, Ap
41	70.5	5.3	464	15	US-10-156-761-9647 Sequence 23, Appl1
42	70.5	5.3	559	14	US-10-001-851-23 Sequence 27, Appl1
43	70.5	5.3	626	14	US-10-001-851-27 Sequence 3506, Ap
44	70.5	5.3	696	15	US-10-128-714-3506 Sequence 8506, Ap
45	70.5	5.3	696	15	US-10-128-714-3506 Sequence 8506, Ap

ALIGNMENTS

US-09-347-064-10	Sequence 10, Application US/09347064A
1	Patent No. US20020045208A1
2	GENERAL INFORMATION:
3	APPLICANT: Eck, Jürgen
4	APPLICANT: Schmidt, Arno
5	APPLICANT: Ralston
6	TITLE OF INVENTION: Ribosome-Inactivating Proteins of the m1stecoe Virus
7	TITLE OF INVENTION: Ribosome-Inactivating Proteins of the m1stecoe Virus
8	FILE REFERENCE: 09282-5
9	CURRENT FILING DATE: 1999-07-02
10	EARLIER FILING DATE: 1999-07-02
11	EARLIER FILING DATE: 1999-07-02
12	EARLIER FILING DATE: 1999-07-02
13	EARLIER FILING DATE: 1999-07-02
14	EARLIER FILING DATE: 1999-07-02
15	EARLIER FILING DATE: 1999-07-02
16	EARLIER FILING DATE: 1999-07-02
17	EARLIER FILING DATE: 1999-07-02
18	EARLIER FILING DATE: 1999-07-02
19	EARLIER FILING DATE: 1999-07-02
20	EARLIER FILING DATE: 1999-07-02
21	EARLIER FILING DATE: 1999-07-02
22	EARLIER FILING DATE: 1999-07-02
23	EARLIER FILING DATE: 1999-07-02
24	EARLIER FILING DATE: 1999-07-02
25	EARLIER FILING DATE: 1999-07-02
26	EARLIER FILING DATE: 1999-07-02
27	EARLIER FILING DATE: 1999-07-02
28	EARLIER FILING DATE: 1999-07-02
29	EARLIER FILING DATE: 1999-07-02
30	EARLIER FILING DATE: 1999-07-02
31	EARLIER FILING DATE: 1999-07-02
32	EARLIER FILING DATE: 1999-07-02
33	EARLIER FILING DATE: 1999-07-02
34	EARLIER FILING DATE: 1999-07-02
35	EARLIER FILING DATE: 1999-07-02
36	EARLIER FILING DATE: 1999-07-02
37	EARLIER FILING DATE: 1999-07-02
38	EARLIER FILING DATE: 1999-07-02
39	EARLIER FILING DATE: 1999-07-02
40	EARLIER FILING DATE: 1999-07-02
41	EARLIER FILING DATE: 1999-07-02
42	EARLIER FILING DATE: 1999-07-02
43	EARLIER FILING DATE: 1999-07-02
44	EARLIER FILING DATE: 1999-07-02
45	EARLIER FILING DATE: 1999-07-02

Thu Dec 11 16:09:49 2003

us-09-601-667c-3.rapb

Page 2

Qy 121 VQTLDTLGGGMLAGNDPAFREVITYGFRDLCSKNSKGSWVETCKSSQXQXWALVGD 180
Db 121 VQTLDTLGGGMLAGNDPAFREVITYGFRDLCSKNSKGSWVETCKSSQXQXWALVGD 179
Qy 181 GSIRPKONODCLTXGRDSVSTVIVTSCSXKXGXQWVFTNEXALINLKKXXXVVAQA 240
Db 180 GSIRPKONODCLTXGRDSVSTVIVTSCSXKXGXQWVFTNEXALINLKKXXXVVAQA 239
Qy 241 NPKLRRIITYPATGKRNQWMLPV 263
Db 240 NPKLRRIITYPATGKRNQWMLPV 262

RESULT 2
US-09-347-064-4
Sequence 4, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
INVENTOR: Schmidt, Irwin J.
APPLICANT: Schmidt, Irwin J.
TITLE OF INVENTION: Ribosome-Inactivating Proteins Based on
TITLE OF INVENTION: album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
EXAMINER APPLICATION NUMBER: ECT/EP98/00009
EXAMINER FILING DATE: 1998-07-02
EXAMINER APPLICATION NUMBER: 1997-10-0012.0
EXAMINER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 267
TYPE: PRT
ORGANISM: Vascum album
US-09-347-064-4

Query Match 95.5%; Score 1267.5; DB 9; Length 267;
Best Local Similarity 95.5%; Pred. No. 426-135;
Matches 241; Conservative 1; Mismatches 20; Indels 1; Gaps 1;
Qy 1 DDTGCSASEPTVIRVGRKGVYVADDDPHGQNIQIWPCKSNNDPQWLTKRDXITRS 60
Db 1 DDTGCSASEPTVIRVGRKGVYVADDDPHGQNIQIWPCKSNNDPQWLTKRDXITRS 60
Qy 61 NSGCLTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYG 120
Db 61 NSGCLTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYGTYG 120
Qy 121 VQTLDTLGGGMLAGNDPAFREVITYGFRDLCSKNSKGSWVETCKSSQXQXWALVGD 180
Db 121 VQTLDTLGGGMLAGNDPAFREVITYGFRDLCSKNSKGSWVETCKSSQXQXWALVGD 179
Qy 181 GSIRPKONODCLTXGRDSVSTVIVTSCSXKXGXQWVFTNEXALINLKKXXXVVAQA 240
Db 180 GSIRPKONODCLTXGRDSVSTVIVTSCSXKXGXQWVFTNEXALINLKKXXXVVAQA 239
Qy 241 NPKLRRIITYPATGKRNQWMLPV 263
Db 240 NPKLRRIITYPATGKRNQWMLPV 262

RESULT 3
US-10-083-336A-1
Sequence 1, Application US/10083336A
Patent No. US2003018665A1
GENERAL INFORMATION:
INVENTOR: Olson, Mark A.
APPLICANT: Mallard, Charles B.
APPLICANT: Byrne, Michael P.
APPLICANT: Mannescher, Robert W.

TITLE OF INVENTION: Racin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 576
TYPE: PRT
ORGANISM: Rictinus communis
US-10-083-336A-1

Query Match 64.0%; Score 849.5; DB 12; Length 576;
Best Local Similarity 60.8%; Pred. No. 2,46-87;
Matches 157; Conservative 29; Mismatches 72; Indels 1; Gaps 1;
Qy 5 CSASEPTVIRVGRKGVYVADDDPHGQNIQIWPCKSNNDPQWLTKRDXITRSNSG 64
Db 318 CMPEPTVIRVGRKGVYVADDDPHGQNIQIWPCKSNNDPQWLTKRDXITRSNSG 377
Qy 65 LTTGYTAGVYVMIIPONTAVREATTIWIWNGTIIIPRSNVLAASSGKGTITLT 124
Db 378 LTTGYTAGVYVMIIPONTAVREATTIWIWNGTIIIPRSNVLAASSGKGTITLT 124
Qy 125 DTLGGGMLAGNDPAFREVITYGFRDLCSKNSKGSWVETCKSSQXQXWALVGDGSR 184
Db 438 IYVAGGMLPTNQQFTVITVGLYGLCLQANSQGWIDCSSEFAEQ-QWALVAGSIR 496
Qy 185 PKONODCLTXGRDSVSTVIVTSCSXKXGXQWVFTNEXALINLKKXXXVVAQNPFL 244
Db 497 PKONODCLTXGRDSVSTVIVTSCSXKXGXQWVFTNEXALINLKKXXXVVAQNPFL 556
Qy 245 RRIITYPATGKRNQWMLPV 263
Db 557 RRIITYPATGKRNQWMLPV 575

RESULT 4
US-10-137-077-17
Sequence 17, Application US/10137077
Patent No. US20030092108A1
GENERAL INFORMATION:
INVENTOR: Hunter, Harry C.
APPLICANT: Goldstein, Irwin J.
TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom L
TITLE OF INVENTION: album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/10/137,077
EXAMINER APPLICATION NUMBER: 2002-05-02
EXAMINER FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/254,322
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 44
TYPE: PRT
ORGANISM: Xizicinus communis
US-10-137-077-17

Query Match 13.6%; Score 180; DB 15; Length 44;
Best Local Similarity 75.0%; Pred. No. 5,46-13;
Matches 33; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
Qy 12 VAIYGRKGVYVADDDPHGQNIQIWPCKSNNDPQWLTKRDXITRS 55
Db 1 VAIYGRKGVYVADDDPHGQNIQIWPCKSNNDPQWLTKRDXITRS 44

RESULT 5
US-10-074-527-5
Sequence 5, Application US/10074527

Thu Dec 11 16:09:49 2003

us-09-601-667c-3.rapb

Page 3

```
Publication No. US20020142426A1
GENERAL INFORMATION:
APPLICANT: Olandt, Peter J.
APPLICANT: Meyers, Rachel B.
APPLICANT: Galvan, Katherine A.
APPLICANT: NIDDK, National Institutes of Health
TITLE OF INVENTION: 3945 A human gene encoding glycocylin transferase and
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: NP12001-01SPICP(M)
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: US/10/074,527
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 45
TYPE: CDS
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus
US-10-074-527-5
```

```
Query Match 12.2%; Score 162; DB 14; Length 145;
Best Local Similarity 32.1%; Pred. No. 2,8e-10;
Matches 44; Conservative 18; Mismatches 61; Indels 14; Gaps 4;
QY 11 TTRIVGRKAKTVDDDFHGNQIQLPKSNNDPQQLMTI--KEDXTIRSG--NGSC 64
DB 7 TLVNSGRKCDVWSSSSSDQVQVNGHSPGQKMSLTYSDSGHSVYNDK 66
QY 65 LTTYGYTAGVYVIFDGNFAVRENTIWOIXNGTINP-----RNDLV--ASSGSG 116
DB 67 LTVNANSPSSVAVLYQDSNDSNOKWELNNDLGNKLLNVTGVLVDYKSGDTONG 126
QY 117 TTVTVQTLDTYTLGGQML 133
DB 127 TKLIVTCSGGRNQML 143
```

```
RESULT 6
US-10-156-761-14970
Sequence 14970, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKA
APPLICANT: HATTORI, YASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14970
LENGTH: 420
TYPE: CDS
ORGANISM: Streptomyces avermitilis
US-10-156-761-14970
```

```
Query Match 11.5%; Score 153; DB 15; Length 420;
Best Local Similarity 30.5%; Pred. No. 1,2e-08;
Matches 43; Conservative 19; Mismatches 69; Indels 10; Gaps 5;
QY 1 DD-VTCASAPPTVIVGRKGVYVDDDFHGNQIQLPKSNNDPQQLMTIKEDXTI 58
```

```
DB 284 DDVAVTTCSSSGAPITLQAGKCVVAGSSSANGAPVQV--DNGTGTQKWTVAADTL 341
QY 59 RSNVSCS--TYYGYTAGVYVIFDGNFAVRENTIWOIXNGTINPNSN--LVYASSGI 114
DB 342 RALGKCLDVTEKGTAGSGTQVQMDGGSANOK--WVTPAGDIVNPQKCLDVTEGNSA 359
QY 115 KETTLVQTLDTYTLGGQMLAG 135
DB 400 NGRHQLQWCSGGRNQKXKG 420
```

```
RESULT 7
US-10-156-761-9724
Sequence 9724, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKA
APPLICANT: HATTORI, YASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9724
LENGTH: 658
TYPE: CDS
ORGANISM: Streptomyces avermitilis
US-10-156-761-9724
```

```
Query Match 10.3%; Score 136.5; DB 15; Length 658;
Best Local Similarity 31.4%; Pred. No. 1.5e-06;
Matches 38; Conservative 17; Mismatches 57; Indels 9; Gaps 5;
QY 17 RPKAKTVYVDDDFHGNQIQLPKSNNDPQQLMTI--KEDXTIRSGSCLTY--GTRAG 73
DB 539 QSRGADIVNNTINQTELM--DNGSPNSWYITSRKELVYKMKLDKXVLSG 596
QY 74 VYVVFQCNVAVRENTIWOIXNGTINPNSVYLA--SSGKGTTLVQTLDTYTLGG 131
DB 597 TKVTVWCGQANOK--WNINSPTITWVAGLCIAVMAATATCTSLVWSCGTGDNK 654
QY 132 W 132
DB 655 W 655
```

```
RESULT 8
US-10-156-761-8170
Sequence 8170, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKA
APPLICANT: HATTORI, YASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
```

Thu Dec 11 16:09:49 2003

us-09-601-667c-3.rapb

Page 4

```
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/ SOURCE: US
/ LENGTH: 536
/ TYPE: PR
/ ORGANISM: Streptomyces avermitilis
US-10-156-761-8170

Query Match
  9.28; Score 121.5; DB 15; Length 536;
Best Local Similarity 29.04; Pred. No. 5.8e-05;
Matches 36; Conservative 16; Mismatches 57; Indels 15; Gaps 5;

QY 22 VVVVDDPHGNOIQIWPSSKSNNDPQWMTI---KRXITRSGS-CLTT- 77
DB 418 IDAVDQVRAEATVQWIKNGITINPSNVLV-----ASSGQIKITLVQITLVQID 474
QY 78 IFCNFAVREKTIQWIKNGITINPSNVLV-----ASSGQIKITLVQITLVQID 131
DB 475 IYTCNGANOK--WSINPQVITQSGICIDVTGSDQSGVAVGTALEMTONGANOQ 532
QY 132 WLQG 135
DB 533 WLQG 536

RESULT 9
US-09-973-457-5
/ Sequence 5, Application US/09973457
/ Patent No. US20020164746A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapeller-Libermann, Rosana
/ TITLE OF INVENTION: AND USES THEREOF
/ FILE REFERENCE: US/09-973-457
/ CURRENT FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/238,849
/ PRIOR FILING DATE: 2000-10-06
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 135
/ TYPE: PR
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match
  9.04; Score 119.5; DB 10; Length 135;
Best Local Similarity 29.14; Pred. No. 1.6e-05;
Matches 41; Conservative 18; Mismatches 61; Indels 21; Gaps 8;

QY 14 IYGRKXGVY--RDDPHGNOIQIWPSSKSNNDPQWMTI---KRXITRSGS-CLTT 67
DB 7 IGAHTGICLDVNGSSSKSDNPVQIMDCHGQ--NQLMELYNESGALRINSDELTV 64
QY 68 YGTAGVYVIFDCNFAV--EATIQWIKNGITINPSNVLVASSGQIKITLVQID 125
DB 65 NG-----TVLYSCDGTGKNGKQWVXKGTIRPK-NKKGVDSG-----LCIDVD 113
QY 126 YTLGGWMLAGNDTAPREVTIY 146
DB 114 GKVQWMTGNSGDAPQKWIIF 134

RESULT 10
US-10-074-527-6
/ Sequence 6, Application US/10074527
/ Patent No. US2002014446A1
/ GENERAL INFORMATION:
/ APPLICANT: Olandt, Peter J.
/ APPLICANT: Meyers, Rachel E.
```

```
/ APPLICANT: Galvín, Katherine A., et al.
/ APPLICANT: Nanyang Technological University, Singapore
/ TITLE OF INVENTION: Human Glycosyltransferase and
/ TITLE OF INVENTION: Uses Thereof
/ FILE REFERENCE: MEI2001-018P(RCPI(M)
/ CURRENT APPLICATION NUMBER: US/10/074,527
/ CURRENT FILING DATE: 2002-02-12
/ PRIOR APPLICATION NUMBER: 60/269202
/ PRIOR FILING DATE: 2001-02-15
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 135
/ TYPE: PR
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: consensus
US-10-074-527-6

Query Match
  9.04; Score 119.5; DB 14; Length 135;
Best Local Similarity 29.14; Pred. No. 1.6e-05;
Matches 41; Conservative 18; Mismatches 61; Indels 21; Gaps 8;

QY 14 IYGRKXGVY--RDDPHGNOIQIWPSSKSNNDPQWMTI---KRXITRSGS-CLTT 67
DB 7 IGAHTGICLDVNGSSSKSDNPVQIMDCHGQ--NQLMELYNESGALRINSDELTV 64
QY 68 YGTAGVYVIFDCNFAV--EATIQWIKNGITINPSNVLVASSGQIKITLVQID 125
DB 65 NG-----TVLYSCDGTGKNGKQWVNDGTIRPK-NKKGVDSG-----LCIDVD 113
QY 126 YTLGGWMLAGNDTAPREVTIY 146
DB 114 GKVQWMTGNSGDAPQKWIIF 134

RESULT 11
US-10-156-761-10246
/ Sequence 10246, Application US/10156761
/ Patent No. US20030119018A1
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: IKEDA, HARUO
/ APPLICANT: ICHIKAWA, YUJI
/ APPLICANT: ISHIMURA, YOSHIO
/ APPLICANT: SHIBA, TAKAYOSHI
/ APPLICANT: SAKAKI, YOSHITAKI
/ APPLICANT: HATTORI, MASAHISA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCE: 249-262
/ CURRENT APPLICATION NUMBER: US/10/156,761
/ CURRENT FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: JP 2001-204089
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/ SOURCE: US
/ LENGTH: 647
/ TYPE: PR
/ ORGANISM: Streptomyces avermitilis
US-10-156-761-10246

Query Match
  8.98; Score 118.5; DB 15; Length 647;
Best Local Similarity 25.04; Pred. No. 0.0016;
Matches 33; Conservative 22; Mismatches 62; Indels 15; Gaps 5;

QY 9 EPTVRLYRKXGVYVDDPHGNOIQIWPSSKSNNDPQWMTI---KRXITRSGS-CLTT 66
DB 520 QGTGSLVLAQKICLDVNGSSSKSDNPVQIMDCHGQ--DCKGSTAGKRTLVKSDSYQAGKICLDVT 577
QY 67 YGTAGVYVIFDCNFAVREKTIQWIKNGITINPSNVLVASSGQIKITLVQID 120
```

Thu Dec 11 16:09:49 2003

us-09-601-667c-3.rapb

Page 5

Db 578 SASSTADAKIQLYQNC-----GTAQNRISNINSTSDVWVTLADKCLDVTGNSANGRRQA 632
 QY 121 VQTLDYITLQGM 132
 Db 633 TNSCTGAANQK 644

```

RESULT 12
US-09-770-621.5
Sequence 5, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: W. Irya, A'rya
APPLICANT: Remaueper, Jari
APPLICANT: Remaueper, Richard
APPLICANT: Lapinto, Rajia
APPLICANT: Palomheo, Maria
APPLICANT: Sumienem, Patrick
APPLICANT: Lahnenen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STEEN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/590,563
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/392,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050 0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
STRANDNESS: No. US20010024815A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-09-770-621.5

```

```

Query Match      8.3%; Score 117.5; DB 9; Length 480;
Best Local Similarity 3.1%; Pred. No. 0.00014;
Matches 32; Conservative 16; Mismatches 49; Indels 5; Gaps 3
QY 22 VVDRDDDFHGDGOTLMSKSNNDNDLTWTFEDXTRISNGS-CITTYGTATGYMIKD 80
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Db 379 IDVPKNGKTDIGVQVQLDCHSSG - NQGVYTHSSGEFR FGNKCLDAGSSNGAVQYIYS 436
 Qy 81 CRRATREALITNQIKNGKITLIPRSLVLAASSGKITLVQ 122
 Db 437 CMGAGNOK - HELDAGITLVGVSSGLCDLVGGATGNGTRIQ 476

RESULT 13
 US-09-770-621-4
 Sequence 4, Application US/09770621
 Patent No. US20010024815A1
 GENERAL INFORMATION:
 APPLICANT: W. HCY, Arja
 APPLICANT: Vagstad, Jari
 APPLICANT: Vagstad, Richard
 APPLICANT: Vagstad, Paul
 APPLICANT: Plothen, Maria
 APPLICANT: Strommen, Mikko
 APPLICANT: Lahnen, Taita
 TITLE OF INVENTION: Production and Secretion of Proteins of
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESSES:
 ADDRESS: STEEN, KESSIE, GOLDSTEIN & FOX, P.L.L.C.
 1000 New York Ave., N.W. Suite 600
 City, Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER TYPE: IBM compatible
 SOFTWARE: DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/770, 621
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/590, 563
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/332, 412
 FILING DATE: 31-OCT-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/282, 001
 FILING DATE: 29-OUL-1994
 ATORNEY/AGENT INFORMATION:
 NAME: Bugalsky, Lawrence B.
 REGISTRATION NUMBER: 35,086
 REFERENCE/DOCKET NUMBER: 1050 0340003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2640
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 4:
 SOURCE: CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-770-621-4

```
Query Match      9.8%; Score 11.75; DB 9; Length 492;
Best Local Similarity 31.4%; Pred. No. 0.00015;
Matches          32; Conservative 16; Mismatches 49; Indels 5; Gaps 3

Ox 22 TTPTDPPDFGNGQVMPMSKSNDDNFTIRDKXTLSSS-CLTYGYTACGYVAIED 80
Db 379 IDVPSTATDTGYQLYDCDSHS--NQGVITYSNGSEFRIIPNNICDLAGSSSGNAVILIS 436
Oy 81 CHTAVREAIQTQIKXGKIINPSSLVLASSGKKTILLIIVQ 122
```

Thu Dec 11 16:09:49 2003

us-09-601-667c-3.rapb

DB 437 CMGANOK--WEHRAJDTTIVGVSGLCDLVGGTGNTRIQ 476

RESULT 14
US-09-770-621-7
Sequence 7, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M ryl, Arja
INVENTOR: M ryl, Arja
APPLICANT: Vennanper, Jari
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
APPLICANT: Suominen, Pirkko
APPLICANT: Lantto, Raito
TITLE OF INVENTION: Production and secretion of proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIA TYPE: CD-ROM
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hagist, Lawrence B.
RESIDENCE/CITY/STATE/ZIP: 10050.0340003
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2640
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDNESS: No. US20010024815A1 Relevant
TOPOLOGY: linear
POSITION IN SEQUENCE:
CHROMOSOME/SEGMENT: AM50
US-09-770-621-7

Query Match 8.9%; Score 117.5; DB 9; Length 492;
Best Local Similarity 31.4%; Pred. No. 0.00015;
Matches 32; Conservative 16; Mismatches 49; Indels 5; Gaps 3;
DB 22 VVRRDDDFHDSNQGLMPSKSNNDPNQLTIKRXITRSNGS-CLTYGYTAGYVMIFD 80
379 IDVPKNTALGTQVQLDCHSGS--NQDWTYSSGSEFRIFPKNCIDAGSSNKAAYVQLIS 436
QY 81 CNTAVREKTIWQIKNGTILNPSNVLAASSGIKETLTIVQ 122
QY 81 CNTAVREKTIWQIKNGTILNPSNVLAASSGIKETLTIVQ 122

DB 437 CMGANOK--WEHRAJDTTIVGVSGLCDLVGGTGNTRIQ 476

RESULT 15
US-10-286-993-4
Sequence 4, Application US/10286993
Publication No. US2003014853A1
GENERAL INFORMATION:
APPLICANT: M ryl, Arja
INVENTOR: M ryl, Arja
APPLICANT: Vennanper, Jari
APPLICANT: Lantto, Raito
APPLICANT: Lantto, Raito
APPLICANT: Suominen, Pirkko
APPLICANT: Lantto, Raito
TITLE OF INVENTION: Production and secretion of proteins in filamentous
FILE REFERENCE: 1716.0340004
CURRENT APPLICATION NUMBER: US/10/286,993
CURRENT FILING DATE: 2002-08-13/20,804
PRIOR APPLICATION NUMBER: 08/09/120,804
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: ECT/PI97/00037
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: US 08/590,563
PRIOR FILING DATE: 1996-01-26
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent version 3.0
SEQ ID NO 4
LENGTH: 492
TYPE: PRT
ORGANISM: Actinobacteria flexuosa
US-10-286-993-4

Query Match 8.9%; Score 117.5; DB 12; Length 492;
Best Local Similarity 31.4%; Pred. No. 0.00015;
Matches 32; Conservative 16; Mismatches 49; Indels 5; Gaps 3;
DB 22 VVRRDDDFHDSNQGLMPSKSNNDPNQLTIKRXITRSNGS-CLTYGYTAGYVMIFD 80
379 IDVPKNTALGTQVQLDCHSGS--NQDWTYSSGSEFRIFPKNCIDAGSSNKAAYVQLIS 436
QY 81 CNTAVREKTIWQIKNGTILNPSNVLAASSGIKETLTIVQ 122
DB 437 CMGANOK--WEHRAJDTTIVGVSGLCDLVGGTGNTRIQ 476
Search completed: December 11, 2003, 14:48:46
Job time : 17.0129 secs

Best Local Similarity 47.7%; Pred. No.2,9e-91;
Matches 254; Conservative 89; Mismatched 162; Indels 29; Gaps 8;

```
QY      9  TQVTVSEYFFPTLLADYVSSGSPENRIPILKOSTIPVSDAKFVLVEITVNGSDSITA 68
Dc      9  TGAQSVKQFTEALREKR-RGGLIHDIPVLDPT-TQENKAYITVELSSNDSEIIV 66
QY      69  AIDPTLVYRXYDAGSGSYIRDPKAGETFLCTSSSSPENGYSPTREKAR-EDQ 127
Db      67  GIDVTNAYVYAAIGSYHFLDKRPSMDLTCTDQHSIFPGYVDLEKMRGSRQ 126
QY      128  IFLGIDLOSVALRPPGSGSPFQVARSILILQIMESAARNPILMAQSYNGASLP 187
Db      127  IFLGKQLTHGISFPFGSGNDIEKRAFLIYIQVLEAKRFRYSRNVDSIQYGAHQ 186
QY      188  PIVYVLELETSMGQSTOVGHSTQYVNNPRLALIPGQVFTLLNRPD-----V 236
Db      187  PPAAMIILENNMNDLSRVOGESVDQDFPQO-----VTLINRINEVPLVDSISPT 236
QY      237  ISGLAILEFVCGSPSSSDVIRFWLVIRFVADVYCSAS-EPVYVIGSNGICVADRD 235
Db      237  VAVALMLFVCP-PAAGS--FLIRIYESKXICSSSPYVPAVIGSDKACVDVYIN 232
QY      236  DRHGNQIQLFESKSNDDPQVLTIRKSGITKSNGLCTITGYAGVYVIFDCAINVAZE 335
Db      233  GHNRNRIKQIKOIRLEHQVQKILSRKIRFVSNKCLTIRFVSNKCLTIRFVSNK 352
QY      336  ATTQNGIMNGKITINPNSVYLAASGIKGTLVQVLTQYDLYTGGQMLAANDPAREVY 415
Db      353  ATYVMIIDNGKITINPESLVLTLASASRMDGTLVQVITNEYLRNGQMTNNISFPVTSIG 412
QY      416  FPDLCQNSNGSYVETCVSSQOQRMALYDQDSIRKQNDQOCLCGRDSVYVINYIS 475
Db      413  YSLDLOMQDSNYVAADDSDNKKRQOMALYTDSDISRYQNTNNCLISDKHQSTILLNG 472
QY      476  CSNAGSGSGRWFTNEGALIMLNKGLANDVQANPFLRRRIITYEAKYNGQNM 528
Db      473  CSNMGASGQWFTNDSIYSLFDQRYVDVAKNSPFLKQIILMFLPTEKRNQNM 525
```

RESULT 6

abryn-c pre

C/Species: *Abrus precatorius* (Indian licorice)

C:\Accession: S16022
B:\Wood y A. Ford T M. Newmarch E T. Dietrich M

Eur. J. Biochem. 198, 723-732, 1991

A: Accession: S16022
A: Reference number: S16022; MUID: 91266957; PMID: 2050141

A;Status: preliminary
A:Molecule type: DNA

A;residuals: 1-562 <NO
A;Cross-references: E

The A and B chains are

C;superfamily: rictm;
C;keywords: duplicati

F:41-280/Domain: rRNA

F: 317-359, 360-400, 403
F: 293-382/ FICUUC: ad

F;108,147,229,230/Bim

F: 130, 201, ACCLAVE SILE
F: 234, 287, 395, 435, 436

F;322,346/Binding site

[illegible]

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

[REDACTED]

Beat Local Similarity 47.8%; Pred. No. 1.le-87;
 Matches 250; Conservative 89; Mismatch. 175; Indels 9; Gaps 7;
 QY THQCTTEBEFFFTLLDIDVYSSCSFSENEPIRLKOSTIPVSDAQRFLVETNQGSDGITA 66
 Db TGAATSGSYKQFTEAKMQRLLTGLLHIDLPALDFTVEEKNKRYITVELSNSESTIEV 100
 QY AIDVTMLRYVAQADQSGFLADPGKAEFLHFTCTSSSLFPHGYSPLERAYAHQQ 127
 Db IGIQIDTAHYVAHAKSGQSYFLADPASSTYLPQTORISLAPDSQYDLERMAQHRE 160
 QY 128 IFLGIDIDLOSVAHAFEGSGSFQRAISILILKQVTEAARNTILMAQAYNSGASFL 187
 Db 161 IELGIDQLTHAIFSLRSGANDERKARTLVIQWAEELAAHYRIANVGSIFPTQAFQ 220
 QY 188 PNYVMELETSQQQSGYQVQHSTGVFNNPIFLALFPGNSVPLTNVDVIALSLMLTV 246
 Db 221 PGPALMSLENNMWNISGVOGVDDFFNNVLISIRINQAPVVDLSHPVIANALMLTV 280
 QY 247 CQERSSSPVRYMFLVRYPIVDIWTCSAS-EPTVRYVRNKMQVADDDPHQNDIQ 305
 Db 281 CNP-FNANS--PILIRISVEEKICSRREYETICGRQGVQVDDYDQXNANMIIA 336
 QY 306 WESGNSNDENQMLTKDQDGTIRNSQSLCTTYGTAGSYVMFLPDCAINREKATINQVNG 366
 Db 337 WICKQRLRENDMLTKDQDGTIRNSQSLCTTYGTAGSYVMFLPDCAINREKATINQVNG 396
 QY 366 TIKNERNLVAASAGIKRITFLTYQTLQYTLAQGLKANDMDAPREUTYVGRRLQMSNG 425
 Db 397 TIINPKSALVYASSSMSGGTLVQINBLYLMQGRQGNNTSPFVTSISGSDLMQAOQ 456
 QY 456 GSAWVEVCVSSQONQRMALVIGGSIIRPKQNDQCCTGCDSTSVYVINTVSCSGASQSQM 485
 Db 457 SHVYALACDNKKEQQAMLVTTQSSIRSYOVNNNCTLSHQKGSFVYLMACSSVMSQSR 516
 QY 486 VFTMEGALINKGLANDVQAQKFLRRLIITYATGKXQNMVL 528
 Db 517 LRFQDSIYNLHDDQWQVDSQDSLAKELIILPHKQKQNMVL 559

RESULT 7

abrin-d precursor - Indian licorice (fragment

C;Species: Abrus precatorius (Indian licorice)

C;Accession: S32431; S34408

J. Mol. Biol. 229, 263-267, 1993

A;Reference number: S32429; MUID:93132798; PM
B;Accession: S32431

A: Molecule type: mRNA
A: Residues: 1-528 (H1N)

A; Cross-references: GE:M98346
P:Hung C : Lee M : Lee T : Lin T

submitted to the EMBL Data Library, March 1999.
A:Reference number: S34408

A;Accession: S34408
A;Molecule type: mRNA

A;Residues: 1-169, 'C', 171-320, 'D', 322-528 <HU
A;Cross-references: GB:M98346

The A and B chains are linked by a single disulfide bond.

C;superfamily: ticin; trna n-glycosidase homo
C;keywords: disulfide bond; duplication; glyc

Fi:7-246/Domain: rRNA N-glycosidase homology <

```

E;261-328/Product: adp1h-a chain B #sequence pr
E;283-325,326-366,369-407,414-449,453-492,495-

```

F;74,113,195,196/Binding site: substrate (Tyr
211/Moaddied site: pyroglutamic acid

F:\104,10//archive site: GUN, ARG #scarcus pried

[illegible]

P:320-537/Pro-act: abrin-b chain B #status experimental RGDH-
P:282-324/325-365: 368-406: 413-449: 452-491: 494-527/Region: 40- residue repeats
P1/Modified site: pyridoxime carboxylic acid (Gln) #status predicted
P:7/113,114,115/Binding site: substrate 'CY', 'YR', 'GU', 'Asn' #status predicted
P:110,160/Binding site: carboxylate (Asn) (covalent) #status predicted
P:113,160/Active site: Glu, Arg #status predicted
P:266-268,285-304,328-345,416-429,435-472/Distalide bonds: #status predicted
P:267,311/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
P:289,520/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 42.3% Score 1197. DB 2: Length 527;
Best Local Similarity 47.2% Pval No. 2.4e-86;
Matches 247; Conservative 91; Mismatches 175; Indels 10; Gaps 8;

QY 9 THQGTGEYRFPITLADVDYSSGSFNSRPLMKSQSTVSDAQRFVLEIYNQGGDITR 68
DB 9 TBNATSSYKQFETLAKQRLTGGALHGIPLVLPDPTLTGERRRIVELNSDPTESIA 66
QY 65 AIVDNLVVAQAGDGSPTFLDAPKAETLFTGTSSLPENQSPDLERAGH-RDQ 127
DB 67 GLDSNAVVAIDAKNSHITLADPTPSASRIETFGVQSLKRNSTIDELRLKQTRQ 126
QY 128 IPEGLDIOGIVLAPPGSGSPRQASRIILTIQNISSARFPIILWRAQYINSGSL 187
DB 127 IPEGLDIAHAIISPLQ-SCGDDEICARTLIYIIQNASAPARFISYRGVSIETWAFQ 185
QY 188 EDVYMLELTSNGQSGSTQVQSHSTGYFNNPRLALPKNPVLTLNV-RVIVSLATMLFV 246
DB 186 FDMANSLSENNMDNISGQVQVDFPAPVALTSVNNQVTVSLTHOSVATLALMFV 245
QY 247 CGERPSSDRIWELIYRIADVDTGASL-EPYTAIVENQNCIDPRDDHFNQGL 305
DB 246 CNP-PNAGS--PLIRAIYERKAIQSRSEPTIRIGNNKQCIDVDYVHGRNIIA 301
QY 306 WPSKSNPNQQLMTKDDGYSINSGSLCTTGYTGAVYWPICNCTVDEATVQIWNQ 365
DB 302 WKCKGLENNQMLTKKDDTKINSKGLCTTGAGAGNVAWIDCTGSAVETATWELMDNG 361
QY 366 TIINPSNLVAASGIRGTLITVQLDYLITGGWAGLQTAAPREVTIYGRDICESNG 425
DB 362 TIINPSNLVAASGIRGTLITVQLDYLITGGWAGLQTAAPREVTIYGRDICESNG 421
QY 428 GSWVETGVSQONQWALYKGSIPPNQDDCTGGRDSVATINIVYASGASGGQW 485
DB 422 SNWVLAYDKNKKEQWALYDGSISASVQNNKCLTSDKDKGSPIVWACSGNSMAQRP 481
QY 486 VFTNCGALINLKNGLADYDAQNAQMKERRIITIVATGKRNQMWL 528
DB 482 LFNQDSITVLDHDKVADYKRSDDLKELIILHFYHQRKNQIML 524

RESULT 9
RNCAG
aggutinin precursor - castor bean
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C:Date: 31-Dec-1993 #sequence_revstatus 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: A24261, A24210
R:Reporter: L.M.; Lamb, L.F.; Peppin, D.J.C.; Lord, J.M.
A:Title: Characterization, Isolation, and Purification of a Ricinus communis agglutinin
A:Reference number: A24261, PMID:86059449; PMID:2993130
A:Accession type: RNA
A:Molecule type: protein
A:Residues: 1-564 <ROB>
A:Cross-references: GB:M12089; NID:9167900; PIDN:AAA3869.1; PID:9167901
B:Araki, T.; Yoshioke, Y.; Nishitani, G.
B:Biochim. Biophys. Acta 872, 277-285, 1986
A:Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin
A:Reference number: A24210
A:Accession type: protein
A:Residues: 303-325, 'E', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-561, 'V',
A:Molecule type: protein

C:Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C:Superfamily: ricin; rRNA N-glycosidase homology; hydrolase; lectin; RNA binding; seed
C:Keyord(s): duplication; agglutinin; glycoprotein; glycosyltransferase; hydrolase; lectin; RNA binding; seed
F:125-290/Product: agglutinin chain A #status predicted <ACD>
F:125-281/Domains: rRNA N-glycosidase homology <RNG>
F:103-564/Product: agglutinin chain B #status experimental <RNG>
F:319-351,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats
F:33,259/Binding site: carbohydrate (asn) (covalent) #status predicted
F:104,147,231,232/Binding site: substrate (tyr, tyr, glu, asn) #status predicted
F:200,203/Active site: glu, arg #status predicted
F:282-306,322-341,365-382,453-466,492-509/Dissulfide bonds: #status predicted
F:334,337,348/Binding site: N-acetylglucosamine (asp, asn, asn) #status predicted
F:357,437/Binding site: carbohydrate (asn) (covalent) #status experimental
F:156,557/Binding site: N-acetylglucosamine (asp, asn) #status predicted

Query Match 42.7% Score 1191.5; DB 1; Length 564;
Best Local Similarity 47.6%; Pred. No. 7,2e-86;
Matches 254; Conservative 84; Mismatches 177; Indels 19; Gaps 10;

QY 9 THQTGEYEPFPTLLADYSSGS-PSNEI-PLI--EGSTIPYSDAGFVVELNQGDSI 66
Db 37 TDAIVESYTFIRAYRSHLTGADVREIPLVPRVGALPS--QPTLVLSNHELSV 94
QY 67 TLAIDVTMLVAVAYQADQSYFLR-DARSGAE--THLPTGTTSS-SLEPNQSPLEKRYA 122
Db 95 TLALDVTMLVAVAYQADQSYFLR-DARSGAE--THLPTGTTSS-SLEPNQSPLEKRYA 122
QY 123 GHRODTPLGIDLIQSYTLARF--PGGSTPTQASLTLLIQMSSEARFPLIRARQY 179
Db 155 GLENTIELGTPELADISALVYYSCTGQVITLASSFWICQIMSEARFVIEGEMER 214
QY 180 INSGAFLEPDIYVLELETSWQGSQTVQSTGVQVFNPRRLAIPGNFVLTVQVDVNAS 239
Db 215 IYKRSADPSVITLSENGSLSTALQSQDAPASIDLERKNSKENVYSLIP 274
QY 240 LALMLVCGEPPSSDVPRVPLVIRPIID--DPTCSASEPTVYKSNQVQVDEDD 296
Db 275 IALMVRCAPEPSSQ---FSLIKRIVYRNNDY-CHDEPIYKAYRNGELTVQVGE 329
QY 297 FHDNOQLMPSKSNPNQNLWTIKDGTIRNSGCLTGYGTAGYVWIFDQNTAVRA 356
Db 330 FPDNPQLMPCSKNTDNLWTIKDGTIRNSGCLTIRKSSPRQGVYVINSSTAVGA 389
QY 357 TTMQWNGTITNPRSNLVAAASGICWTLTYQTLDTYLGQWLANDPAPREVTYIG 416
Db 390 TFMQWNTITNPRSGVLATLSSNGSKLVTNITVAVSQMLPNNTQPTPTVITGA 449
QY 417 RDLCSNGSGWTCVYSSQGNQVAVYAGSIPKQNDQCTCGRDSVTVINYS 476
Db 450 YKCLQNSGKVMEDCTSEKABQRMALVAGSIPKQNDQCTCGTDAIKGVKILSG 509
QY 477 SAGSGQWFTNKGALINLKNGLANDVQANPGLRIIYPAKCKRNMQLPV 530
Db 510 GPASGQWFTNKGALINLKNGLANDVQANPGLRIIYPAKCKRNMQLPV 530
RESULT 10
Agglutinin I precursor - European elder
C:Species: Sambucus nigra
C:Accession: S62627
C:ReleaseDate: 19860227
C:Revision: 11-Mar-1997 #text_change 20-Aug-1999
P:van Damme, B.J.M.; Barte, A.; Rouge, P.; van Leuven, F.; Pennaers, W.J.
Eur. J. Biochem. 235, 128-137, 1996
A:Title: The Nucleo-alpha-2,6-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)
A:Reference number: S62619; MIM:96202926; PMID:8631319
A:Accession: S62627
A:Status: preliminary
A:Status: preliminary
A:Molecule type: rRNA
A:Residues: 1-570 <VMN>
A:Cross-References: EMBL:U27122; NID:G1141772; PION:AA649158.1; PID:G1141773
A:Accession: S62619

A:Status: preliminary
A:Molecule type: protein
A:Residues: 25-39,109-219 <VAZ>
C:Superfamily: ricin; rRNA N-glycosidase homology
F:37-283/Domains: rRNA N-glycosidase homology <RNG>

Query Match 33.9% Score 947.5; DB 2; Length 570;
Best Local Similarity 40.7%; Pred. No. 1,2e-86;
Matches 220; Conservative 82; Mismatches 206; Indels 33; Gaps 15;

QY 8 YTHQTG-EEYEPFPTLLADYSSGS-PSNEI-PLI--EGSTIPYSDAGFVVELNQGDSI 66
Db 37 TDAIVESYTFIRAYRSHLTGADVREIPLVPRVGALPS--QPTLVLSNHELSV 94
QY 67 TLAIDVTMLVAVAYQADQSYFLR-DARSGAE--THLPTGTTSS-SLEPNQSPLEKRYA 122
Db 95 TLALDVTMLVAVAYQADQSYFLR-DARSGAE--THLPTGTTSS-SLEPNQSPLEKRYA 122
QY 123 GHRODTPLGIDLIQSYTLARF--PGGSTPTQASLTLLIQMSSEARFPLIRARQY 179
Db 155 GLENTIELGTPELADISALVYYSCTGQVITLASSFWICQIMSEARFVIEGEMER 214
QY 180 INSGAFLEPDIYVLELETSWQGSQTVQSTGVQVFNPRRLAIPGNFVLTVQVDVNAS 239
Db 215 IYKRSADPSVITLSENGSLSTALQSQDAPASIDLERKNSKENVYSLIP 274
QY 240 LALMLVCGEPPSSDVPRVPLVIRPIID--DPTCSASEPTVYKSNQVQVDEDD 296
Db 275 IALMVRCAPEPSSQ---FSLIKRIVYRNNDY-CHDEPIYKAYRNGELTVQVGE 329
QY 297 FHDNOQLMPSKSNPNQNLWTIKDGTIRNSGCLTGYGTAGYVWIFDQNTAVRA 356
Db 330 FPDNPQLMPCSKNTDNLWTIKDGTIRNSGCLTIRKSSPRQGVYVINSSTAVGA 389
QY 357 TTMQWNGTITNPRSNLVAAASGICWTLTYQTLDTYLGQWLANDPAPREVTYIG 416
Db 390 TFMQWNTITNPRSGVLATLSSNGSKLVTNITVAVSQMLPNNTQPTPTVITGA 449
QY 417 RDLCSNGSGWTCVYSSQGNQVAVYAGSIPKQNDQCTCGRDSVTVINYS 476
Db 450 YKCLQNSGKVMEDCTSEKABQRMALVAGSIPKQNDQCTCGTDAIKGVKILSG 509
QY 477 SAGSGQWFTNKGALINLKNGLANDVQANPGLRIIYPAKCKRNMQLPV 530
Db 510 GPASGQWFTNKGALINLKNGLANDVQANPGLRIIYPAKCKRNMQLPV 530
RESULT 11
Ricin B - caenor bean (fragment)
M:Context(s): chain B, rRNA N-glycosidase (EC 3.2.2.22) (chain A)
C:Species: Ricinus communis
C:Accession: S06330
C:ReleaseDate: 19860227
C:Revision: 31-Mar-1990 #text_change 20-Aug-1999
P:Bladin, B.F.; Murray, B.B.; Halling, A.C.; Tilkakare, N.; Long, G.
Plant Mol. Biol. 9, 287-295, 1987
A:Title: Characterization of a cDNA encoding ricin B, a hybrid ricin-Ricinus communis
A:Reference number: S06330
A:Accession: S06330
A:Status: not compared with conceptual translation
A:Molecule type: rRNA
A:Residues: 1-263 <LAD>
A:Cross-References: EMBL:M17631; NID:G159714; PION:AA6506.1; PID:G169715
A:Accession: S06331
A:Status: preliminary
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-191, 191-200, 1987
A:Cross-References: EMBL:U27122; NID:G1141772; PION:AA649158.1; PID:G1141773
A:Accession: S06331

A/Residues: 1-69, 'P', 'S', 'T', 'A', 'V', '211-241, 243-250, 'V', 252-263 <ABA>
A/Experimental source: seed
C/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase
F/1-263/Product: ricin B chain B #status experimental <BCH>
F/1-263/60-100/103-141, 148-183, 187-228, 229-263/Region: 40-residue repeats
F/10-35/Binding site: carboxylate (Asn) (covalent) #status experimental
F/195, 115/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 31.9%; Score 891.5; DB 2; Length 263;
Best Local Similarity 62.5%; Pred. No. 1, 1e-62;
Matches 162; Conservative 34; Mismatches 62; Indels 1; Gaps 1;

QY 273 CSASEPTVAVSNMCDVDDDFDQNDQNTQMPKSNNDPNDLTKDQITRSNASC 332
DB 4 CNDPEPTVAVSNMCDVDDDFDQNDQNTQMPKSNNDPNDLTKDQITRSNASC 63

QY 333 LTVYGTAGVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 392
DB 64 LTVYGTAGVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 123

QY 393 DYLQGGWLAGVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 452
DB 124 DYLQGGWLAGVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 183

QY 453 KQNDQCLTCGRDSTVAVSNMCDVDDDFDQNDQNTQMPKSNNDPNDLTKDQITRSNASC 511
DB 184 KQNDQCLTCGRDSTVAVSNMCDVDDDFDQNDQNTQMPKSNNDPNDLTKDQITRSNASC 243

QY 512 RNTTTPATKGRVQNTLEFV 530
DB 244 RNTTTPATKGRVQNTLEFV 262

RESULT 12
C39761
abrin (clone 7.2) precursor - Indian jicorice (fragment)
N/Contents: rRNA N-glycosidase (BC 3.2.2.22)
C/Species: Abrus precatorius (Indian jicorice)
C/Date: 21-Feb-1992 #sequence, revision 31-Dec-1993 #ext. change 20-Aug-1999
A/Accession: C39761, S14471, S14471, S14471, S14471, S14471, S14471, S14471
J. Biol. Chem. 266:6848-6852, 1991
A/Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A/Reference number: A39761; MUID:91201329; PMID:2026300
A/Accession: C39761
A/Molecule type: DNA
A/Residues: 1-251 <EV>
R. Svensen, G. Mathiesen, A. Sundan, A.
submitted to the EMU Data Library, October 1990
A/Description: Direct molecular cloning of two distinct abrin A-chains.
A/Reference number: S14471
A/Accession: S14471
A/Molecule type: DNA
A/Residues: 1-251 <EV>
A/Cross-references: EMBL:X54872; NID:916088; PIRN:CA38654.1; PID:916089
C/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycosidase; hydrolase; lacticin; toxin
F/1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F/74, 113, 195, 196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/164, 167/Active site: Glu, Arg #status predicted

Query Match 16.5%; Score 462; DB 2; Length 251;
Best Local Similarity 44.4%; Pred. No. 6, 3e-25;
Matches 107; Conservative 38; Mismatches 92; Indels 4; Gaps 4;

QY 9 TQGTGEEPTVAVSNMCDVDDDFDQNDQNTQMPKSNNDPNDLTKDQITRSNASC 68
DB 9 TQGTGEEPTVAVSNMCDVDDDFDQNDQNTQMPKSNNDPNDLTKDQITRSNASC 66

QY 69 AIDVTNLYVAVSNMCDVDDDFDQNDQNTQMPKSNNDPNDLTKDQITRSNASC 127

QY 69 AIDVTNLYVAVSNMCDVDDDFDQNDQNTQMPKSNNDPNDLTKDQITRSNASC 127

DB 67 GIDVTNLYVAVSNMCDVDDDFDQNDQNTQMPKSNNDPNDLTKDQITRSNASC 126
QY 128 IPGLDQLOSVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 187
DB 127 IPGLDQLOSVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 186

QY 188 PDVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 246
DB 187 PDVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 246

QY 247 C 247
DB 247 C 247

RESULT 13
S25560
rRNA N-glycosidase (BC 3.2.2.22) momordin II - balsam apple
C/Species: Momordica balsamina (balsam apple)
C/Date: 25-Feb-1994 #sequence, revision 03-Aug-1995 #ext. change 20-Aug-1999
A/Accession: S25560, M14871, M14871, M14871, M14871, M14871, M14871, M14871
J. Biol. Chem. 269:1992-1997, 1994
A/Title: Momordin II, a ribosome inactivating protein from Momordica balsamina, is a
Nucleic Acid Res 20, 4662, 1992
A/Reference number: S25560; MUID:93027170; PMID:1408771
A/Accession: S25560
A/Molecule type: mRNA
A/Status: preliminary
A/Cross-references: EMBL:U12175; NID:919525; PIRN:CA47816.1; PID:919526
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C/Keywords: glycosidase; hydrolase
F/27-264/Domain: rRNA N-glycosidase homology <RNG>

Query Match 13.3%; Score 344.5; DB 2; Length 286;
Best Local Similarity 34.8%; Pred. No. 1, 5e-19;
Matches 88; Conservative 54; Mismatches 92; Indels 19; Gaps 9;

QY 13 TGEYPTVAVSNMCDVDDDFDQNDQNTQMPKSNNDPNDLTKDQITRSNASC 69
DB 33 TGEYPTVAVSNMCDVDDDFDQNDQNTQMPKSNNDPNDLTKDQITRSNASC 86

QY 70 IPGLDQLOSVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 127
DB 67 IPGLDQLOSVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 145

QY 128 IPGLDQLOSVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 187
DB 146 IPGLDQLOSVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 201

QY 188 PDVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 246
DB 187 PDVYVAFDQNTVRENTTQIMQNGTITPSSNIVAASSGIRKTTVPQTL 246

QY 247 C 247
DB 247 C 247

RESULT 14
JC4840
rRNA N-glycosidase (BC 3.2.2.22) trichogangula - snake gourd
C/Species: Trichosanthes anguina (snake gourd)
C/Date: 15-Aug-1995 #sequence, revision 24-Oct-1997 #ext. change 05-Dec-1997
A/Accession: JC4840, J07071, J07071, J07071, J07071, J07071, J07071, J07071
J. Biol. Chem. 270:1992-1997, 1995
A/Title: Snake gourd rRNA N-glycosidase homology <RNG>
A/Accession: JC4840
A/Molecule type: protein
A/Residues: 1-132, 'S', 'T', 'A', 'V', 134-245 <CHOI>
A/Experimental source: seed

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 5.1251 seconds

2736.539 Million cell updates/sec

Title: US-09-601-667C-4

Perfect score: 2791

Sequence: 1 YERLRRLVHTQGTGEYFRP.....NRITVPAKGNOMLPPV 531

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1339.5	48.0	264	1 MBE_VTSAL	P081830 viscum albu
2	1308	46.7	526	1 R1P1_RICCO	P024875 ricinus com
3	1289.5	45.1	528	1 ABRP_ABRP	P11440 album abna
4	1259.5	43.5	528	1 ABRP_ABRP	P128990 abna abna
5	1244.5	42.9	527	1 ABRP_ABRP	P06077 abna abna
6	1197	42.7	564	1 AGGL_RICCO	P06150 ricinus com
7	1191.5	42.7	563	1 NIGB_SANNI	P33181 sambucus ni
8	895.5	32.1	563	1 NIGB_SANNI	P33181 sambucus ni
9	350	12.5	282	1 R1P2_BRIDI	P98184 bryonia dio
10	344.5	12.3	286	1 R1P2_BRIDI	P293133 momordica b
11	327.5	11.7	294	1 R1P1_TRIAN	P293133 momordica b
12	326	11.7	289	1 R1P1_TRIAN	P09988 crichosanth
13	325	11.6	289	1 R1P1_TRIAN	P24478 crichosanth
14	318.5	11.1	286	1 R1P1_TRIAN	P09128 cucumis fig
15	318.5	11.1	286	1 R1P1_TRIAN	P09128 cucumis fig
16	294.5	10.6	250	1 R1P1_BRIDI	P33181 sambucus ni
17	291.5	10.4	277	1 R1P1_BRIDI	P00465 luffa cylin
18	284.5	10.2	286	1 R1P1_BRIDI	P12694 momordica c
19	280	10.0	250	1 R1P1_BRIDI	P22851 luffa cylin
20	249.5	8.9	278	1 R1P1_MIRNA	P10297 phytolecta
21	215	7.7	313	1 R1P1_MIRNA	P10297 phytolecta
22	213.5	7.6	261	1 R1P1_PHYAM	P23339 phytolecta
23	208	7.5	261	1 R1P1_PHYAM	P23339 phytolecta
24	180.5	6.5	253	1 R1P5_SAPOR	P04189 saponaria o
25	180.5	6.5	253	1 R1P5_SAPOR	P04189 saponaria o
26	178.5	6.4	253	1 R1P7_SAPOR	P04191 saponaria o
27	177.5	6.2	252	1 R1P2_SAPOR	P22753 saponaria o
28	168.5	5.4	310	1 R1P2_SAPOR	P22753 saponaria o
29	165.5	5.1	293	1 R1P2_SAPOR	P22753 saponaria o
30	142.5	5.0	236	1 R1P1_DIACA	P24476 diunhus ca
31	140	5.0	236	1 R1P1_DIACA	P24476 diunhus ca
32	138.5	5.0	236	1 R1P1_DIACA	P24476 diunhus ca
33	127	4.6	315	1 SLTA_BP119	P08026 bacterioph

ALIGNMENTS

RESULT 1	MBE_VTSAL	STANDARD	PRT	264 AA
1	MBE_VTSAL	STANDARD	PRT	264 AA
2	MBE_VTSAL	STANDARD	PRT	264 AA
3	MBE_VTSAL	STANDARD	PRT	264 AA
4	MBE_VTSAL	STANDARD	PRT	264 AA
5	MBE_VTSAL	STANDARD	PRT	264 AA
6	MBE_VTSAL	STANDARD	PRT	264 AA
7	MBE_VTSAL	STANDARD	PRT	264 AA
8	MBE_VTSAL	STANDARD	PRT	264 AA
9	MBE_VTSAL	STANDARD	PRT	264 AA
10	MBE_VTSAL	STANDARD	PRT	264 AA
11	MBE_VTSAL	STANDARD	PRT	264 AA
12	MBE_VTSAL	STANDARD	PRT	264 AA
13	MBE_VTSAL	STANDARD	PRT	264 AA
14	MBE_VTSAL	STANDARD	PRT	264 AA
15	MBE_VTSAL	STANDARD	PRT	264 AA
16	MBE_VTSAL	STANDARD	PRT	264 AA
17	MBE_VTSAL	STANDARD	PRT	264 AA
18	MBE_VTSAL	STANDARD	PRT	264 AA
19	MBE_VTSAL	STANDARD	PRT	264 AA
20	MBE_VTSAL	STANDARD	PRT	264 AA
21	MBE_VTSAL	STANDARD	PRT	264 AA
22	MBE_VTSAL	STANDARD	PRT	264 AA
23	MBE_VTSAL	STANDARD	PRT	264 AA
24	MBE_VTSAL	STANDARD	PRT	264 AA
25	MBE_VTSAL	STANDARD	PRT	264 AA
26	MBE_VTSAL	STANDARD	PRT	264 AA
27	MBE_VTSAL	STANDARD	PRT	264 AA
28	MBE_VTSAL	STANDARD	PRT	264 AA
29	MBE_VTSAL	STANDARD	PRT	264 AA
30	MBE_VTSAL	STANDARD	PRT	264 AA
31	MBE_VTSAL	STANDARD	PRT	264 AA
32	MBE_VTSAL	STANDARD	PRT	264 AA
33	MBE_VTSAL	STANDARD	PRT	264 AA
34	MBE_VTSAL	STANDARD	PRT	264 AA
35	MBE_VTSAL	STANDARD	PRT	264 AA
36	MBE_VTSAL	STANDARD	PRT	264 AA
37	MBE_VTSAL	STANDARD	PRT	264 AA
38	MBE_VTSAL	STANDARD	PRT	264 AA
39	MBE_VTSAL	STANDARD	PRT	264 AA
40	MBE_VTSAL	STANDARD	PRT	264 AA
41	MBE_VTSAL	STANDARD	PRT	264 AA
42	MBE_VTSAL	STANDARD	PRT	264 AA
43	MBE_VTSAL	STANDARD	PRT	264 AA
44	MBE_VTSAL	STANDARD	PRT	264 AA
45	MBE_VTSAL	STANDARD	PRT	264 AA

1. MBE_VTSAL (rel. 41, Created)
2. MBE_VTSAL (rel. 41, Last annotation update)
3. MBE_VTSAL (rel. 41, Last annotation update)
4. MBE_VTSAL (rel. 41, Last annotation update)
5. MBE_VTSAL (rel. 41, Last annotation update)
6. MBE_VTSAL (rel. 41, Last annotation update)
7. MBE_VTSAL (rel. 41, Last annotation update)
8. MBE_VTSAL (rel. 41, Last annotation update)
9. MBE_VTSAL (rel. 41, Last annotation update)
10. MBE_VTSAL (rel. 41, Last annotation update)
11. MBE_VTSAL (rel. 41, Last annotation update)
12. MBE_VTSAL (rel. 41, Last annotation update)
13. MBE_VTSAL (rel. 41, Last annotation update)
14. MBE_VTSAL (rel. 41, Last annotation update)
15. MBE_VTSAL (rel. 41, Last annotation update)
16. MBE_VTSAL (rel. 41, Last annotation update)
17. MBE_VTSAL (rel. 41, Last annotation update)
18. MBE_VTSAL (rel. 41, Last annotation update)
19. MBE_VTSAL (rel. 41, Last annotation update)
20. MBE_VTSAL (rel. 41, Last annotation update)
21. MBE_VTSAL (rel. 41, Last annotation update)
22. MBE_VTSAL (rel. 41, Last annotation update)
23. MBE_VTSAL (rel. 41, Last annotation update)
24. MBE_VTSAL (rel. 41, Last annotation update)
25. MBE_VTSAL (rel. 41, Last annotation update)
26. MBE_VTSAL (rel. 41, Last annotation update)
27. MBE_VTSAL (rel. 41, Last annotation update)
28. MBE_VTSAL (rel. 41, Last annotation update)
29. MBE_VTSAL (rel. 41, Last annotation update)
30. MBE_VTSAL (rel. 41, Last annotation update)
31. MBE_VTSAL (rel. 41, Last annotation update)
32. MBE_VTSAL (rel. 41, Last annotation update)
33. MBE_VTSAL (rel. 41, Last annotation update)
34. MBE_VTSAL (rel. 41, Last annotation update)
35. MBE_VTSAL (rel. 41, Last annotation update)
36. MBE_VTSAL (rel. 41, Last annotation update)
37. MBE_VTSAL (rel. 41, Last annotation update)
38. MBE_VTSAL (rel. 41, Last annotation update)
39. MBE_VTSAL (rel. 41, Last annotation update)
40. MBE_VTSAL (rel. 41, Last annotation update)
41. MBE_VTSAL (rel. 41, Last annotation update)
42. MBE_VTSAL (rel. 41, Last annotation update)
43. MBE_VTSAL (rel. 41, Last annotation update)
44. MBE_VTSAL (rel. 41, Last annotation update)
45. MBE_VTSAL (rel. 41, Last annotation update)

FT VARIANT 231 231 N -> S OR T.
FT VARIANT 231 233 NGL -> KGP.
FT VARIANT 232 235 GLAM -> SLWV.
SQ SEQUENCE 264 AA; 28981 MW; 7D0DC326CC6F5M4 CRC64;
Query Match 48.0%; Score 1339.5; DB 1; Length 264;
Best Local Similarity 95.8%; Pred. No. 1.7e-99;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
QY 269 DDTYCSASEPTVATVGRNWRVDFRDPFHNGQQLMPSKSNNDPQMLTIEGCTIS 60
DB 1 DDTYCSASEPTVATVGRNWRVDFRDPFHNGQQLMPSKSNNDPQMLTIEGCTIS 60
QY 329 NGSCLTITGYAGVYVWIFPCNTAVRATVWQIMWNGTILNRSNVLAAASGIGKTLT 388
DB 61 NGSCLTITGYAGVYVWIFPCNTAVRATVWQIMWNGTILNRSNVLAAASGIGKTLT 120
QY 389 VQTLDTTLAQGLMAGNDTAPREVTIYGRDLCNENSGSVWETCVSSQONO-FMALYD 447
DB 121 VQTLDTTLAQGLMAGNDTAPREVTIYGRDLCNENSGSVWETCVSSQONKQALYD 180
QY 448 GSIRPNODQCTGSDSYVYVNIYSCSSGQPRFTREGATILKRCALMDYDQ 507
DB 181 GSIRPNODQCTGSDSYVYVNIYSCSSGQPRFTREGATILKRCALMDYDQ 240
QY 508 NPKLRRIIYPATGKNQMLPV 530
DB 241 NPKLRRIIYPATGKNQMLPV 263
RESULT 2
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
AC P02879; P02880; FT; 576 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-SEP-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ricin precursor [contains: Ricin A chain (RNA N-glycosidase)]
DB (EC 3.2.2.22); Ricin B chain).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotyledons; Malvales; Euphorbiales; Ricinus.
OC UniProtKB:TaxId:3986;
RN 111 Ricin A chain; 576 AA.
RP SOURCE FROM N.A.
RX MEDLINE=8606724; PubMed=2399712;
RA Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,
RA Weaver R.P.;
RT "Genomic cloning and characterization of a ricin gene from Ricinus
RT communis";
RL Nucleic Acids Res. 13:8019-8033(1985).
RN 121 SOURCE FROM N.A.
RX MEDLINE=92163016; PubMed=1171405;
RA Tregear J.W., Roberts L.M.;
RT "The lectin gene family of Ricinus communis: cloning of a functional
RT ricin gene and three lectin pseudogenes";
RL Plant Mol. Biol. 18:515-525(1992).
RN 131
RP SEQUENCE OF 12-576 FROM N.A.
RX MEDLINE=85179479; PubMed=3839723;
RA Lamb A., Roberts L.M., Lord J.M.;
RT "Nucleotide sequence of cloned cDNA coding for preproricin";
RL J. Biochem. 116:265-270(1985).
RN 141
RP SEQUENCE OF 36-302.
RX Yoshitake S., Funatsu G., Funatsu M.;
RT "Isolation and sequences of peptide peptides, and the complete
RT sequence of the chain of ricin-D";
RL Agric. Biol. Chem. 42:1267-1274(1978).
RN 151
RP SEQUENCE OF 315-576.

Funatsu G., Kimura M., Funatsu M.;
"Purification of ricin D chain";
Agric. Biol. Chem. 43:2221-2224(1979).
(6)
CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
RX MEDLINE=90344223; PubMed=1368517;
RA Kimura Y., Kusuhiko H., Tada M., Takagi S., Funatsu G.;
RT "Structural analyses of sugar chains from ricin A-chain variant";
RL Agric. Biol. Chem. 54:157-162(1990).
RN 161
RX MEDLINE=21480122; PubMed=11595654;
RA Olmes S., Kozlov J.V.;
RT "Ricin";
RL Toxicol. 39:1723-1728(2001).
RN 181
X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=87165983; PubMed=3558397;
RA Monfort M., Vallatrance J.E., Monzingo A.F., Ernst S.R., Katzin B.,
RA Rueber B., Xuong N.H., Hamlin R., Robertus J.D.;
RT "The three-dimensional structure of ricin at 2.8 A";
RL J. Biol. Chem. 262:5398-5403(1987).
RN 191
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=91352004; PubMed=1881861;
RA Katzin B.J., Collins E.J., Robertus J.D.;
RT "Structure of ricin A-chain at 2.5 A";
RL Proteins 10:251-259(1991).
RN 101
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
RX MEDLINE=91352005; PubMed=1881882;
RA Rueber B., Robertus J.D.;
RT "Structure of ricin B-chain at 2.5-A resolution";
RL Proteins 10:260-269(1991).
RN 111
X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=95082010; PubMed=790130;
RA Weston S.A., Tucker A.D., Thatcher D.R., Darbyshire D.J.;
RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution";
RL J. Mol. Biol. 244:410-422(1994).
RN 121
X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
RX MEDLINE=96374222; PubMed=8780513;
RA Day P.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,
RA Molinari-Svahn M.C., Robertus J.D.;
RT "Ricin A-chain and activity of an active site substitution of ricin A
RT chain";
RL Biochemistry 35:11098-11103(1996).
RN 131
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=97240820; PubMed=9066280;
RA Yan X., Hollis T., Swinh M., Day F., Monzingo A.F., Milne G.M.,
RA Robertus J.D.;
RT "Structure-based identification of a ricin inhibitor";
RL J. Mol. Biol. 266:1043-1049(1997).
RN 141
RX MEDLINE=93165632; PubMed=1287657;
RA Kin Y., Robertus J.D.;
RT "Analysis of several key active site residues of ricin A chain by
RT mutagenesis and X-ray crystallography";
RL Protein Eng. 5:775-779(1992).
RN 151
-1- FUNCTION: Ricin is highly toxic to animal cells and to a less
RN extent to plant cells. The A chain is responsible for inhibiting
RN protein synthesis through the catalytic inactivation of 60S
RN ribosomal subunits. It acts as a glycosidase that removes a
RN specific adenine residue from an exposed loop of 28S ribosomal
RN protein. This loop is involved in the binding of elongation
RN factors. The A chain can inactivate these factors. The report protein
RN per minute, thus inactivating them faster than the cell can make
RN new ones. A single A-chain molecule can therefore kill an animal

CC	call. The B chain binds to cell receptors and facilitates the
CC	entry into the cell of the A chain; B chains are also responsible
CC	for cell agglutination (lectin activity). It binds to beta-D-
CC	galactopyranoside moieties.
CC	-1 CATALYTIC ACTIVITY: Endopolylys of the N-glycosidic bond at one
CC	specific adenosine on the 28S rRNA.
CC	-1 SUBUNIT: Disulfide-linked dimer of A and B chains.
CC	-1 SUBSTRATE: Polysaccharide chains. The A chain domain
CC	consists of 3 homologous subdomains (alpha, beta, gamma).
CC	-1 PFM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE
CC	MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 27.
CC	-1 SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
CC	INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.
CC	-1 SIMILARITY: Contains 2 rich B-type lectin domains.
CC	-1 CATION: REF. 4 AND REF. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
CC	WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
CC	NOTE: THIS IS A PROPOSED NAME.
CC	-1 OTHER NAME: 31 of February 2003
CC	WWW: http://www.expasy.org/spolish/articles/spolish3.html ."
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on ways
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	DR EMIL, X03179; CAA26939.1; -
DR	EMIL; X52908; CAA37095.1; -
DR	EMIL; X02388; CAA26230.1; -
DR	EMIL; A12892; CAA01058.1; -
DR	PIR; A24041; RLCSO.
DR	PDB; 2A41; 31-JAN-94.
DR	PDB; 1A6G; 31-JAN-94.
DR	PDB; 1F8Z; 31-OCT-93.
DR	PDB; 11F7; 14-JAN-98.
DR	PDB; 11F9; 14-JAN-98.
DR	PDB; 1R7C; 31-OCT-93.
DR	PDB; 10B1; 16-JUN-97.
DR	PDB; 1B85; 02-SEP-98.
DR	PDB; 1B86; 02-SEP-98.
DR	PDB; 11J3; 16-JAN-92.
DR	PDB; 11J4; 16-JAN-92.
DR	PDB; 11J5; 16-JAN-92.
DR	GlycoStitch: R02979.
DR	InterPro: IPR000772; Ricin_B_lectin.
DR	InterPro: IPR001574; RIP.
DR	Pfam: PF00562; Ricin_B_lectin; 6.
DR	Pfam: PF00161; RIP; 1.
DR	PRINTS; PR00396; SHIGARICIN.
DR	SMART; SMO0458; RICIN; 2.
DR	PROSITE; PSS0231; RICIN_B_LECTIN; 2.
DR	PROSITE; PSS00275; SHIG_RICIN; 1.
DR	GLUE (define): HYDROL; Ricin synthesis inhibitor; Toxin; Repeat;
KW	Glucose,Hydrolysis,Hydrolysis,Hydrolysis,Hydrolysis,Hydrolysis,
FT	SIGNAL, 1
FT	CHAIN 36 302
FT	PEPTIDE 303 314
FT	CHAIN 315 576
FT	DOMAIN 321 448
FT	DOMAIN 451 575
FT	REPEAT 331 373
FT	REPEAT 377 416
FT	REPEAT 416 446
FT	REPEAT 462 497
FT	REPEAT 501 540
FT	REPEAT 543 570
FT	ACT_SITE 212 212
FT	DISULFID 294 318
FT	DISULFID 334 353
	INTERCHAIN.

Query Match	Similarity	Score	DB 1	Length	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB
-------------	------------	-------	------	--------	------	------	------	------	------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	----

[illegible]

ID	ABRP	STANDARD	PRT	528 AA
AD	ABRP	P28589		
AC	P1110	P28589		
DT	01-JUL-1989	(Rel. 11, Created)		
DT	01-JUN-1994	(Rel. 29, Last sequence update)		
DE	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Abirin-a precursor [Comments: Abirin-a A chain (rRNA N-glycosidase)]			
DE	HEC 3.2.2(22); Abirin-a B chain;			
DE	Abus preacatorius (Indian alligator) (Crab's eye)			
CC	Abus preacatorius (Indian alligator) (Crab's eye)			
CC	Spermatophytes Magnoliophyta Eudicotyledons Core eudicots Residue;			
CC	eucotids I; Fabales; Fabaceae; Papilionoideae; Abysae; Abus;			
CC	NCBI_TaxID=3816;			
CC	[1]			
CC	SEQUENCE FROM N.A.			
CC	MEDLINE=9132796; PubMed=8421313;			
CC	Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;			
CC	Primary structure of three distinct isobins determined by cDNA			
CC	sequencing, conservation and significance."			
CC	J. Mol. Biol. 253:265-267(1995).			
CC	[2]			
CC	SEQUENCE OF 1-251			
CC	TISSUE=Seed;			
CC	Funatsu G., Teguchi Y., Kameosono M., Yanaka M.;			
CC	"The complete amino acid sequence of the A-chain of abirin-a, a toxic			
CC	protein from the seeds of Abus preacatorius."			
CC	Agric. Biol. Chem. 52:1095-1097(1988).			
CC	[3]			
CC	SEQUENCE OF 1-251 FROM N.A.			
CC	TISSUE=Leaf;			
CC	MEDLINE=9120129; PubMed=154300;			
CC	Evensen G., Mathiesen A., Sundan A.;			
CC	"Direct molecular cloning and expression of two distinct abirin			
CC	A-chains."			
CC	J. Biol. Chem. 266:6848-6852(1991).			
CC	[4]			
CC	SEQUENCE OF 262-528			
CC	MEDLINE=92371856; PubMed=105674;			
CC	Chen Y.-C., Chen Y.-C., Lin J.-Y.;			
CC	"The complete primary structure of abirin-a B chain."			
CC	FEBS Lett. 309:115-118(1992).			
CC	[5]			
CC	X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).			
CC	MEDLINE=95313188; PubMed=7608980;			
CC	Tahirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;			
CC	"Crystal structure of abirin-a at 2.14 A."			
CC	J. Mol. Biol. 280:354-367(1995).			
CC	SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 40S PROSOMAL			
CC	SUBUNIT BY REMOVING AMINO ACID FROM POSITION 4,324 OF 28 S RRNA.			
CC	ABIRIN-A IS MORE TOUGH THAN FCIN.			
CC	-1 FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT			
CC	FACILITATES THE BINDING OF ABIRIN TO THE CELL MEMBRANE THAT			
CC	PRECEDES ENDOCYTOSIS.			
CC	-1 CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one			
CC	specific aspartic residue on the 28S RRNA.			
CC	-1 DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS. EACH DOMAIN			
CC	CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).			
CC	-1 SIMILARITY: IN THE N-TERMINAL SECTION BELONGS TO THE RIBOSOME-			
CC	INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.			
CC	-1 SIMILARITY: Contains 2 richin B-type lectin domains.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use. The entry is available under the terms of the EMBL/EBI/Genbank			
CC	modified and this statement is not removed by any means. For commercial			
CC	entails requires a license agreement (see http://www.ebi.ac.uk/sequence/			
CC	or send an email to license@ebi.ac.uk).			
CC	EMBL; M98344; AAA2624.1; ALT INT.			
CC	EMBL; X54872; -; NOT ANNOTATED CDS			

DB 187 PDAMSLNNMNDLSGVQSVQDVFPRQ-----VTLNINIRNRPVDSLSHPT 236
 QY 237 TATSLAINRUCGSRSSSVRWVYVIRPVADVTCSAS-EPTVAIVGNMVCVDRD 295
 DB 237 VAVLALMFLVNP-PNANOS---PLILMSIVKSKCSSEIEPTVIGSDMNCVDVYN 292
 QY 296 DFHGMQGLWPSKSNNDPNOLMTIRBDGTIRNSGCTTGTGAGYVWIPCTWPRE 355
 DB 293 GYHNGRIIMWCKDRLIEMQVLTLSKRTIRSNKCLTTGYAPSYWIDCTSNAB 352
 QY 356 ATIWQWNGFTIINRSLNVLASGIGKTTLTVOYTDYLGQWLAGNDLPAPRYTIG 415
 DB 353 ATWELWNGFTIINRSLNVLASGIGKTTLTVOYTDYLGQWLAGNDLPAPRYTIG 412
 QY 416 FRULCESNGSVWETCVSSQGNMALTGDSIRPNQDQCTGCRDSVTVINIVS 475
 DB 413 YSDLCMQAGSNVWADCDNKGQCMALDTGDSIRPNQDQCTGCRDSVTVINIVS 472
 QY 476 CSAGSGQWVTFNEGALINLNGLANMAYANPRLITITTPKXNQMFL 528
 DB 473 CSNGASQWVTFNEGALINLNGLANMAYANPRLITITTPKXNQMFL 525

RESULT 5

ABCOABRR STANDARD; FRT; 562 AA.

AC P26530
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Abirin-c precursor [Contains: Abirin-c A chain (rRNA N-glycosidase)]
 DE (EC 3.2.2.22); Abirin-c B chain]
 DE Abirus pectatorius (Indian licorice) (Crab's eye).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eutrosids I; Papales; Fabaceae; Papilionoideae; Abiraceae; Abirus.
 DX NCBI Taxid=3816;
 RX SOURCE FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=9126697; PubMed=2050149;
 RT Wood K.A., Lord J.M., Nawrzymczak E.J., Platak M.,
 RT "Preproabirin: genomic cloning, characterization and the expression of
 RT the A-chain in Escherichia coli.";
 RL Eur. J. Biochem. 198;723-732(1991).
 CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE
 CC B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
 CC BINDING OF ABIRIN TO THE CELL MEMBRANE THAT FREEDS ENDOCYTOSIS.
 CC -1- CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one
 CC specific adenosine.
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS. EACH DOMAIN
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
 CC The sequence data has been submitted to the EMBL outstation on its
 CC use by non-profit institutions. There are no restrictions on its
 CC modified and this statement is not removed as its content is in no way
 CC entitles requires a license agreement (See <http://www.isb.slb.ch/annouce/>
 CC or send an email to license@isb.slb.ch).

DR Pfam: PF00652; Ricin_B_lectin; 6.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR SMART: SM00458; RICIN; 2.
 DR PROSITE: PS00231; RICIN B LECTIN; 2.
 DR PROSITE: PS00275; SHIGA; RICIN; 1.
 KW plant defense; Hydrolase; Protein synthesis inhibitor; toxin; Repeat;
 KW glycoprotein; Lectin; Signal; Pyroglutamate carboxylic acid.
 FT CHAIN 35 288
 FT PREPIDE 286 295
 FT CHAIN 296 562
 FT DOMAIN 437 561
 FT DOMAIN 437 561
 FT REPEAT 317 359
 FT REPEAT 360 400
 FT REPEAT 403 435
 FT REPEAT 448 483
 FT REPEAT 487 526
 FT REPEAT 529 562
 FT ACETATE 188 198
 FT ACETATE 201 203
 FT DISULFID 321 380
 FT DISULFID 363 380
 FT DISULFID 451 464
 FT DISULFID 490 507
 FT MOD RES 35 35
 FT CARBOHYD 234 234
 FT CARBOHYD 395 395
 FT CARBOHYD 435 435
 SQ SEQUENCE 562 AA; 62817 NM; 1PQDA0C7DBA6278 C6C64;
 Query Match 43.5%; Score 1214.5; DB 1; Length 562;
 Best local similarity 47.8%; Evid. No. 1.3e-62;
 Matches 250; Conservative 99; Mismatches 179; Indels 9; Gaps 7;
 QY 9 TQQTGGSEYRPFITLIRPVYSSGNSNRPILRQSTIRPSDAGPVLVETLNCQGPSITL 68
 DB 43 TGAATSGYKQFTEALRQL-TCGLIHDPVLPDPT-TVEENRYITVELNSRESIEV 100
 QY 69 AIDVNLVYVQNDQSYFLDAPRQETLFTGTSSLPFNGSPDLRYAAG-RDQ 127
 DB 101 GIDVNAVYVIRPAGSGYFLDAPASATYLPFGTQYSLRFDSDYDLRYAAGQTRER 160
 QY 128 IRLGIDLOSTYALRPFQSGRTQASLLIQLMTASARNPILRQYINSGASF 187
 DB 161 IRLGIDLOSTYALRPFQSGARNDEKRTLYIQLVNSARARISRYGSGIRQTRFQ 220
 QY 188 PPTVWLEETSGQSGTQVQSHGTQGV-NNRPLALPPKAPPTLNNRDVYASALMFLPV 246
 DB 221 PPTVALSLNNMNDLSGVQSVQDVFPRVYVDSISNRPVYVDSLSHPTVAVLALMFLPV 280
 QY 247 CSEPRSSSVRWVYVIRPVADVTCSAS-EPTVAIVGNMVCVDRDDFHGMQGL 305
 DB 281 CWP-PNANOS---PLILMSIVKSKCSSEIEPTVIGSDMNCVDYDYNMRLTA 336
 QY 306 KESKSNNDPNOLMTIRBDGTIRNSGCTTGTGAGYVWIPCTWPRE 365
 DB 337 WCKDRIEMQVLTLSKRTIRSNKCLTTGYAPSYWIDCTSNAB 396
 QY 366 TTIINRSLNVLASGIGKTTLTVOYTDYLGQWLAGNDLPAPRYTIG 425
 DB 397 TTIINRSLNVLASGIGKTTLTVOYTDYLGQWLAGNDLPAPRYTIG 456
 QY 426 GSIVWETCVSSQGNMALTGDSIRPNQDQCTGCRDSVTVINIVS 485
 DB 457 SIVWADCDNKGQCMALDTGDSIRPNQDQCTGCRDSVTVINIVS 516
 QY 486 VTFNEGALINLNGLANMAYANPRLITITTPKXNQMFL 528
 DB 517 LFNQDGSIVNLDHMDVWADVWVQSDSKELIINRPNKRNQML 559

RA Siegal C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
 RA Marguier H.,
 RT Characterization of ribosome-inactivating proteins isolated from
 RT Bryonia dioica and their utility as carcinoma-reactive
 RT immunokonjugates. 423-428(1994).
 CC 1. FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
 CC 1. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J34238; -; NOT ANNOTATED_CDS.
 DR HSP: P09989; 1MBJ.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGA_RICIN; 1.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 DR KX Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin;
 KW Maltigene family; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 282 RIBOSOME-INACTIVATING PROTEIN BRYONIN II.
 FT ACT SITE 183 183 BY SIMILARITY.
 FT CATH 25 25 N-LINKED (GLCNAc..) (POTENTIAL).
 FT CROHD 282 AA; 30754 MW; 62828268737696 CRC64;
 SQ SEQUENCE 282 AA; 30754 MW; 62828268737696 CRC64;
 Query Match 12.5%; Score 350; DB 1; Length 282;
 Best Local Similarity 3.3%; Pred. No. 2e-20;
 Matches 90; Conservative 40; Mismatches 95; Indels 16; Gaps 8;
 Db 13 TGEYRPFTLLADVSSGS-PSAEIPILRQSTIPVSDQRFVVELTNGQGSITAAID 71
 32 TQATYKTFIRLRTKLVGPPVYDIIVIRMAAGLA--RQVLTLYNGSVYALD 88
 QY 72 VTNLYVAVAGQGSYFLNAPRQVNHFTGTTSSLPNGSYPDILRYVAGH--RQCI 129
 Db 89 VNVVYVAVRAGNTAFPLASTBANNVLEGNHVRALPGATDGLTAAGISRENI 148
 QY 130 LGIDQLIGSTAL--RFGQSTRTQASILLQISZAAEPNIIIMRAGYNSGSEL 187
 Db 149 LGFSEISLIGMFRHNGSY--PLGVIIQIVSAAKFKIIRGVSS--NGTKR 203
 QY 188 PNYVMELETSGQSTQVQ--HSTGVNPNRIRLIPQNFVLTINVAD--VIALAM 244
 Db 204 PDPATSLQNMGSLSEQIQIQTSGCEPAPVRLTSTFTVINAVSVKGIALL 263
 QY 245 F 245
 Db 264 Y 264
 RESULT 10
 ID RIP2 MOMBA STANDARD; PRT; 286 AA.
 AC P29339;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribosome-inactivating protein momordin II precursor (rRNA
 DE N-glycosidase) (EC 3.2.2.22).
 OS Momordica balsamina (Bitter melon) (Balsam pear).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliopsida; euclidocladons; core eudicots; Rosidae;
 CC eustosids I; Cucurbitales; Cucurbitaceae; Momordica.

CC NGBI_TextID=3672;
 RA 1. SOURCE FROM N.A.
 RT TRISUB-Seal
 RX MEDLINE=31027170; PubMed=1408771;
 RA Orliga M., Better M.,
 RT "Momordin II, a ribosome inactivating protein from Momordica
 RT balsamina, is homologous to other plant proteins.";
 RL Nucleic Acids Res. 20:4662-4662(1992).
 CC -1. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z12275; C25490;
 DR EMBL: Z12275; C25490;
 DR PDB: 1C25; 07-JUN-99.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGA_RICIN; 1.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
 KW 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 286 RIBOSOME-INACTIVATING PROTEIN MOMORDIN
 FT ACT SITE 181 181 BY SIMILARITY.
 FT CATH 24 286
 FT CROHD 286 AA; 32031 MW; 3859FPAE25396 CRC64;
 SQ SEQUENCE 286 AA; 32031 MW; 3859FPAE25396 CRC64;
 Query Match 12.3%; Score 344.5; DB 1; Length 286;
 Best Local Similarity 34.8%; Pred. No. 3.4e-20;
 Matches 88; Conservative 54; Mismatches 92; Indels 19; Gaps 9;
 Db 13 TGEYRPFTLLADVSSGS--SIPILRQSTIPVSDQRFVVELTNGQGSITAA 69
 33 TACTYKTFIRLRTKLVGPPVYDIIVIRMAAGLA--RQVLTLYNGSVYALD 88
 QY 70 IDVTNLYVAVAGQGSYFLNAPRQVNHFTGTTSSLPNGSYPDILRYVAGH--RQ 127
 Db 89 IDVTNLYVAVAGQGSYFLNAPRQVNHFTGTTSSLPNGSYPDILRYVAGH--RQ 145
 QY 128 IPGIDQLIGSTAL--RFGQSTRTQASILLQISZAAEPNIIIMRAGYNSGSEL 187
 Db 149 LGFSEISLIGMFRHNGSY--PLGVIIQIVSAAKFKIIRGVSS--NGTKR 203
 QY 188 PNYVMELETSGQSTQVQ--HSTGVNPNRIRLIPQNFVLTINVAD--VIALAM 244
 Db 204 PDPATSLQNMGSLSEQIQIQTSGCEPAPVRLTSTFTVINAVSVKGIALL 263
 QY 245 F 245
 Db 262 L-NSRPADEENF 273
 RESULT 11
 ID RIP1 TRIAN STANDARD; PRT; 294 AA.
 AC P5626; Q92071;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-SEP-2003 (Rel. 41, Last annotation update)
 DE Type 1 ribosome-inactivating protein (rRNA
 DE N-glycosidase) (EC 3.2.2.22) (RIP) (Trichosanin).
 OS Trichosanthes anguina (Snake gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euphorbiales; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=50544;
 RN 111
 RP SEQUENCE FROM N.A. PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=cy. Anguina; TISSUE=seed.
 RX MEDLINE=99132006; PubMed=991318;
 RA Chow L.-P., Chou M.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H.,
 RA Lin J.-Y.;
 RA "Purification, characterization and molecular cloning of trichosanthin,
 RT a novel type I ribosome-inactivating protein from the seeds of
 RT Trichosanthes anguina.";
 RL Biochem. J. 338:211-219(1999).
 RN 120
 RP SEQUENCE OF 20-264.
 RC TISSUE=seed.
 RA Chow L.-P., Kamo M., Lin J.-Y., Wang S.-H., Tang Y., Tang J.A.;
 RA "Amino acid sequence of trichosanthin, a ribosomal-inactivating
 RT protein from Trichosanthes anguina seeds.";
 RL J. Biomed. Sci. 3:178-186(1996).
 CC -1- FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPURINATING 28S RNA IN
 CC RIBOSOMES.
 CC -1- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one
 CC specific adenosine on the 28S RNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC -1- TYPE 1 RIP SUBFAMILY.
 CC
 CC This SWISS-Prot entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute for Bioinformatics and the EMBL collection
 CC the European Bioinformatics Institute. The data are made available on the
 CC use by non-profit institutions as long as its content is not modified
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb.ch).
 CC
 CC EMBL; AF055086; A020468.1; -.
 DR HSSP; F93185; 1SERV.
 DR Fasta; F93185; 1SERV.
 DR Fasta; F93185; 1SERV.
 DR PRINTS; P80025; SHIGA_RICIN.
 DR PROSITE; P80025; SHIGA_RICIN.
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
 KW Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 264
 FT TYPE 1 RIBOSOME-INACTIVATING PROTEIN
 FT TRICHOSANTHIN.
 FT PROPEP 265 294
 FT ACT_SITE 177 177
 FT ACT_SITE 180 180
 FT CARBOHYD 220 220
 FT CONFLICT 51 51
 FT CONFLICT 65 65
 FT CONFLICT 84 84
 FT CONFLICT 152 152
 FT CONFLICT 174 174
 FT CONFLICT 245 245
 FT SEQUENCE 294 AA; 32234 MW; DA4F8B7CE3290994 CRC64;
 Query Match 11.7%; Score 327.5; DB 1; Length 234;
 Best local 34.0%; Freq. No. 8e-19;
 Matches 85; Conservative 47; Mismatches 105; Indels 13; Gaps 6;
 Oy 13 TGEYFRITLADYVSGSSNSMIPILQSTIPVQAPQVULVHLMGSGSITLADY 72
 Db 29 TKKSYSTIOLDALTOGVGCIPLPST--ASGSQWRPRLNIVYDSTITVAWV 85
 Oy 73 TMLVVAQAGDSYPLNDAPRGAHFLFTGTTSASIPLNGSYPDLEKAVG-HEDQIPG 131
 Db 86 TMLVVAQADAVSYFEDTFAEFLFAGTKTKVLPISGNDYKLSGVGQRMIEIG 145
 Oy 132 IDQLQSYTALRPGSTTYQASILLIOMISAKARFPLWRAQRTINSAGSLPDEVY 191

Db 146 IPLASLITNWV--YDQSTALALVLQCTAARAKRYIEQVSSHS--NYPQCA 201
 Oy 192 MLELTSGQSQSTQVQ--HSTQVFNRPRIALPGQVFTLLTVRD--VIASLAIMLFV 246
 Db 202 VISLNNKALSKQIDIMNRTHQGFENHVLNPDGFRSFTNSAGVYKNTKILLY 261
 Oy 247 CGRRGSSPY 256
 Db 262 KASVGSFYDI 271

RESULT 12
 RIPT_TRIKI STANDARD; RT; 289 AA.
 AC P09589;
 DT 01-MAR-1989 (rel. 10, Created)
 DT 01-SEP-1990 (rel. 16, Last sequence update)
 DT 01-SEP-2003 (rel. 42, Last annotation update)
 DE R1387-2003 (rel. 42, Last annotation update)
 DE (rRNA N-glycosylase) (EC 3.2.2.22) (Alphabeta)
 DE Trichosanthes kirilowii (Mongolian snake-gourd)
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euphorbiales; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=4677;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN=Maximowicz;
 RX MEDLINE=91153657; PubMed=199291;
 RA Shaw P.C., Hung K.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
 RA "Isolation and DNA sequence of a gene encoding alpha-trichosanthin,
 RT a type I ribosome-inactivating protein.";
 RL J. Biol. Chem. 265:8670-8674(1990).
 RN 121
 RP SEQUENCE OF 24-270.
 RC STRAIN=Maximowicz;
 RX MEDLINE=9026789; PubMed=2343399;
 RA Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
 RA Wu P., Huang K., Piatek M.;
 RA "Primary amino acid sequence of alpha-trichosanthin and molecular
 RT models for abrin A-chain and alpha-trichosanthin.";
 RL J. Biol. Chem. 265:865-869(1990).
 RN 144
 RP SEQUENCE OF 24-270.
 RC STRAIN=Maximowicz;
 RX MEDLINE=9344383; PubMed=7613070;
 RA Tian G.Y., Ni C.Z., Gu Z.M., Jin S.W., Zhang L.Q., Xia Z.X.,
 RA "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
 RT application.";
 RL Pure Appl. Chem. 58:789-798(1996).
 RN 151
 RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
 RX MEDLINE=94344957; PubMed=8066085;
 RA Zhou F., Fu Z., Chen W., Lin Y., Pan K.;
 RA "Structure of trichosanthin at 1.88-A resolution.";
 RL Proteins 19:4-15(1994).
 RN 161
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=9534383; PubMed=7613070;
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
 RA "Studies on crystal structures, active-centre geometry and
 RT dehydrating mechanism of two ribosome-inactivating proteins.";
 RL Biochem. J. 309:285-298(1995).
 CC -1- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS


```
CC -----
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB000666; BAA1786.1; -
DR PIR; JCS606; JCS606.
DR PIR; J00393; J00393.
DR HSP; P09989; 1MRJ.
DR InterPro; IP001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KV Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KV Toxin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 270 KARASURIN-C.
FT PROPEP 271 289 REMOVED IN MATURE FORM.
FT ACT SITE 183 BY SIMILARITY.
SQ SEQUENCE 289 AA; 31704 MW; 98303E32287B26 CRC64;

Query Match
Best Local Similarity 11.6%; Score 325; DB 1; Length 289;
Matches 88; Conservative 50; Mismatches 87; Indels 14; Gaps 9;

QY 13 TGEYFRFTLRDYSSGSFSENEIPRLROSTIEVDNQRFVLTINQGDSTIAIDVTN 72
DB 33 TSSYGVFISNKKALPYERKXIDIFILR-STLPS--QRYLTHIMVNDERISVAILV 89
QY 73 TELYVAVQAGDSYFLDA-PRGEYHLFTGTRG-SLPFGSYDLEERYAGH-RQIIP 129
DB 90 TNYVYGRADDTYFFREKSTAKVYFEDAKKRYLTPYSGVYERQIDAKKRENIIP 149
QY 130 LQIDQLQSVTLARPPGSTRQARISILILQWISBARNFILMARQYNSGSELPD 189
DB 150 LQPRALDSNITLIF--YNNNSNMAAMVLLQSTSEBAKRTKIQSGSRVDA--TFLS 205
QY 190 VYMLFETSWGQSTVOQ--HSTQGVNPNRILAPPGNVTYTNTRD--VTSIALML 244
DB 206 LAISLENSWALSNOQIQASTNGQETFEVVLINQCHQVITINDVAGVTSINALL 264

RESULT 14
RIPQ GELMU STANDARD; PRT; 286 AA.
ID RIPQ GELMU
AC Q9FEX4;2001 (Rel. 40, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
DE (EC 3.2.2.22).
OS Cucumis figareli.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Cucumns.
OX NCBI_TaxID=131071;
RN 11
RS SEQUENCE FROM N.A.
RA Nolan P.A., Garritson D.A., Beller M.;
RT Cloning and analysis of a cDNA coding a putative ribosome-
RT inactivating protein from Cucumis figareli."
RL Plant Biotechnol. 17:337-340(2000)
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
```

```
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB045560; BAB19677.1; -
DR HSP; P16094; 1AHC.
DR InterPro; IP001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KV Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KV Toxin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 286 PUTATIVE RIBOSOME-INACTIVATING PROTEIN.
FT ACT SITE 185 185 BY SIMILARITY.
FT CARBOHYD 189 193 N-LINKED (GLUCNAc . . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLUCNAc . . .) (POTENTIAL).
SQ SEQUENCE 286 AA; 31771 MW; 4ERD966E504DA1 CRC64;

Query Match
Best Local Similarity 11.1%; Score 310.5; DB 1; Length 286;
Matches 78; Conservative 53; Mismatches 93; Indels 13; Gaps 7;

QY 15 EYEFYFTLRDYSSGSFSENEIPRLROSTIEVDNQRFVLTINQGDSTIAIDVTN 74
DB 38 KSYKRFYISNKKALPYERKXIDIFILVPS--ISGSRITLMQLSNYSBNTFYAAVDVN 94
QY 75 LLYVAVQAGDSYFLDA-PRGEYHLFTGTRGSLPFGSYDLEERYAGH-RQIIP 132
DB 99 VYIMGLVNGTGYFENETDAQLSNFTGTRGSLTPYSGVYERQIDAKKRENIIP 154
QY 133 LQIDQLQSVTLARPPGSTRQARISILILQWISBARNFILMARQYNSGSELPD 191
DB 155 MALDSYSLTYL--YNSRANAFVILQPTAEAKRKXI---EKQIIDISGVSDIA 209
QY 192 MLEFETSWGQSTVOQ--HSTQGVNPNRILAPPGNVTYTNTRD--VTSIALML 246
DB 210 ALSENENSLSKQIQASTNGQETFEVVLINQCHQVITINDVAGVTSINALL 266

RESULT 15
RIPQ GELMU STANDARD; PRT; 316 AA.
ID RIPQ GELMU
AC P33186;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein gelonin precursor (rRNA N-glycosidase)
DE (EC 3.2.2.22).
OS Gelonium multiflorum (Euphorbiaceae: huihualeae)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Malpighiales; Euphorbiaceae; Gelonium.
OX NCBI_TaxID=3979;
RN 11
RS SEQUENCE FROM N.A.
RA MEDLINE=94085781; PubMed=7916721;
RA Nolan P.A., Garritson D.A., Beller M.;
RT Cloning and expression of a gene encoding gelonin, a ribosome-
RT inactivating protein from Gelonium multiflorum."
RL Gene 134:223-227(1993).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
```

R	Lapdi D.;
RA	"N-terminal sequence of some ribosome-inactivating proteins.";
RT	Int. J. Pept. Protein Res. 33:263-267(1989).
LN	[3]
LN	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RP	MEDLINE=95331189; PubMed=7608981;
RX	Hosur M.V., Nair B., Sankaranarayanan P., Masquith S., Surroli A.,
CC	"X-ray structure of gelatin at 1.8-A resolution."
CC	J. Mol. Biol. 250:169-180(1995).
CC	-1- CARPAMYCIN ACTIVITY. Endonucleolytic cleavage of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC	-1- SUBUNIT: Homodimer.
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC	TYPE I RIP SUBFAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use provided it is not profit institutions as long as its content is in no way used for advertising or promotional purposes without the prior written consent of the EBI. The EBI does not assume any legal liability for errors or omissions in the database. For more information please visit http://www.ebi.ac.uk/ebis/biops/cn/announce/ .
CC	-- or send an email to license@ebi.slb.ch --
DR	PDB; 1J2Z43; AAA6332.1; "
DR	EML; J07053; J07053.
DR	HSSP; P09989; IMRI.
DR	InterPro; IPRO01574; RIP.
DR	Ffam; PF00161; RIP_1.
DR	PRINTS; PR00396; SHIGAGICIN.
DR	PROSITE; PS00275; SHIGA_RICIN; FALSE NEG.
KM	Plant defense, protein synthesis inhibitor; Hydrolase; Toxin; Signal;
KN	Gelatin defense, protein synthesis inhibitor; Hydrolase; Toxin; Signal;
FT	Stoichiometry: 1
FT	PROPEP 27 46
FT	CHAIN 47 297
FT	PROPEP 298 316
FT	DISEULFID 90 96
FT	CARBOHYD 235 235
FT	ACT SITE 212 212
FT	CONFLICT 90 90
FT	CONFLICT 93 93
SQ	SEQUENCE 316 AA; 1252387B10901885 CRC64;
Query Match	
Best Local	10.2% Score 305.5 DB 1; Length 316;
Matches	Similarity 2.3% Freq. No. Se -17 Indels 21; Gaps 5;
	Matches 89; Conservative 37; Mismatches 109;
Qy	9 THQTGSEKFFRLTLRRPYVSGSGFSNR-----IFLRQSTIPMSADAEVL 55
Db	42 TSKLTGLDTVSFKATATLYTNLEHRYKLPEGRSHGPIFLRKCK--DPGKCIVL 99
Qy	56 VETLVQGGSITAIIVTNLYVAQAQDGQSIFLARARGAFHLFGTTNSLPSPNSGY 115
Db	100 VALSDNDGQLAELIADIVSYVVGQVRNRSFPFKADDAAYEGSFNIKIKTRHFQASY 159
Qy	116 PLDERVLAGHQDIPLGIDOL---IQSVYLIRPGSGTFQRASILLIOMISBAEAPVI 172
Db	160 FLBSRHQAKRTLDLDEYLAELIKGDENALIMPTETLSLSLVLTQMWSBAEPFI 219
Qy	173 LWRARQINSAGSLDYPMYLEMTSGMSQYCHCS--TGCPYRIKRLAPGNVTILT 231
Db	220 ENQIRN--NFQGRIPAAINTISLEMKGLSPDLTPFSANGMFSEAVLEBRNGKYTVI 277
Qy	232 NYRDVATISALINEFY 246
Db	278 ADVQYKEKALKREV 292

Search completed: December 11, 2003, 14:09:03
Job time : 10.2084 secs

Matches 522; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 YERLRLATVHTQTTGEYFRITLLADYVSAGSFENETPLRQSTIPVSDAORFVLVELTN 60
Db 1 YERLRLATVHTQTTGEYFRITLLADYVSAGSFENETPLRQSTIPVSDAORFVLVELTN 60

QY 61 QGGDSITTAIDVNTLVYVAOAGQSYFLRDAFGAETHLFTGTRSSLPENSGYPLER 120
Db 61 QGGDSITTAIDVNTLVYVAOAGQSYFLRDAFGAETHLFTGTRSSLPENSGYPLER 120

QY 121 YAGHDQIPFLGIDLIQSVTALRPFQSGTRTQASLILILQMISEARFPIFLARQYI 180
Db 121 YAGHDQIPFLGIDLIQSVTALRPFQSGTRTQASLILILQMISEARFPIFLARQYI 180

QY 181 NSGASFLPDVYMLEETSMQOOSTVOQSTDCVFNNEPRLAIPGNFVTLTVNADVASTL 240
Db 181 NSGASFLPDVYMLEETSMQOOSTVOQSTDCVFNNEPRLAIPGNFVTLTVNADVASTL 240

QY 241 AITMLFVCGERSSSDVRYMPLVIRPVADVTCSAEPYRLVGRNQKCVADVDHEDG 300
Db 241 AITMLFVCGERSSSDVRYMPLVIRPVADVTCSAEPYRLVGRNQKCVADVDHEDG 300

QY 301 NOIQAPSKSNNDPQMTWKTKDGTIRNSGCLTGYGTAGYVMIPOCNVREATHNQ 360
Db 301 NOIQAPSKSNNDPQMTWKTKDGTIRNSGCLTGYGTAGYVMIPOCNVREATHNQ 360

QY 361 IWNGGTIIPRSNLVLAASSGKGTLLVOTLDYTLQGGMLAGNDAPREVTYGFDDLC 420
Db 361 IWNGGTIIPRSNLVLAASSGKGTLLVOTLDYTLQGGMLAGNDAPREVTYGFDDLC 420

QY 421 MESNGSVWVETCSQONRVALYGDGSIHPQKQDDCLTCGRDVSATVINTVCSNGS 480
Db 421 MESNGSVWVETCSQONRVALYGDGSIHPQKQDDCLTCGRDVSATVINTVCSNGS 480

QY 481 SCGRVYVTEGATILNKGADVDYQSNRKLRIITVPAIGKPNQMLFVP 531
Db 481 SCGRVYVTEGATILNKGADVDYQSNRKLRIITVPAIGKPNQMLFVP 531

RESULT 2

Q8W243 PRELIMINARY; PRT; 565 AA.

AC 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE VCA precursor (EC 3.2.2.22) (rRNA N-glycosidase).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RA Fark N.-B., Liu S.;
RT Cloning of Viscum album subsp. coloratum (Korean mistletoe)."
BT 5 (520)
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF369961; ALA0417.1; -
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR PRINTS; PR00161; RLP; 1.
DR PROSITE; PS00321; RICHIN_B_LECTIN; 2.
DR SIGNAL; 1.
FT CHAIN 23 273 VCA ALPHA CHAIN.
FT CHAIN 309 565 VCA BETA CHAIN.
SQ SEQUENCE 565 AA; 62401 MW; 991E3994DA005F11 CRC64;

Query Match 85.7%; Score 2392.5; DB 10; Length 565;
Best Local Similarity 85.6%; Pred. No. 9.3e-190;
Matches 459; Conservative 27; Mismatches 41; Indels 9; Gaps 2;

QY 1 YERLRLATVHTQTTGEYFRITLLADYVSAGSFENETPLRQSTIPVSDAORFVLVELTN 60
Db 1 YERLRLATVHTQTTGEYFRITLLADYVSAGSFENETPLRQSTIPVSDAORFVLVELTN 60

QY 34 YERLRLATVHTQTTGEYFRITLLADYVSAGSFENETPLRQSTIPVSDAORFVLVELTN 93
Db 34 YERLRLATVHTQTTGEYFRITLLADYVSAGSFENETPLRQSTIPVSDAORFVLVELTN 93

QY 61 QGGDSITTAIDVNTLVYVAOAGQSYFLRDAFGAETHLFTGTRSSLPENSGYPLER 120
Db 61 QGGDSITTAIDVNTLVYVAOAGQSYFLRDAFGAETHLFTGTRSSLPENSGYPLER 120

QY 94 QGGDSITTAIDVNTLVYVAOAGQSYFLRDAFGAETHLFTGTRSSLPENSGYPLER 153
Db 94 QGGDSITTAIDVNTLVYVAOAGQSYFLRDAFGAETHLFTGTRSSLPENSGYPLER 153

QY 121 YAGHDQIPFLGIDLIQSVTALRPFQSGTRTQASLILILQMISEARFPIFLARQYI 180
Db 121 YAGHDQIPFLGIDLIQSVTALRPFQSGTRTQASLILILQMISEARFPIFLARQYI 180

QY 154 YAGHDQIPFLGIDLIQSVTALRPFQSGTRTQASLILILQMISEARFPIFLARQYI 213
Db 154 YAGHDQIPFLGIDLIQSVTALRPFQSGTRTQASLILILQMISEARFPIFLARQYI 213

QY 181 NSGASFLPDVYMLEETSMQOOSTVOQSTDCVFNNEPRLAIPGNFVTLTVNADVASTL 240
Db 181 NSGASFLPDVYMLEETSMQOOSTVOQSTDCVFNNEPRLAIPGNFVTLTVNADVASTL 240

QY 214 NSGASFLPDVYMLEETSMQOOSTVOQSTDCVFNNEPRLAIPGNFVTLTVNADVASTL 273
Db 214 NSGASFLPDVYMLEETSMQOOSTVOQSTDCVFNNEPRLAIPGNFVTLTVNADVASTL 273

QY 241 AITMLFVCGERSSSDVRYMPLVIRPVADVTCSAEPYRLVGRNQKCVADVDHEDG 300
Db 241 AITMLFVCGERSSSDVRYMPLVIRPVADVTCSAEPYRLVGRNQKCVADVDHEDG 300

QY 274 AITMLFVCGERSSSDVRYMPLVIRPVADVTCSAEPYRLVGRNQKCVADVDHEDG 333
Db 274 AITMLFVCGERSSSDVRYMPLVIRPVADVTCSAEPYRLVGRNQKCVADVDHEDG 333

QY 296 DFDHNOIQAPSKSNNDPQMTWKTKDGTIRNSGCLTGYGTAGYVMIPOCNVREATHNQ 355
Db 296 DFDHNOIQAPSKSNNDPQMTWKTKDGTIRNSGCLTGYGTAGYVMIPOCNVREATHNQ 355

QY 334 KFTNPNPIQMPW---DPOIWTIRBDGTISNGRCLTGYGTAGYVMIPOCNVREATHNQ 389
Db 334 KFTNPNPIQMPW---DPOIWTIRBDGTISNGRCLTGYGTAGYVMIPOCNVREATHNQ 389

QY 356 AITWQMGNGTIIIPRSNLVLAASSGKGTLLVOTLDYTLQGGMLAGNDAPREVTYGFDDLC 415
Db 356 AITWQMGNGTIIIPRSNLVLAASSGKGTLLVOTLDYTLQGGMLAGNDAPREVTYGFDDLC 415

QY 390 AITWQMGNGTIIIPRSNLVLAASSGKGTLLVOTLDYTLQGGMLAGNDAPREVTYGFDDLC 449
Db 390 AITWQMGNGTIIIPRSNLVLAASSGKGTLLVOTLDYTLQGGMLAGNDAPREVTYGFDDLC 449

QY 416 FRLCHESNGSVWVETCSQONRVALYGDGSIHPQKQDDCLTCGRDVSATVINTVCSNGS 475
Db 416 FRLCHESNGSVWVETCSQONRVALYGDGSIHPQKQDDCLTCGRDVSATVINTVCSNGS 475

QY 450 FRLCHESNGSVWVETCSQONRVALYGDGSIHPQKQDDCLTCGRDVSATVINTVCSNGS 509
Db 450 FRLCHESNGSVWVETCSQONRVALYGDGSIHPQKQDDCLTCGRDVSATVINTVCSNGS 509

QY 476 CSAGSGQWVFTMEGALINIKGADVDYQSNRKLRIITVPAIGKPNQMLFVP 531
Db 476 CSAGSGQWVFTMEGALINIKGADVDYQSNRKLRIITVPAIGKPNQMLFVP 531

QY 510 CSAGSGQWVFTMEGALINIKGADVDYQSNRKLRIITVPAIGKPNQMLFVP 565
Db 510 CSAGSGQWVFTMEGALINIKGADVDYQSNRKLRIITVPAIGKPNQMLFVP 565

RESULT 3

Q84B93 PRELIMINARY; PRT; 560 AA.

AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE VCA precursor (EC 3.2.2.22) (rRNA N-glycosidase).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI_TaxID=15429;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Q., Gong Z.Z., Liu X.Y.;
RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamom proteins and study of their expression patterns."
BT 5 (520)
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF039803; AA082460.1; -
DR InterPro; IPR001574; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR PRINTS; PR00161; RLP; 1.
DR PROSITE; PS00321; RICHIN_B_LECTIN; 2.
DR SIGNAL; 1.
FT CHAIN 23 273 VCA ALPHA CHAIN.
FT CHAIN 309 565 VCA BETA CHAIN.
SQ SEQUENCE 565 AA; 62401 MW; 991E3994DA005F11 CRC64;

KW Hydrolase; Signal; Toxin. POTENTIAL.
 FT SIGNAL 1 32 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CHAIN 33 580 CINNAMOMIN II
 SQ SEQUENCE 580 AA; 64421 MW; 940010P01E7P558 CRC64;
 Query Match 48.6%; Score 1361; DB 10; Length 580;
 Best Local Similarity 53.0%; Pred No. 3 5e-104;
 Matches 287; Conservative 76; Mismatches 157; Indels 22; Gaps 11;

QY 9 THQTGEYPRFTLLADYSSGSPNEIPILRO-STIPVSDAQRVAVELVETNOGDS-I 66
 DB 40 TKNAIKSYTGFELALRQALASGEHPHGPVMEKSTVTP-DSKRFILVELSNMAADSPV 97
 QY 67 TAAIDVTMLVYVAQAGDSYFLR-DAFRGABTHLFTGTSSSLPTNGSYPLERYAG-H 124
 DB 98 TLAVDVYNAIVYVATRSQSFLEEDNEDPALEMLPTKRTFFPSGSYTLDERVAGER 157
 QY 125 RDQIPGIDOLIOSYTLAFPG-GSTRTOASLILILIONISGAAPFLIMRAQYING 183
 DB 158 REEILGNDPLENRLISLMTSNLNOGALASLIYQVAVAFVRFPIXYVESITRA 217
 QY 184 ASFLPDVYMLEFTSMQGSQTOVQSTG-DVFNPPRLALPFGNPLYLTVND-VIASLA 241
 DB 218 EMFRPPPMALSLNNKMSALSNVQSGVSSPEVLEISNKPYYGVSRYISGLA 277
 QY 242 IMLFVVC-GERPSSDVRVYPLVIRPVAD-----DYTCSASEPTVIRVGNQC 289
 DB 278 IMLFICGSTDSQSFIDELMLRPLLDVAVATDADNDTCADPEPTVIRISGNGLC 337
 QY 290 VDVRDDPHDNOIQILPESKSNDDPNOLATIKEDGIRSNAGCLTYGTAGYVMAFPG 349
 DB 338 VDVRDKKNKNPILQMPCKNSDVQMLTRDGTIRNSGCLTNGYSAGDYVMIYC 397
 QY 350 NTAVREATTIOWMGNTIINPRSNVLAASGIKGTLTVQTLDTLQGMAGNDAPR 409
 DB 398 RPYVTASIMQFVANGTIIPOSALVLSBESGPRITLTVQADLYASRQMLAGNTEFP 457
 QY 410 EYTVGFRLCMESNGSVWATCVSSQGNQNALYGDGSIIPKQNDQCLT-CGRDSVS 468
 DB 458 VTSIVGFNOLCMQAGNDMMVYVCESSKRAEGNALPFGSIRPHQDDKCLTSTNHSQ 517
 QY 469 TVINIVSGAGSGGQRTVTEGAILINXGALANDVACANRELRITTYANGXNQML 528
 DB 518 SIIILSSCSFGSGQRTVTEGAILINXGALANDVACANRELRITTYANGXNQML 577
 QY 529 PV 530
 DB 578 PL 579

RESULT 4
 ID Q99W4 PRELIMINARY; PRT; 580 AA.
 AC Q94BW4
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinnamonin II precursor
 DE (EC 3.2.2.22) (rRNA N-glycosidase).
 OS Cinamomum camphora (Camphor tree).
 OC Spermatophyta; Magnoliopsida; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Laurales; Lauraceae; Cinamomum.
 RX NCBI_TaxID=13429;
 RP SEQUENCE FROM N.A.
 RA Yang O., Gong Z.Z., Liu W.Y.
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinamomn proteins and study of their expression
 RT patterns.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; A039602; AK82459.1; "-"
 DR Interpro; IPR000772; Ricin_B_lectin.
 DR Interpro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR SMART; SM00458; RICTN_2; 2.
 DR SMART; SM00458; RICTN_2; 2.
 KW Hydrolase; Signal; Toxin; 2.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CHAIN 33 580 CINNAMOMIN II
 SQ SEQUENCE 580 AA; 64265 MW; 3784289SC0CBDFP CRC64;
 Query Match 48.6%; Score 1357; DB 10; Length 580;
 Best Local Similarity 52.8%; Pred No. 5e-104;
 Matches 286; Conservative 74; Mismatches 180; Indels 22; Gaps 11;

QY 9 THQTGEYPRFTLLADYSSGSPNEIPILRO-STIPVSDAQRVAVELVETNOGDS-I 66
 DB 40 TKNAIKSYTGFELALRQALASGEHPHGPVMEKSTVTP-DSKRFILVELSNMAADSPV 97
 QY 67 TAAIDVTMLVYVAQAGDSYFLR-DAFRGABTHLFTGTSSSLPTNGSYPLERYAG-H 124
 DB 98 TLAVDVYNAIVYVATRSQSFLEEDNEDPALEMLPTKRTFFPSGSYTLDERVAGER 157
 QY 125 RDQIPGIDOLIOSYTLAFPG-GSTRTOASLILILIONISGAAPFLIMRAQYING 183
 DB 158 REEILGNDPLENRLISLMTSNLNOGALASLIYQVAVAFVRFPIXYVESITRA 217
 QY 184 ASFLPDVYMLEFTSMQGSQTOVQSTG-DVFNPPRLALPFGNPLYLTVND-VIASLA 241
 DB 218 EMFRPPPMALSLNNKMSALSNVQSGVSSPEVLEISNKPYYGVSRYISGLA 277
 QY 242 IMLFVVC-GERPSSDVRVYPLVIRPVAD-----DYTCSASEPTVIRVGNQC 289
 DB 278 IMLFICGSTDSQSFIDELMLRPLLDVAVATDADNDTCADPEPTVIRISGNGLC 337
 QY 290 VDVRDDPHDNOIQILPESKSNDDPNOLATIKEDGIRSNAGCLTYGTAGYVMAFPG 349
 DB 338 VDVRDKKNKNPILQMPCKNSDVQMLTRDGTIRNSGCLTNGYSAGDYVMIYC 397
 QY 350 NTAVREATTIOWMGNTIINPRSNVLAASGIKGTLTVQTLDTLQGMAGNDAPR 409
 DB 398 RPYVTASIMQFVANGTIIPOSALVLSBESGPRITLTVQADLYASRQMLAGNTEFP 457
 QY 410 EYTVGFRLCMESNGSVWATCVSSQGNQNALYGDGSIIPKQNDQCLT-CGRDSVS 468
 DB 458 VTSIVGFNOLCMQAGNDMMVYVCESSKRAEGNALPFGSIRPHQDDKCLTSTNHSQ 517
 QY 469 TVINIVSGAGSGGQRTVTEGAILINXGALANDVACANRELRITTYANGXNQML 528
 DB 518 SIIILSSCSFGSGQRTVTEGAILINXGALANDVACANRELRITTYANGXNQML 577
 QY 529 PV 530
 DB 578 PL 579

RESULT 5
 ID Q99W4 PRELIMINARY; PRT; 549 AA.
 AC Q94BW4
 DT 01-DEC-2001 (Tremblrel. 15, Created)
 DT 01-DEC-2001 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Type II ribosome-inactivating protein cinnamonin (EC 3.2.2.22) (rRNA
 DE N-glycosidase) (Fragment).
 OS Cinamomum camphora (Camphor tree).
 OC Spermatophyta; Magnoliopsida; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Laurales; Lauraceae; Cinamomum.
 RX NCBI_TaxID=13429;

Thu Dec 11 16:09:55 2003

us-09-601-667c-4.xbpt

Page 4

[illegible][illegible]

Db 303 WKCDRLBNQTLTKNDLITKNSKCLTTEGTAAGVYVNIYDCTSAVAEATWEIWDNG 362
Qy 366 TTPRSNVLVLAASGKIGTTLTVOITLDTLGGGGLAGNDTAPREVTIYGFRLDMESNG 425
Db 363 TTPRSKALVLAASGSSGGLTVOITNEMLRQGRGNTSPVVISISGSDLOMOAG 422
Qy 426 GSVAWETVSSQGMKALYGGSTIRPKQNDCTTCGSDSVSTVITVSCASGSGQW 485
Db 423 SNVWADQNRKQGMALYDSSISVQNTNCLIKHKGSGPIYLAQSWMSQGN 482
Qy 486 VPTNBAIINLKNGLANDVAQNPRLRIITYPACGKQMWL 528
Db 483 LPKDGSISLYDMDVMDVGSQPSIKQIITIMPYGKPNQWL 525

RESULT 9

Q91KQ2 PRELIMINARY; PRT; 263 AA.

AC Q91KQ2:2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lectin chain B isoform 2 (fragment).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=15976;
RN [1]
RS SEQUENCE FROM N.A.
RA MEDLINE:20102702; PubMed:1170524;
RA PubMed:1166572; PubMed:1166573;
RA PubMed:1166574; PubMed:1166575;
RA Do M.-S., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RT "CDNA cloning and sequence analysis of the lectin genes of the Korean
mistlecra (Viscum album coloratum).";
RL Mol. Cells 12:215-220(2001).
RN [2]
RS SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF505918; AK046936.1; B.
DR GenBank; AF505918; AK046936.1; B.
DR PIR; P00652; R1CIN_B.lectin.5.
DR SMART; SMO0456; R1CIN_2.
DR PROSITE; PS50231; R1CIN_B_LECTIN; 2.
FT NON TER 1 1
FT TER 263 263
SQ SEQUENCE 263 AA; 29150 MW; B685CB7C49C8D1F CRC64;

Query Match 42.6%; Score 1189; DB 10; Length 263;
Best Local Similarity 82.5%; Pred. No. 2e-90; Indels 0; Gaps 0;
Matches 217; Conservative 20; Mismatches 26;
Qy 269 DPTVCSAPPTIRVGRGKQVDDDDHGGQNGIQWRKSNDDPQMLTKKGGTTS 328
Db 1 DGGCTASPTVRIYVGLMGCTDVYNGKHGNGFIQWPKCKNDNRQMLTTRDDTTS 60
Qy 329 NSGCLTGYGTAGVYVMEFGDCAVREATITQWNGGIIINPSSVLVLAASGKIGTTL 388
Db 61 NSKCLTYGREGVYVIMYQCAVREATITQWNGGIIINPSSVLVLAASGKIGTTL 120
Qy 389 VQITDYLTAQGMALAGNDTAPREVTIYGFRLDMESNGSVWETVSSQGMKALYDG 448
Db 121 VQITDYLTAQGMALAGNDTAPREVTIYGFRLDMESNGSVWETVSSQGMKALYDG 180
Qy 449 STPKQNDQCTTCGSDSVSTVITVSCASGSGQWPTTBAITLKNGLANDVAQNP 508
Db 181 STPKQNDQCTTCGSDSVSTVITVSCASGSGQWPTTBAITLKNGLANDVAQNP 240
Qy 509 PKLRRIITYPACGKQMWLPV 531

Db 241 PSIRRIITYPACGKQMWLPV 263

RESULT 10

Q9M6E9 PRELIMINARY; PRT; 547 AA.

AC Q9M6E9:2002 (TrEMBLrel. 15, Created)
DT 01-OCT-2002 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Preproagglutinin (EC 3.2.2.22) (RNA N-glycosidase).
GN AAG.
OS Abrus precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosida I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OX NCBI_TaxID=3816;
RN [1]
RS SEQUENCE FROM N.A.
RA MEDLINE:20102702; PubMed:10636890;
RA PubMed:1166572; PubMed:1166573;
RA PubMed:1166574; PubMed:1166575;
RA Liu C.Y., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Hwang M.J.,
RT "Primary Structure and Function Analysis of the Abrus precatorius
agglutinin A chain by site-directed mutagenesis: Protein of Amphiphilic
U. Biol. Chem. 275:1897-1901(2000).
RL U. Biol. Chem. 275:1897-1901(2000).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; AF190173; AK28309.1; -.
CC GenBank; AF190173; AK28309.1; -.
CC PIR; P00157; R1P.
DR EMBL; AF190173; AK28309.1; B.
DR GenBank; AF190173; AK28309.1; B.
DR PIR; P00157; R1P.
DR SMART; SMO0456; R1CIN_2.
DR PROSITE; PS50231; R1CIN_B_LECTIN; 2.
DR PROSITE; PS50231; R1CIN_B_LECTIN; 2.
DR HYDROLASE; Toxin.
SQ SEQUENCE 547 AA; 61248 MW; 355A325254A1BD CRC64;

Query Match 41.7%; Score 1164.5; DB 10; Length 547;
Best Local Similarity 45.5%; Pred. No. 6.4e-88;
Matches 242; Conservative 87; Mismatches 174; Indels 29; Gaps 8;
Qy 9 THQCTEEYERFTLLADVSSGSPENRPLRQSTPVSQARFVLVELTQGGDSTTA 68
Db 28 TGSATVAYNQFDLBERLGLIYQ-IVLRDPS-TERPKQVYVLAESDVSVDL 85
Qy 69 AIDVNLVYVAYQAGDSSFTLADPAPGAEHTLFTCTTSSGTFPNSGPIEDERYAGH-RQ 127
Db 86 GIDVNLVYVAYQAGDSSFTLADPAPGAEHTLFTCTTSSGTFPNSGPIEDERYAGH-RQ 145
Qy 128 FGLDNLQVYVAYQAGDSSFTLADPAPGAEHTLFTCTTSSGTFPNSGPIEDERYAGH-RQ 187
Db 146 FGLDNLQVYVAYQAGDSSFTLADPAPGAEHTLFTCTTSSGTFPNSGPIEDERYAGH-RQ 205
Qy 188 PPTVMELETSSWQGSQVQSTGVFNRRIRLAPRGVFTLTVNRD-----V 236
Db 206 PPTVMELETSSWQGSQVQSTGVFNRRIRLAPRGVFTLTVNRD-----V 236
Qy 237 TASLALMEVQGERSSSVRRVYLVRPIVADVTGSAS-EPVTVVGNRQCTVDRD 295
Db 256 VSAHALMEVQGERSSSVRRVYLVRPIVADVTGSAS-EPVTVVGNRQCTVDRD 295
Qy 296 DPTVCSAPPTIRVGRGKQVDDDDHGGQNGIQWRKSNDDPQMLTKKGGTTS 328
Db 312 ANNGNPFIIMKQDQFENQWMLKSKTIRSKKLTITTVYAPQNVYMDGSAVMA 371
Qy 372 ATYQWNGGIIINPSSVLVLAASGKIGTTLTVOITLDTLGGGGLAGNDTAPREVTIY 415
Db 372 ATYQWNGGIIINPSSVLVLAASGKIGTTLTVOITLDTLGGGGLAGNDTAPREVTIY 415

[illegible]

RESULT 11

```

ID      Q8R3H7;          PRELIMINARY;          PRT: 249 AA.
AC      Q8R3H7;
DT      01-JUN-2002 (YEEMBLrefl, 21, Created)
DT      01-JUN-2002 (YEEMBLrefl, 21, Last sequence update)
DT      01-MAR-2003 (YEEMBLrefl, 23, Last annotation update)
DE      Lectin chain A isoform 2 (EC 3.2.2.22) (RNA N-glycosidase)
DR      (Fragment)
DS      (Fragment)
OS      Viscum album (European mistletoe)
OC      Caryophyllales; Ericaceae; Viscaceae; Myricophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Santalales; Viscaceae; Viscum.
NCBI    taxid:3972;
RN      [1]
RX      SEQUENCE FROM N.A.
RC      TISSUE=leaf;
RA      Paramanasiyam M., Srinivasan A., Singh T.P.;
RA      "Viscum Album (Indian) mRNA for Mistletoe Lectin Chain A, isoform 2."
RL      Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RC      -;
CC      CATALYTIC ACTIVITY: RHODODENDROUS OF THE N-GLYCOSIDIC BOND RT ONE
CC      -1; SIMILARITY: PROTEIN OF THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC      EMBL: A001148; A0487005.1;
CC      InterPro: IPR001574; RfP.
DR      Pfam: PF00161; RfP. 1.
DR      Hydrolase; Toxin.
FT      NON_TER          1
FT      NON_TER          1
FT      NON_TER          1
SQ      SEQUENCE      249 AA; 27944 MW; 89FAFE78309A8B35 CRC64;

```

Query Match	41.5%;	Score 1159;	DB 10;	Length 249;
Best Local Similarity	91.2%;	Pred. No. 5.7e-88;		
Matches 227; Conservative	9;	Mismatches 13;	Indels 0;	Gaps 0;

```

OY  YESLRLRHTQTLGEXPFITLLNDYVSSGSFNEPLNGOSTPVSAQSPFLVELTN 60
Db  1 YESLRLRHTQTLGEXPFITLLNDYVSSGSFNEPLNGOSTPVSAQSPFLVELTN 60
OY  QCSDSITLADIVLKYVAYVADGDSYFLNDAPGATLFTPTQTSLEPFVSGSYDLEI 120
Db  61 EGSDSTLADIVLKYVAYVADGDSYFLNDAPGATLFTPTQTSLEPFVSGSYDLEI 120
OY  YAGHRDQPLVAGIDLIQSYTLAPRGSSITTOAGSILLIOMTSANRNPILWAKRQTI 180
Db  121 YAGHRDQPLVAGIDLIQSYTLAPRGSSITTOAGSILLIOMTSANRNPILWAKRQTI 180
OY  YAGHRQPLQEFLEELIQSYSLKRPQSTHIAKNSILLIOMTSANRNPILWAKRQTI 180
Db  122 YAGHRQPLQEFLEELIQSYSLKRPQSTHIAKNSILLIOMTSANRNPILWAKRQTI 180
OY  NSAGSLPQPLDYMLEFTSGQSGOSTOYHSGSDVDVNNPILAPPGNPFYLTAVSDYIABL 240
Db  181 NSAGSLPQPLDYMLEFTSGQSGOSTOYHSGSDVDVNNPILAPPGNPFYLTAVSDYIABL 240
OY  NSGSEFLPDYMLEFTSGQSGOSTOYHSGSDVDVNNPILASTGKFFYLSNVEDYIABL 240
Db  181 NSGSEFLPDYMLEFTSGQSGOSTOYHSGSDVDVNNPILASTGKFFYLSNVEDYIABL 240
OY  AILMLFVCGE 249
Db  241 AILMLFVCGE 249

```

RESULT 12

ID	Q&A	PRELIMINARY;	PRT;	254 AA.
Q&A06				
AC	Q&A06			
DT	01-OCT-2002	(TRENDArel. 22,	Created)	
DT	01-OCT-2002	(TRENDArel. 22,	last sequence update)	
DT	01-MAR-2003	(TRENDArel. 23,	last annotation update)	

[illegible]

RESULT 13

	PRISM10MNR.F	PRT	263 AA.
9D	08JLK01		
1D	08JLK01		
2D	01-OCT-2002	(TREM)Pr1. 22, (Created)	
3D	01-OCT-2002	(TREM)Pr1. 22, (Last sequence update)	
4D	01-OCT-2002	(TREM)Pr1. 22, (Last annotation update)	
5D	01-MAR-2003	(TREM)Pr1. 23, (Fragment)	
6D	Lection chain B	Isoterm 3 (Fragment)	
7D	Viscum album subsp. colosatum.		
8D	Eukaryota, Viridiplantae: Streptophyta, Embryophyta, Tracheophyta.		
9D	CC Spermatophyta: Magnoliopsphyta: eudicotyledons: core eudicots:		
0D	CC Santalales: Viscaceae: Viscum.		
1D	NCBI_Taxid=153976; (1)		
2D	SEQUENCE FROM N.A.		
3D	MEDLINE=21566752; PubMed=11710524;		

RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RL Mol. Cells 12:215-220(2001).
RN (2)
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF508919; AM46931.1; -
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR SMART: SM00458; RICIN_2.
DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
FT NON_TER 1 1
FT NON_TER 263 263
SQ SEQUENCE 263 AA; 29071 MW; 389CADAB60F061D CRC64;
Query Match 41.4%; Score 1155; DB 10; Length 263;
Best Local Similarity 80.6%; Pred. No. 1,3e-87;
Matches 212; Conservative 21; Mismatches 30; Indels 0; Gaps 0;
CY 269 DNYTCSASPTPEIVGENGCVCVDPDDPHQMCQLMPKSKNDNOLITIRDTGIS 328
DB 1 DDGCTPSEPTWIVGLNGLCVDFHKGKFDGMPQLMPCKANTDNQWLTIRDTGIS 60
CY 329 NQSCLTGYAGVYVMIPDCNTVREATVQWINGCTIIPRGNVYLAASGIGCTLT 388
DB 61 NSKCLTYGDMYVMYVNCVAVRATVQWINGCTIIPRGNVYLAASGIGCTLT 120
CY 389 VQTLDTTLCQGLKANDTAPREVTITGFRDLCNESNGSWVETCVSSQGNALYGG 448
DB 121 VQVQNSLQGLKASHDAPREVTITGFRDLCNESNGSWVETCVSSQGNALYGG 180
CY 449 SIRPKMOPCLTCQSDSVTINIVSGASSGGQWPTNKGALINTKGLAMPVQAN 508
DB 181 SIRPKMOPCLTCQSDSVTINIVSGASSGGQWPTNKGALINTKGLAMPVQAN 240
CY 509 PLARITTPATCKPQWMLPVP 531
DB 241 PLARITTPATCKPQWMLPVP 263
RESULT 14
ID O8LK03 PRELIMINARY; PRT; 249 AA.
AC O8LK03;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Lectin chain A isoform 2 (IPC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment).
OS Viscum album subsp. coloratum.
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Euphorbiales; Vitaceae; Viscum.
OC NCBI_TaxID=159976;
RN [1]_TaxID=159976;
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
RT "CDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RN Mol. Cells 12:215-220(2001).
RN (2)
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
RT "CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF508919; AM46931.1; -
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGALICIN.
DR HYDROLase; Toxin.
FT NON_TER 1 1
FT NON_TER 249 249
SQ SEQUENCE 249 AA; 27821 MW; 3C5870E8338BDA5 CRC64;
Query Match 40.8%; Score 1140; DB 10; Length 249;
Best Local Similarity 89.1%; Pred. No. 2,2e-86;
Matches 220; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
CY 1 YERLRLVHTQTEGEYFRFTLLLDYVSSGSPFNEIPLRGSTIPVSDAOPVYELTN 60
DB 1 YERLRLVHTQTEGEYFRFTLLLDYVSSGSPFNEIPLRGSTIPVSDAOPVYELTN 60
CY 61 QCGGRTNALDPTWYVYVNOAGDSYFEPDAPRGAEFTLFTGTRESLPPYGSYDLEK 120
DB 61 QCGGRTNALDPTWYVYVNOAGDSYFEPDAPRGAEFTLFTGTRESLPPYGSYDLEK 120
CY 121 YAGHDDQIPGHDLQSYTLRFPGQSPRTQASILLIQWISAPRNPILPRARQYI 180
DB 121 YAGHDDQIPGHDLQSYTLRFPGQSPRTQASILLIQWISAPRNPILPRARQYI 180
CY 181 NSGASFLPDVYMLELSTWQGSQSTGVGSHSDGVNPNRLALPPGNPVTLLVWEDYASL 240
DB 181 NSGASFLPDVYMLELSTWQGSQSTGVGSHSDGVNPNRLALPPGNPVTLLVWEDYASL 240
CY 241 AMLRPG 247
DB 241 AMLRPG 247
RESULT 15
ID O8LK03 PRELIMINARY; PRT; 266 AA.
AC O8LK03;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Lectin chain B isoform 1 (Fragment).
OS Viscum album subsp. coloratum.
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Vitaceae; Viscum.
OC NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
RT "CDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RN Mol. Cells 12:215-220(2001).
RN (2)
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
RT "CDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RN Mol. Cells 12:215-220(2001).
RN (2)
FT NON_TER 266 266
FT NON_TER 266 266
SQ SEQUENCE 266 AA; 29537 MW; 4A51473C7B94C73 CRC64;
Query Match 38.0%; Score 1060.5; DB 10; Length 266;
Best Local Similarity 72.6%; Pred. No. 9,4e-80;
Matches 193; Conservative 29; Mismatches 41; Indels 3; Gaps 1;

Qy 269 DDTCSASEPTVAIVGNMVCVDRDDFDHGNQIOLMPSKANNPNOLMTIKRDGITS 328
 Db 1 DDTCTTSEPTVAIVGNMVCVDRDDFDHGNQIOLMPSKANNPNOLMTIKRDGITS 60
 Qy 329 NSGCTTGYTAQVWTFECNTRVREATTWIMKNGTINRSNLT--AASGIXT 385
 Db 61 NGRCLTGYTHASYIMYDCNRGNDLTWIRNGIILNFRSMWIGTSSGSGTGT 120
 Qy 386 TLVQTLDTYTCQGWLAGNDTAPREVTIYGFRLCMESNGSVWETCVSSQGNQWALY 445
 Db 121 TPLQTLGSLGQWLAGNDTAPREVTIYGFRLCMESNGSVWETCVSSQGNQWALY 180
 Qy 446 GPSIRPKNDQCLTCGRDSYSTINIVSCAGSSQGRVFTNEGAILINXGLANDYA 505
 Db 181 GPSIRPKRYDQCLTCGRDSYSTINIVSCAGSSQGRVFTNEGAILINXGLANDYA 240
 Qy 506 GANPKRRIITYPATKRNOMLPP 531
 Db 241 RSNPSLRRIITYPATKRNOMLPP 266

Search completed: December 11, 2003, 14:01:00
 Job time : 41.9287 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 52.4693 Seconds
(without a1:imworo)

Title: US-09-601-667C-4

Sequence: 1 YERLRRLRVTHQTGGEYFRF.....RRIITYPATGKPNQMWLPVP 531

Scoring table: BLOSUM62

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

```
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

1:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1960.DMT
2:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1961.DMT
3:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1962.DMT
4:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1963.DMT
5:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1964.DMT
6:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1965.DMT
7:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1966.DMT
8:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1967.DMT
9:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1968.DMT
10:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1969.DMT
11:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1970.DMT
12:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1971.DMT
13:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1972.DMT
14:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1973.DMT
15:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1974.DMT
16:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1975.DMT
17:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1976.DMT
18:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1977.DMT
19:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1978.DMT
20:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI1979.DMT
21:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI2000.DMT
22:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI2001.DMT
23:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI2002.DMT
24:	/SIDS1.gcgdat4.genseq.genseqp-emb1/AAI2003.DMT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	ID	Description
1	2791	100.0	53	AA25878	Mistletoe lectin I
2	2791	100.0	52	AA25875	Mistletoe lectin I
3	2791	100.0	53	AA25882	Mistletoe lectin I
4	2770	99.2	564	AAW10021	Pedro mistletoe I
5	2770	99.2	564	AAW90127	Mistletoe lectin P
6	2519	90.3	533	AA25870	Mistletoe lectin P
7	2519	90.3	533	AA25876	Mistletoe lectin P
8	2525	84.3	551	ABW91850	Mistletoe lectin B
9	1450	50.9	263	AA259855	Glycose lectin B

[illegible]

PT Preparation of mistletoe lectins in heterologous systems.
PT particularly for use as anticancer agents and immunostimulants
XX
XX Claim 7, Fig 1b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a mistletoe lectin I protein fragment.
XX
SQ Sequence 531 AA:
Query Match 100.0%; Score 2791; DB 20; Length 531;
Best Local Similarity 100.0%; Pred. No. 2, 8e-244;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YERLRARVHTQGTGEYFRFTLLRDYVSSGSFSENEIPILRSGTIPVSDAQRFVLELN 60
DB 1 YERLRARVHTQGTGEYFRFTLLRDYVSSGSFSENEIPILRSGTIPVSDAQRFVLELN 60
QY 61 QGGSDITAIADVTMLVVAOAGDSYFLRDPAGAEHLFTGTSSLPFGSGYDLER 120
DB 61 QGGSDITAIADVTMLVVAOAGDSYFLRDPAGAEHLFTGTSSLPFGSGYDLER 120
QY 121 YAGHRDIPFGIDQLIGSTALRPFQGSRTQASILLTOMISPAARNPILMARQYI 180
DB 121 YAGHRDIPFGIDQLIGSTALRPFQGSRTQASILLTOMISPAARNPILMARQYI 180
QY 181 NSGASFLPDVYMLELTSWGQSTOVQSTGVFNRIPLAIPPGAPVTLNVRDVA 240
DB 181 NSGASFLPDVYMLELTSWGQSTOVQSTGVFNRIPLAIPPGAPVTLNVRDVA 240
QY 241 AMLFVCGERSSSDVRYMPLVIRPVADVTCSASEPTVIRGNMCCVDRDDPHG 300
DB 241 AMLFVCGERSSSDVRYMPLVIRPVADVTCSASEPTVIRGNMCCVDRDDPHG 300
QY 301 NOILMPKSSNDPQGLMTIRKDTIRNSGCLITTYGTVNIPPCNTNVRALNTQ 360
DB 301 NOILMPKSSNDPQGLMTIRKDTIRNSGCLITTYGTVNIPPCNTNVRALNTQ 360
QY 361 INWNGTIIINPSSNVLAAASGKGTLLVQTLDTYLLGGMLAGNDAPREVITYGFDLC 420
DB 361 INWNGTIIINPSSNVLAAASGKGTLLVQTLDTYLLGGMLAGNDAPREVITYGFDLC 420
QY 421 MESNGSFWETVCSQONKALYDGSIRPKONOCULTGONDSVTYINVSAGS 480
DB 421 MESNGSFWETVCSQONKALYDGSIRPKONOCULTGONDSVTYINVSAGS 480
QY 481 SCGRWVFNNEGAILNLKNGLANADVAKMPKRIIITTPATGKPPQWTFPV 531
DB 481 SCGRWVFNNEGAILNLKNGLANADVAKMPKRIIITTPATGKPPQWTFPV 531
RESULT 2
AAZ5982
XZ AAZ5982 standard; Protein; 532 AA.
XZ
XZ AAZ5982;
XZ
XZ 18-OCT-1999 (first entry)
XZ
XZ Mistletoe lectin I (variant) protein fragment.
XZ
XZ Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;
KM

KV ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW particularly for use as anticancer agents and immunostimulants
KW cancer; cytotoxicity; antigen; isoform; lectin I.
XX
XX Viscum album.
XX
XX DEL9804210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
XX
XX Morris P, Stiefel T, Voelter W, Welters P;
XX
XX WPI: 1999-445335/38.
XX
XX N-PSDB: AA209106.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Disclosure; Fig 4b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin I protein variant.
XX
SQ Sequence 532 AA:
Query Match 100.0%; Score 2791; DB 20; Length 532;
Best Local Similarity 100.0%; Pred. No. 2, 8e-244;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YERLRARVHTQGTGEYFRFTLLRDYVSSGSFSENEIPILRSGTIPVSDAQRFVLELN 60
DB 1 YERLRARVHTQGTGEYFRFTLLRDYVSSGSFSENEIPILRSGTIPVSDAQRFVLELN 60
QY 61 QGGSDITAIADVTMLVVAOAGDSYFLRDPAGAEHLFTGTSSLPFGSGYDLER 120
DB 61 QGGSDITAIADVTMLVVAOAGDSYFLRDPAGAEHLFTGTSSLPFGSGYDLER 120
QY 121 YAGHRDIPFGIDQLIGSTALRPFQGSRTQASILLTOMISPAARNPILMARQYI 180
DB 121 YAGHRDIPFGIDQLIGSTALRPFQGSRTQASILLTOMISPAARNPILMARQYI 180
QY 181 NSGASFLPDVYMLELTSWGQSTOVQSTGVFNRIPLAIPPGAPVTLNVRDVA 240
DB 181 NSGASFLPDVYMLELTSWGQSTOVQSTGVFNRIPLAIPPGAPVTLNVRDVA 240
QY 241 AMLFVCGERSSSDVRYMPLVIRPVADVTCSASEPTVIRGNMCCVDRDDPHG 300
DB 241 AMLFVCGERSSSDVRYMPLVIRPVADVTCSASEPTVIRGNMCCVDRDDPHG 300
QY 301 NOILMPKSSNDPQGLMTIRKDTIRNSGCLITTYGTVNIPPCNTNVRALNTQ 360
DB 301 NOILMPKSSNDPQGLMTIRKDTIRNSGCLITTYGTVNIPPCNTNVRALNTQ 360
QY 361 INWNGTIIINPSSNVLAAASGKGTLLVQTLDTYLLGGMLAGNDAPREVITYGFDLC 420
DB 361 INWNGTIIINPSSNVLAAASGKGTLLVQTLDTYLLGGMLAGNDAPREVITYGFDLC 420

QY 421 MESNGSVWVETCVSSQONRMALVGDGSIKPKONODCLTCGRDSVSVINIVSCSAGS 480
DB 421 MESNGSVWVETCVSSQONRMALVGDGSIKPKONODCLTCGRDSVSVINIVSCSAGS 480
QY 481 SGGKRVFTNEGALINIKGELMDVYQANPFLKRIITITPATGKPNOMLPP 531
DB 481 SGGKRVFTNEGALINIKGELMDVYQANPFLKRIITITPATGKPNOMLPP 531

RESULT 3
AAM10021
ID AAM10021 standard; Protein; 564 AA.

18-DEC-1997 (first entry)

Prepro mistletoe lectin.

Mistletoe; lectin; cytotoxic; A chain; B chain; dimer.

Viscum album.

BE751221-A1.

02-JAN-1997.

26-JUN-1995; 95EP-0109949.

26-JUN-1995; 95EP-0109949.

(MADU) MADUS KOEHLN AG.

Baur A, Eck J, Lentzen H, Zinke H;

WEI; 1997-054678/06.

N-PSDB; AAT70473.

Nucleic acid encoding prepro form of mistletoe lectin - for therapeutic or diagnostic use

Claim 12, Fig 4c; 30pp; German.

Mistletoe lectin is a cytotoxic agent that has been used for tumour therapy. It can be used in immunotoxins and medicaments. Nucleic acid fragments can be used in diagnostic methods. Mistletoe lectin (AAT70473) comprises an A chain (AAT70474) and a B chain (AAT70475).

Sequence 564 AA;

Query Match 99.2%; Score 2770; DB 18; Length 564;

Best Local Similarity 99.1%; Pred. No. 2.4e-242;

Matches 526; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 YERLRATVHTGTEGFEYRETLADYSSGSFSENIPLRQSTIPYDAGQFVLELNM 60
DB 34 YERLRATVHTGTEGFEYRETLADYSSGSFSENIPLRQSTIPYDAGQFVLELNM 93
QY 61 QGDSITAIIDVNLVVAOAGQSYFLRARGAEHLFTGTRSLPNSGSPDLER 120
DB 94 QGDSITAIIDVNLVVAOAGQSYFLRARGAEHLFTGTRSLPNSGSPDLER 153
QY 121 YAGRDITPLGIDLIQSVTARPGSSTKQASITLILQMSAARNTILMARQIT 180
DB 154 YAGRDITPLGIDLIQSVTARPGSSTKQASITLILQMSAARNTILMARQIT 213
QY 181 NSGASFLPDVYNLELSTMGQSTQVGHSTGVFNNPRLATPGNFVTLNRYVLSL 240
DB 214 NSGASFLPDVYNLELSTMGQSTQVGHSTGVFNNPRLATPGNFVTLNRYVLSL 273
QY 241 AITLFCGEPSSSEVRYWPLVIRPVADVTCSASEPTVIRVGNMGCVDVDDDFDQ 300

DB 274 AITLFCGEPSSSEVRYWPLVIRPVADVTCSASEPTVIRVGNMGCVDVDDDFDQ 333
QY 301 NOTLAPSSKNDNQLTIKADGTFISNGSLTYTGAGVYVITCKNAVEKTIWQ 360
DB 334 NOTLAPSSKNDNQLTIKADGTFISNGSLTYTGAGVYVITCKNAVEKTIWQ 393
QY 361 INGNSTINPBNLVAASGIGKTLTYQLDYTLGGQMLAGNDIAPREVTYGRDLC 420
DB 394 INGNSTINPBNLVAASGIGKTLTYQLDYTLGGQMLAGNDIAPREVTYGRDLC 453
QY 421 MESNGSVWVETCVSSQONRMALVGDGSIKPKONODCLTCGRDSVSVINIVSCSAGS 480
DB 454 MESNGSVWVETCVSSQONRMALVGDGSIKPKONODCLTCGRDSVSVINIVSCSAGS 513
QY 481 SGGKRVFTNEGALINIKGELMDVYQANPFLKRIITITPATGKPNOMLPP 531
DB 514 SGGKRVFTNEGALINIKGELMDVYQANPFLKRIITITPATGKPNOMLPP 564

RESULT 4

AAM90127
ID AAM90127 standard; Protein; 564 AA.

AAM90127;

20-MAR-2003 (updated)

30-APR-1995 (first entry)

Mistletoe lectin prepro-protein.

Mt; mistletoe; lectin; Mt; transgenic plant; glycosylation; dimer; immunotoxin; large-scale production; diagnosis; therapeutic; cancer.

Viscum album.

EP84388-A1.

16-DEC-1998.

26-JUN-1995; 95EP-0105660.

26-JUN-1995; 95EP-0109949.

26-JUN-1995; 95EP-0105660.

(MADU) MADUS KOEHLN AG.

Baur A, Eck J, Lentzen H, Zinke H;

WEI; 1999-026592/03.

N-PSDB; AAV74182.

New transgenic plant expressing mistletoe lectin - useful for producing recombinant lectin in e.g. cancer diagnosis and therapy

Claim 1a; Fig 4c; 30pp; German.

This invention describes a novel transgenic plant transformed with a vector capable of encoding a mistletoe (Viscum album) lectin preproprotein or a biologically active fragment. The specific lectin also describes a polypeptide produced by a plant where the polypeptide exhibits at least one enzymatic modification other than the glycosylation that occurs in viscum album of the polypeptide is a fusion protein, a mistletoe lectin polypeptide dimer and an immune used for large-scale production of mistletoe lectin for diagnostic or therapeutic purposes (e.g. in cancer therapy). This sequence represents the mistletoe lectin used in the method of the invention.

(Updated on 20-MAR-2003 to correct pf field.)

Sequence 564 AA;

Query Match 99.2%; Score 2770; DB 20; Length 564;

Best Local Similarity 99.1%; Pred. No. 2,4e-242;
Matches 526; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 YERLRATVQGTGEYFRFTLLROYVSSGSPSNEIFLLRQSTIPVSDAQRFVLVLIN 60
DB 34 YERLRATVQGTGEYFRFTLLROYVSSGSPSNEIFLLRQSTIPVSDAQRFVLVLIN 93
QY 61 QGSESTTAIDVNLVYVAYAGPQSYTLADAPRQATHLPTGTPSSALPNSYPLER 120
DB 94 QGSESTTAIDVNLVYVAYAGPQSYTLADAPRQATHLPTGTPSSALPNSYPLER 153
QY 121 YAGHRDQIPLGIDPLQISVTAAPPGASTRTQASIIILIQMISEAARFPIIMARQYI 180
DB 154 YAGHRDQIPLGIDPLQISVTAAPPGASTRTQASIIILIQMISEAARFPIIMARQYI 213
QY 181 NSGASFLPDVYMLELSTNGQOSTOVSHSTDGVFNNTIKALPPGNVTLTNRDYASL 240
DB 214 NSGASFLPDVYMLELSTNGQOSTOVSHSTDGVFNNTIKALPPGNVTLTNRDYASL 273
QY 241 AMLFVCEHRPSSDVPYMLYIEPVIADVTCSASEPTVRIVERNQCVDVADDDFDG 300
DB 274 AMLFVCEHRPSSDVPYMLYIEPVIADVTCSASEPTVRIVERNQCVDVADDDFDG 333
QY 301 NCGLMPKSNNDPQMLATIKKDGTRHNSCLTTGTAGVYVIMPCNTAREACTIQ 360
DB 334 NCGLMPKSNNDPQMLATIKKDGTRHNSCLTTGTAGVYVIMPCNTAREACTIQ 393
QY 361 IWNGCTIINPRSNLVLAASGIKGTLLVQTLDTYLQGMAGNDIARREVTIYGFDDLC 420
DB 394 IWNGCTIINPRSNLVLAASGIKGTLLVQTLDTYLQGMAGNDIARREVTIYGFDDLC 453
QY 421 MESNGSVVETVCSQGNRMALKQASIRPNQVQCLTCGSDVSTVINIVSGAS 480
DB 454 MESNGSVVETVCSQGNRMALKQASIRPNQVQCLTCGSDVSTVINIVSGAS 513
QY 481 SGQRWFTNEGATILNKLAMVDQAQPKLREIIITYPATGPKQWMLPVP 531
DB 514 SGQRWFTNEGATILNKLAMVDQAQPKLREIIITYPATGPKQWMLPVP 564

RESULT 5
AAV25970
ID AAV25970 standard; protein; 533 AA.
XX
XX AAV25970;
DT 18-OCT-1999 (first entry)
XX
XX
DE Mistletoe lectin protein consensus sequence 1.
XX
XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
KW ribozyme 26S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX
XX cancer; cytotoxicity; antigen; isoform.
OS
XX Viscum album.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 15 /label= Asp, Glu
FT Misc-difference 63 /label= Gly, Gln
FT Misc-difference 66 /label= Ile, Val
FT Misc-difference 107 /label= Leu, Ala
FT Misc-difference 113 /label= Asp, Arg or none
FT Misc-difference 117 /label= Asn, Thr
FT Misc-difference 134 /label= Pro, Thr

FT /label= Asp, Glu
FT Misc-difference 141 /label= Ser, Thr
FT Misc-difference 145 /label= Phe, Tyr
FT Misc-difference 152 /label= Thr, Ala
FT Misc-difference 177 /label= Ala, Tyr
FT Misc-difference 185 /label= Tyr, Asp
FT Misc-difference 185 /label= Ala, Glu
FT Misc-difference 191 /label= Val, Met
FT Misc-difference 219 /label= Ile, Phe
FT Misc-difference 224 /label= Pro, Ser
FT Misc-difference 225 /label= Pro, Thr
FT Misc-difference 236 /label= Thr, Ser
FT Misc-difference 236 /label= Asp, Ser
FT Misc-difference 267 /label= Asn, Ser
FT Misc-difference 290 /label= Cys, Arg
FT Misc-difference 325 /label= Gly, Asn
FT Misc-difference 364 /label= Gly, Asp
FT Misc-difference 420 /label= Val, Asp
FT Misc-difference 439 /label= Gln, Lys
FT Misc-difference 442 /label= Gly or none
FT Misc-difference 443 /label= Arg, Lys
FT Misc-difference 464 /label= Cys, Ser, Val
FT Misc-difference 480 /label= Ala, Gly
FT Misc-difference 481 /label= Gly, Ala
FT Misc-difference 483 /label= Ser, Gly
FT Misc-difference 484 /label= Gly, Ser
FT Misc-difference 493 /label= Met, Val
FT Misc-difference 500 /label= Asn, Ser, Thr, Lys
FT Misc-difference 501 /label= Ser, Gly
FT Misc-difference 502 /label= Leu, Pro
FT Misc-difference 503 /label= Ala, Met
FT Misc-difference 504 /label= Met, Val
FT Misc-difference 533 /label= Pro, Phe
DE19804210-A1.
12-AUG-1999.
PO 03-FEB-1998; 98DE-1004210.

FT MISC-difference 180 /label= Tyr, Asp
 FT MISC-difference 183 /label= Ala, Glu
 FT MISC-difference 191 /label= Val, Met
 FT MISC-difference 219 /label= Ile, Phe
 FT MISC-difference 224 /label= Pro, Ser
 FT MISC-difference 225 /label= Thr, Ser
 FT MISC-difference 232 /label= Thr, Ser
 FT MISC-difference 236 /label= Asp, Ser
 FT MISC-difference 287 /label= Asn, Ser
 FT MISC-difference 290 /label= Cys, Arg
 FT MISC-difference 325 /label= Gly, Asn
 FT MISC-difference 364 /label= Gly, Asp
 FT MISC-difference 426 /label= Gly, Gln
 FT MISC-difference 435 /label= Val, Asp
 FT MISC-difference 438 /label= Gln, Lys
 FT MISC-difference 442 /label= Gly, none
 FT MISC-difference 443 /label= Arg, Lys
 FT MISC-difference 464 /label= Cys, Ser, Val
 FT MISC-difference 480 /label= Ala, Gly
 FT MISC-difference 481 /label= Ser, Gly, Ala
 FT MISC-difference 483 /label= Ser, Gly
 FT MISC-difference 484 /label= Gly, Ser
 FT MISC-difference 493 /label= Gly, Tyr
 FT MISC-difference 500 /label= Asn, Ser, Thr, Lys
 FT MISC-difference 501 /label= Ser, Gly
 FT MISC-difference 503 /label= Leu, Pro
 FT MISC-difference 504 /label= Ala, Met
 FT MISC-difference 533 /label= Met, Val
 FT MISC-difference 533 /label= Pro, Phe
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL, GMBH.
 XX Morris F, Stiefel T, Voelter W, Welters P;
 XX WPI, 1999-44535/38.
 XX

FT Preparation of mistletoe lectins in heterologous systems,
 FT particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 40; Page 37-38; 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (WLA)
 CC of mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Mistletoe lectin (I) contains a unique domain (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a consensus sequence of the mistletoe lectin described in the
 CC specification.
 XX
 SQ Sequence 533 AA;
 Query Match 90.3%; Score 2519; DB 20; Length 533;
 Best Local Similarity 92.5%; Pred. No. 1,4e-219;
 Matches 492; Conservative 0; Mismatches 38; Indels 2; Gaps 2;
 QY 1 YERLRLVHTQTEGEYFRPTLLADYSSGSFSENEIPLRSGTTPVSDARFVLELTN 60
 1 YERLRLVHTQTEGEYFRPTLLADYSSGSFSENEIPLRSGTTPVSDARFVLELTN 60
 DB 61 QGDSITAIIDYTNLIVVAIQGDSTFRLDAPRGAEHLFTGTR-SGLPNSGPDLR 119
 61 QGDSITAIIDYTNLIVVAIQGDSTFRLDAPRGAEHLFTGTR-SGLPNSGPDLR 119
 QY 120 RYKGRROQPGIDOLIOGYVLAEPGSGSTRQARSHIILIMISEARFPIIMAPAOY 179
 120 RYKGRROQPGIDOLIOGYVLAEPGSGSTRQARSHIILIMISEARFPIIMAPAOY 179
 DB 121 RYKGRROQPGIDOLIOGYVLAEPGSGSTRQARSHIILIMISEARFPIIMAPAOY 180
 121 RYKGRROQPGIDOLIOGYVLAEPGSGSTRQARSHIILIMISEARFPIIMAPAOY 180
 QY 180 INSGASLPDYVMELETSWGQSTVOVCHSTDGVFNNKRLAIXXGPFVTLXNRYVAS 239
 180 INSGASLPDYVMELETSWGQSTVOVCHSTDGVFNNKRLAIXXGPFVTLXNRYVAS 239
 DB 181 INSGASLPDYVMELETSWGQSTVOVCHSTDGVFNNKRLAIXXGPFVTLXNRYVAS 240
 181 INSGASLPDYVMELETSWGQSTVOVCHSTDGVFNNKRLAIXXGPFVTLXNRYVAS 240
 QY 240 LAIMEFCGERSSSPVWYFVIRVADVTCSASEPTVIRVGNKQCVADDDPHD 299
 240 LAIMEFCGERSSSPVWYFVIRVADVTCSASEPTVIRVGNKQCVADDDPHD 299
 DB 241 LAIMEFCGERSSSPVWYFVIRVADVTCSASEPTVIRVGNKQCVADDDPHD 300
 241 LAIMEFCGERSSSPVWYFVIRVADVTCSASEPTVIRVGNKQCVADDDPHD 300
 QY 300 GNOICLWPKSNNDPQWLMTIKEDTIRNSGCLITTYGTVAYVMFPCNTAVRATITW 360
 300 GNOICLWPKSNNDPQWLMTIKEDTIRNSGCLITTYGTVAYVMFPCNTAVRATITW 360
 DB 301 GNOICLWPKSNNDPQWLMTIKEDTIRNSGCLITTYGTVAYVMFPCNTAVRATITW 360
 301 GNOICLWPKSNNDPQWLMTIKEDTIRNSGCLITTYGTVAYVMFPCNTAVRATITW 360
 QY 360 QITNGGIIINPRSNVLAASSGSKOTLLVOTIDYTLQCGMLAGNDTAREETIYFFDL 419
 360 QITNGGIIINPRSNVLAASSGSKOTLLVOTIDYTLQCGMLAGNDTAREETIYFFDL 419
 DB 361 QITNGGIIINPRSNVLAASSGSKOTLLVOTIDYTLQCGMLAGNDTAREETIYFFDL 420
 361 QITNGGIIINPRSNVLAASSGSKOTLLVOTIDYTLQCGMLAGNDTAREETIYFFDL 420
 QY 420 QESNGSGWETCTSSQONO-RNALFGSGIIPKQNDODCLTCGRSVSTYINIVGSA 478
 420 QESNGSGWETCTSSQONO-RNALFGSGIIPKQNDODCLTCGRSVSTYINIVGSA 478
 DB 421 QESNGSGWETCTSSQONO-RNALFGSGIIPKQNDODCLTCGRSVSTYINIVGSA 480
 421 QESNGSGWETCTSSQONO-RNALFGSGIIPKQNDODCLTCGRSVSTYINIVGSA 480
 QY 479 GSGGQWVFTNEGILINIXXGMLNDVQANPKLRRIIYPAKXKNQWMLPV 530
 479 GSGGQWVFTNEGILINIXXGMLNDVQANPKLRRIIYPAKXKNQWMLPV 530
 DB 481 KXXQWVFTNEGILINIXXGMLNDVQANPKLRRIIYPAKXKNQWMLPV 532
 481 KXXQWVFTNEGILINIXXGMLNDVQANPKLRRIIYPAKXKNQWMLPV 532
 XX
 RESULT 8
 AB879450 standard; Protein, 551 AA.
 XX
 AB879450;
 XX
 08-JUL-2002 (first entry)
 XX
 Galactose-recognising mistletoe lectin.
 XX

Thu Dec 11 16:09:53 2003

us-09-601-667c-4.rag

Page 8

XW	Mistlec;	galactose-recognising mistleec lectin; MIII.
OS	Viscum album.	
XX	Key	Location/Qualifiers
FH	Misc-difference 223	/note= "Encoded by ATG"
FT	Misc-difference 251	/note= "Encoded by TTT"
FT	Misc-difference 344	/note= "Encoded by TCG"
FT	Misc-difference 380	/note= "Encoded by GGC"
FT	Misc-difference 448	/note= "Encoded by GTG"
FN	D810044027-A1.	
FX	14-MAR-2002.	
PF	06-SEP-2000; 2000DB-1044027.	
PR	06-SEP-2000; 2000DB-1044027.	
PA	(VISC-) VISCUM AG.	
XX	Kieff S;	
PI	WPI; 2002-316737/36.	
DR	N-PDB; AML56947.	
PT	New nucleic acid encoding preprolactin of mistleec lectin, useful as diagnostic and therapeutic agents, also encodes polypeptide -	
PS	Claim 1; Fig 1; 6pp; German.	
CC	The invention relates to a nucleic acid molecule (AML56947) that encodes a preprotein (AB879450) which, after maturation, has the biological activity of the galactose-recognising mistleec lectin (MIII). The MIII encoding nucleic acid molecule, primers specific to it or complements of it, and encoded (Oligomeric) polypeptides are useful as diagnostic and therapeutic agents.	
SQ	Sequence 551 Aa;	
Query Match	84.3%; Score 2352.5; DB 23; Length 551;	
Best Local Similarity	88.0%; Pred. No. 1.9e-204;	
Matches 449;	Conservative 21; Mismatches 35; Indels 5; Gaps 1	
OY	1 YEKILRVMHQITTEEFFPFLILDLYSSGSFSNEIPRLKOSTIFVPDAORFVYLZLN 60	
Db	34 YEKLIRLVHQITDEFFPFLILDLYSSGSFSNBIPLKOSTIFVPDAORFVLZLN 93	
OY	61 OGSDIRPALDPTLVAVAYAGDSYFEDAPSGAEIIECTGRSLFRNGSYDLR 120	
Db	94 OGDSDIRDALDVTLVAVAYAGDSYFLMDAPGNRHLLTGTTRSSLPTFGSYDLR 153	
OY	121 YAAHDQDPGLGIDQLQSVTLAFPGSPTPOASLTIIOMTSSEANFPILWPAAQYT 180	
Db	154 YAAHDQDPGLGLELQSVALYSALYSGSTFAQASIIITIIOMTSKANPFIWPKRWODI 213	
OY	181 NSGASFLEPDVYTELISLWSGOSTOVCHSDTGATNNPRLAIPDNFVLIINVEDVIASL 240	
Db	214 NTSQSFGEPPSSDDRYNPALTYRT-----ADDTSCASPEPTRIYKMGCKVDROD 295	
OY	241 AINTVGCPHETLALBLSNSGOSTVQSDTDGYNNPRLAISGVNFVLSXWDVIALSL 273	
Db	274 AINTVGCPHESSEFEVRVWLPVLRVPLMSGANGVDVTCAASEPTRIIVGDELCAVVRG 333	
OY	296 DFDNDNQIQAWSSKNNDNLQTLTKRGTFIKNSGCLTVYGTVAGYYVIFDCNARYE 355	
Db	334 KFINSNPQLQAWCKCFNIDNQPWLIRBDGINSNGRLTIYGVAGYYVIFDCNARYE 353	

[illegible]

QY 329 NSCLTGYTAGYVWIFDCNFAVRENTIWOIMNGTIIINPRSNLVLAASSGKGTTLT 388
DB 61 NSCLTGYTAGYVWIFDCNFAVRENTIWOIMNGTIIINPRSNLVLAASSGKGTTLT 120
QY 389 VOTLDYTLGGSMLAGNDTAPREVTIYGFRLCNSNGSSVWETCVSSQONQRMALYGDG 448
DB 121 VOTLDYTLGGSMLAGNDTAPREVTIYGFRLCNSNGSSVWETCVSSQONQRMALYGDG 180
QY 449 SIRPKONQDCLTCGRDSVSTVINIVSCSAGSSQGRWFTNKGALINLKNGLAMDVQAN 508
DB 181 SIRPKONQDCLTCGRDSVSTVINIVSCSAGSSQGRWFTNKGALINLKNGLAMDVQAN 240
QY 509 PKLRRIIIVPATGKPNQMWLPVP 531
DB 241 PKLRRIIIVPATGKPNQMWLPVP 263

RESULT 10

AAV25991
ID AAV25991 standard; Protein: 264 AA.

AC AAV25991;

DT 18-OCT-1999 (first entry)

DE Mistletoe lectin B variant protein fragment.

XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;

KW lymphoma; lung cancer; non-cytotoxic; T-cell activation; immune response;

KW cancer; cytotoxicity; antigen; isoform; lectin B.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

PA (BIOS-) BIOGVN ARZNEIMITTEL GMBH.

PI Morris P, Stiefel T, Voelter W, Welters P;

DR WP1; 1999-445335/38.

DR N-PSDB; AA209115.

PT Preparation of mistletoe lectins in heterologous systems,

PT particularly for use as anticancer agents and immunostimulants

XX Disclosure; Fig 13B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments

CC which have antitumor and immunostimulatory activity. The A-chain (MIA)

CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and

CC lymphokine-producing macrophages, so stimulate immunity. (I) and its

CC fragments are used to treat uncontrolled cell growth (particularly

CC (tumour-associated lymphoma). The method allows production of the

CC mistletoe lectin, and its individual fragments. Many different isoforms

CC and on a large scale, at any time of the year. The products are

CC free from toxins present in natural mistletoe extracts. This sequence

XX Sequence 264 AA:

Query Match

Best Local Similarity

50.9%; Score 1420; DB 20; Length 264;

100.0%; Pred. No. 2,6e-120;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 269 DVTCSASRPVRIIVGRMCKCTDRDDPHNQCULMBKSNDDPVQIMTIRKQITIR 328
DB 1 DVTCSASRPVRIIVGRMCKCTDRDDPHNQCULMBKSNDDPVQIMTIRKQITIR 60
QY 329 NSCLTGYTAGYVWIFDCNFAVRENTIWOIMNGTIIINPRSNLVLAASSGKGTTLT 388
DB 61 NSCLTGYTAGYVWIFDCNFAVRENTIWOIMNGTIIINPRSNLVLAASSGKGTTLT 120
QY 389 VOTLDYTLGGSMLAGNDTAPREVTIYGFRLCNSNGSSVWETCVSSQONQRMALYGDG 448
DB 121 VOTLDYTLGGSMLAGNDTAPREVTIYGFRLCNSNGSSVWETCVSSQONQRMALYGDG 180
QY 449 SIRPKONQDCLTCGRDSVSTVINIVSCSAGSSQGRWFTNKGALINLKNGLAMDVQAN 508
DB 181 SIRPKONQDCLTCGRDSVSTVINIVSCSAGSSQGRWFTNKGALINLKNGLAMDVQAN 240
QY 509 PKLRRIIIVPATGKPNQMWLPVP 531
DB 241 PKLRRIIIVPATGKPNQMWLPVP 263

RESULT 11

AAW64662
ID AAW64662 standard; Protein: 263 AA.

AC AAW64662;

DT 23-OCT-1998 (first entry)

DE Mistletoe TMB variant protein.

XX lectin B-chain; mistletoe; xMB; fusion protein; effector; cytotoxic;

KW intracellular; immunostimulant; cancer; disease; targeting module;

KW autoimmune disease; allergy; tumor; lectin; translocation.

XX Viscum album.

XX Key

FT Protein

XX W09829540-A2.

XX 09-JUL-1998.

XX 02-JAN-1998; 98WO-EP00009.

XX 02-JAN-1997; 97EP-010012.

PA (BRAI-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.

PI Beck J, Schmidt A, Zinke H;

DR WP1; 1998-38122/33.

DR N-PSDB; AAV51344.

PT Disclosure; Fig 11b; 115pp; German.

XX This sequence represents a variant mistletoe lectin B-chain, TMB. This

CC sequence can be used in the construction of a fusion protein which

CC processing module covalently bonded to the effector module and

CC the surface of a cell, as a processing module, able to bind specifically to

CC the surface of a cell, as a processing module, able to bind specifically to

CC the surface of a cell, as a processing module, able to bind specifically to

CC involving proliferation and/or elevated activation of cells, especially
 CC autoimmune disease, allergy and tumours. The proteins can be administered
 CC e.g. by injection or topically but especially by intravenous injection.
 CC The proteins are used in a dose of 100 µg to 500 µg/ml.
 CC Fusion proteins can be used, toxic activity in the cells.
 CC The processing module prevents extracellular dissociation and
 CC fusion proteins based on mistletoe lectin A-chain are far more active
 CC than those based on ricin and do have the associated problems of
 CC non-specific toxicity. The protein may be expressed in a non-glycosylated
 CC form that does not bind to sugar receptors in the liver, and which has a
 CC long half-life in the blood. Where the mistletoe lectin B-chain is used,
 CC it actively assists in translocation of the ML A-chain from the
 CC endoplasmic reticulum to the cytoplasm.

Sequence 263 AA;

Query Match 50.4%; Score 1406; DB 19; Length 263;
 Best Local Similarity 98.9%; Pred. No. 4.9e-119;

Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 269 DVTCSASEPTVIRIVGNKCVVDHDDPFQDNQIQMPKSKNDPNQMTIKDGTIRS 328
 DB 1 DVTCSASEPTVIRIVGNKCVVDHDDPFQDNQIQMPKSKNDPNQMTIKDGTIRS 60
 QY 329 NGSCITTYGTAQVYVWIPCNVAVREATVQWNGTIINPRSNVLAASGIGKTLT 388
 DB 61 NGSCITTYGTAQVYVWIPCNVAVREATVQWNGTIINPRSNVLAASGIGKTLT 120
 QY 389 VQTLDTYLGQGLAGNDTAPREVTIYGFRLCMESNGSWVETCVSSQONRMALYGD 448
 DB 121 VQTLDTYLGQGLAGNDTAPREVTIYGFRLCMESNGSWVETCVSSQONRMALYGD 180
 QY 449 SIFRKQNDQCLTCGRDSVSTVNIYVSCASGSGQWVFTNEGALINLNGGLAMVQAQ 508
 DB 181 SIFRKQNDQCLTCGRDSVSTVNIYVSCASGSGQWVFTNEGALINLNGGLAMVQAQ 240
 QY 509 PTLRRITTYPATGKQNMWLPVP 531
 DB 241 PTLRRITTYPATGKQNMWLPVP 263

RESULT 12

AA010023

AA010023 standard; Protein; 264 AA.

XX

XX

XX 18-DEC-1997 (first entry)

XX Pregro mistletoe lectin B chain.

XX Mistletoe, lectin; cytotoxic; A chain; B chain; dimer.

XX Viscum album.

XX EP751221-A1.

XX 02-JAN-1997.

XX 26-JUN-1995; 95EP-0109949.

XX 26-JUN-1995; 95EP-0109949.

XX (MADU) MADUS KOEHL AG.

XX Baur A, Eck J, Lentzen H, Zinke H;

XX WPI; 1997-054678/06.

XX N-PSDB; AAV70475.

XX Nucleic acid encoding pre-pro form of mistletoe lectin - for

XX Therapeutic or diagnostic use

PS Claim 12; Fig 4B; 30pp; German.

XX Mistletoe lectin is a cytotoxic agent that has been used for tumour

XX therapy. It can be used in immunotoxins and medicaments. Nucleic

XX acids encoding the protein have been used in immunotoxins. The

XX (MADU) comprises an A chain (AAV70475) and a B chain (AAV70475).

XX Sequence 264 AA;

Query Match 50.4%; Score 1406; DB 18; Length 264;
 Best Local Similarity 98.9%; Pred. No. 4.9e-119;

Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 269 DVTCSASEPTVIRIVGNKCVVDHDDPFQDNQIQMPKSKNDPNQMTIKDGTIRS 328
 DB 2 DVTCSASEPTVIRIVGNKCVVDHDDPFQDNQIQMPKSKNDPNQMTIKDGTIRS 61
 QY 329 NGSCITTYGTAQVYVWIPCNVAVREATVQWNGTIINPRSNVLAASGIGKTLT 388
 DB 62 NGSCITTYGTAQVYVWIPCNVAVREATVQWNGTIINPRSNVLAASGIGKTLT 121
 QY 389 VQTLDTYLGQGLAGNDTAPREVTIYGFRLCMESNGSWVETCVSSQONRMALYGD 448
 DB 122 VQTLDTYLGQGLAGNDTAPREVTIYGFRLCMESNGSWVETCVSSQONRMALYGD 181
 QY 449 SIFRKQNDQCLTCGRDSVSTVNIYVSCASGSGQWVFTNEGALINLNGGLAMVQAQ 508
 DB 182 SIFRKQNDQCLTCGRDSVSTVNIYVSCASGSGQWVFTNEGALINLNGGLAMVQAQ 241
 QY 509 PTLRRITTYPATGKQNMWLPVP 531
 DB 242 PTLRRITTYPATGKQNMWLPVP 264

RESULT 13

AA090126

AA090126 standard; Protein; 264 AA.

XX

XX 20-MAR-2003 (updated)

XX 30-APR-1999 (first entry)

XX Mistletoe ML B-chain protein.

XX ML; mistletoe, lectin; MLB; B-chain; transgenic plant; glycosylation;

XX dimer; immunotoxin; large-scale production; diagnosis; therapeutic;

XX Viscum album.

XX EP864388-A1.

XX 16-DEC-1998.

XX 26-JUN-1995; 98EP-0105660.

XX 26-JUN-1995; 95EP-0109949.

XX 26-JUN-1995; 98EP-0105660.

XX (MADU) MADUS KOEHL AG.

XX Baur A, Eck J, Lentzen H, Zinke H;

XX WPI; 1999-026592/03.

XX N-PSDB; AAV74181.

XX New transgenic plant expressing mistletoe lectin - useful for

XX producing recombinant lectin in e.g. cancer diagnosis and therapy

XX Disclosure; Fig 4b; 30pp; German.

XX This invention describes a novel transgenic plant transformed with a

Thu Dec 11 16:09:53 2003

us-09-601-667c-4.rag

```
XX 03-FEB-1998; 98DE-1004210.
PF 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
PR 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX
XX Morris P, Stiefel T, Voelter W, Walters P;
XX MPI; 1999-44535/38.
XX N-PSDE; AA209110.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 9; Fig 8b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (WLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different hosts
XX and on a large scale, at any time of the year. Mistletoe products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B1 protein.
XX
XX Sequence 264 AA:
SQ
Query Match 48.0%; Score 139.5; DB 20; Length 264;
Best Local Similarity 95.8%; Pred. No. 5.4e-13;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
QY 269 DVTCSASEPTVIVGNKNCYDRDDHDSQIQMPSKANDPQLTIKEDTIR 328
DB 1 DVTCSASEPTVIVGNKNCYDRDDHDSQIQMPSKANDPQLTIKEDTIR 328
QY 329 NSGCTVGTAGVWIMPCNTAVREATIMQIMKNTINPSENVLASGIGKTLT 388
DB 61 NSGCTVGTAGVWIMPCNTAVREATIMQIMKNTINPSENVLASGIGKTLT 120
QY 389 VQTLDTYLGQGNLANDTAPREVITVGFADLCMSNGSVMWETCVSSQONQ 447
DB 121 VQTLDTYLGQGNLANDTAPREVITVGFADLCMSNGSVMWETCVSSQONQ 447
QY 448 GSIRKONODQCTFGRDSYVTINIVSCAGSSQKRWFTNEGATINRGLACTYQA 507
DB 181 GSIRKONODQCTFGRDSYVTINIVSCAGSSQKRWFTNEGATINRGLACTYQA 507
QY 508 NRKLRRIITVPATCKRQMWLPV 530
DB 241 NRKLRRIITVPATCKRQMWLPV 263
```

Search completed: December 11, 2003, 14:07:42
Job time : 53.4693 secs

Thu Dec 11 16:09:54 2003

us-09-601-667c-4.rapb

Page 2

```

Qy 389 VQTLDTLGGWLAGNDTAPRRTYVGRFLCMESNGSVWETCVSSQGNRMALYGG 448
Db 121 VQTLDTLGGWLAGNDTAPRRTYVGRFLCMESNGSVWETCVSSQGNRMALYGG 180
Qy 449 SIRPKONODCLTCGRDSVSTVIVSCSSGSGGVFTMEGALINLKNGLANDVAQAN 508
Db 181 SIRPKONODCLTCGRDSVSTVIVSCSSGSGGVFTMEGALINLKNGLANDVAQAN 240
Qy 509 PCLRRITITPATKRNQWMLPVP 531
Db 241 PCLRRITITPATKRNQWMLPVP 263

RESULT 2
US-09-347-064-4
/ Sequence 4, Application US/09347064A
/ Patent No. US20020045208A1
/ GENERAL INFORMATION:
/ APPLICANT: Eck, Jurgen
/ APPLICANT: Schmidt, Arno
/ TITLE OF INVENTION: Recombinant Fusion Proteins Based on
/ TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe viscum
/ TITLE OF INVENTION: Album
/ FILE REFERENCE: 09282-5
/ CURRENT APPLICATION NUMBER: US/09/347, 064A
/ EARLIER FILING DATE: 1999-07-02
/ EARLIER APPLICATION NUMBER: PCT/EP98/00009
/ EARLIER FILING DATE: 1998-01-02
/ EARLIER APPLICATION NUMBER: EP 97 10 0012.0
/ EARLIER FILING DATE: 1997-01-02
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 467
/ TYPE: PRT
/ ORGANISM: Viscum Album
US-09-347-064-4

Query Match 50.4%; Score 1406; DB 9; Length 267;
Best Local Similarity 98.9%; Pred. No. 3,6e-128;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 269 DDTYCSASPTTAVIYARNKCTVDYRDDDFHDSNOICLMPKSNNDNOLATIKGTITG 328
Db 1 DDTYCSASPTTAVIYARNKCTVDYRDDDFHDSNOICLMPKSNNDNOLATIKGTITG 60
Qy 329 NSGCLTYGTAGVYVIMFPCCTAVREATIMQWNGIINPRNLTVAASGIGKTTT 388
Db 61 NSGCLTYGTAGVYVIMFPCCTAVREATIMQWNGIINPRNLTVAASGIGKTTT 120
Qy 389 VQTLDTLGGWLAGNDTAPRRTYVGRFLCMESNGSVWETCVSSQGNRMALYGG 448
Db 121 VQTLDTLGGWLAGNDTAPRRTYVGRFLCMESNGSVWETCVSSQGNRMALYGG 180
Qy 449 SIRPKONODCLTCGRDSVSTVIVSCSSGSGGVFTMEGALINLKNGLANDVAQAN 508
Db 181 SIRPKONODCLTCGRDSVSTVIVSCSSGSGGVFTMEGALINLKNGLANDVAQAN 240
Qy 509 PCLRRITITPATKRNQWMLPVP 531
Db 241 PCLRRITITPATKRNQWMLPVP 263

RESULT 3
US-10-083-336A-1
/ Sequence 1, Application US/10083336A
/ Publication No. US2003018165A1
/ GENERAL INFORMATION:
/ APPLICANT: Hoffmann-La Roche Mark A
/ APPLICANT: Millard, Charles B
/ APPLICANT: Byrne, Michael P
/ APPLICANT: Wainmacher, Robert W
US-10-083-336A-1

Query Match 46.7%; Score 1304; DB 12; Length 576;
Best Local Similarity 51.0%; Pred. No. 9,8e-118;
Matches 273; Conservative 81; Mismatches 161; Indels 20; Gaps 11;

Qy 9 THQTVSEVFRITLKRQVSSG--FSNEIPL-RQSTIPVSDQRFVLEIVNQGDNI 66
Db 48 TACATVOSTYNFIRAVRGLTALADVHEHLEPLNKGALPLN--QRFILHLSNEALSV 105
Qy 67 TAAITNTLYVAVQNGDSYIF-DAPKAE--THSTGT-FRESLPFGSDPEEVA 122
Db 106 TLADLVNAYVGYKNGSAIFPHDQEDBAITLFTDQMEYVATAGNYDRLEQA 165
Qy 123 GH-FOIPIGIDIOISVTAIR--FGSSTRQASLILIIQWISAPAFPIIMRAQ 178
Db 166 GNFRENELANGPLEALSAIVYSTGQULPTLARSFICQMSAPAFQYIEGSKT 225
Qy 179 YINSGAFIPDVMLELTSWQOSTVQSHSTGVNPRILAPFNVTILNVDVIA 238
Db 226 RIKRNSAPDPSYITLNSKSLTALDSNQARASIQLOKRNKSAFYIVNSILP 285
Qy 233 SLATLTYGCGRPSSDYRTYPIYIRPLND--DPTCSASPTTAVIYARNKCTVDY 295
Db 286 TILAVYRCAPPSQ---FSLIRPYVNNNDV-CODEDEYFRIVGNCCLCVVRG 340
Qy 356 ATTMQWNGIINPRNLTVAASGIGKTTTQTLDTLGGWLAGNDTAPRRTYVGR 415
Db 341 RFRNGLAIQWPCSKVTDANQWLTAKDNTIRNSKCLTYGSGVYVIMDCTIARD 400
Qy 416 FRLCMESNGSVWETCVSSQGNRMALYGGIRPKONODCLTCGRDSVSTVIVS 475
Db 461 ATRMQWNGIINPRNLTVAASGIGKTTTQTLDTLGGWLAGNDTAPRRTYVGR 460
Qy 461 LYLCLQNGGQVIEKDSKRAEQNALYAGSIRPKONODCLTCGRDSVSTVIVS 520
Db 521 CGPSSGQGRMFRNDGITLINTYGLVADVPASDPSIKQIILYELGDPNDIWL 575

RESULT 4
US-09-347-064-8
/ Sequence 8, Application US/09347064A
/ Patent No. US20020045208A1
/ GENERAL INFORMATION:
/ APPLICANT: Eck, Jurgen
/ APPLICANT: Schmidt, Arno
/ APPLICANT: Zinke, Holger
/ TITLE OF INVENTION: Recombinant Fusion Proteins Based on
/ TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe viscum
/ TITLE OF INVENTION: Album
/ FILE REFERENCE: 09282-5
/ CURRENT APPLICATION NUMBER: US/09/347, 064A
/ EARLIER FILING DATE: 1999-07-02
/ EARLIER APPLICATION NUMBER: PCT/EP98/00009
/ EARLIER FILING DATE: 1998-01-02
/ EARLIER APPLICATION NUMBER: EP 97 10 0012.0
/ EARLIER FILING DATE: 1997-01-02
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: PatentIn Ver. 2.1
US-09-347-064-8
```

SEQ ID NO 8
LENGTH: 252
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-8

Query Match
Best Local Similarity: 46.0%; Score 1285; DB 9; Length 252;
Best Local Similarity: 39.6%; Pred. No. 1, 9e-16;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YERLRVTHQTGEYFRITLLADYSSGSFSNIEPLLRQSTIPVSDAQRFVLYELIN 60
DB 1 YERLRVTHQTGEYFRITLLADYSSGSFSNIEPLLRQSTIPVSDAQRFVLYELIN 60
QY 61 QGGSITAIADVTNLVYVAYAGDSYFLRDAFRGAETHLFTGTRSSILPNSSYPLER 120
DB 61 QGGSITAIADVTNLVYVAYAGDSYFLRDAFRGAETHLFTGTRSSILPNSSYPLER 120
QY 121 VAGHRDQIFLGIQDILQSVYALRFGSGSTRQARSILILQWISBAARFVILMARQYI 180
DB 121 VAGHRDQIFLGIQDILQSVYALRFGSGSTRQARSILILQWISBAARFVILMARQYI 180
QY 181 NSGASFLPDVYMLEETSMQGSQVQVSHTDGVFNPRILAIPEGVYTLINRVIASI 240
DB 181 NSGASFLPDVYMLEETSMQGSQVQVSHTDGVFNPRILAIPEGVYTLINRVIASI 240
QY 241 AMLFVCGERP 252
DB 241 AMLFVCGERP 252

RESULT 5
US-09-347-064-2
Sequence 2, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Eck, Jurgen
APPLICANT: Schindt, Arno
APPLICANT: Zinke, Holger
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
FILE REFERENCE: US20020045208A1
CURRENT APPLICATION NUMBER: US/09/347,064A
PRIOR FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 252
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-2

Query Match
Best Local Similarity: 45.9%; Score 1281; DB 9; Length 252;
Best Local Similarity: 39.6%; Pred. No. 4, 8e-116;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YERLRVTHQTGEYFRITLLADYSSGSFSNIEPLLRQSTIPVSDAQRFVLYELIN 60
DB 1 YERLRVTHQTGEYFRITLLADYSSGSFSNIEPLLRQSTIPVSDAQRFVLYELIN 60
QY 61 QGGSITAIADVTNLVYVAYAGDSYFLRDAFRGAETHLFTGTRSSILPNSSYPLER 120
DB 61 QGGSITAIADVTNLVYVAYAGDSYFLRDAFRGAETHLFTGTRSSILPNSSYPLER 120
QY 121 VAGHRDQIFLGIQDILQSVYALRFGSGSTRQARSILILQWISBAARFVILMARQYI 180
DB 121 VAGHRDQIFLGIQDILQSVYALRFGSGSTRQARSILILQWISBAARFVILMARQYI 180

QY 181 NSGASFLPDVYMLEETSMQGSQVQVSHTDGVFNPRILAIPEGVYTLINRVIASI 240
DB 181 NSGASFLPDVYMLEETSMQGSQVQVSHTDGVFNPRILAIPEGVYTLINRVIASI 241
QY 241 AMLFVCGERP 251
DB 241 AMLFVCGERP 252

RESULT 6
US-10-282-935-3
Sequence 3, Application US/10282935
Publication No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SHALISHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: TOXIC INHIBITORS OF COMPOUNDS
FILE REFERENCE: US20020045208A1
CURRENT APPLICATION NUMBER: US/10/282,935
PRIOR FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126,826
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 3
LENGTH: 251
TYPE: PRT
ORGANISM: Abrus precatorius
US-10-282-935-3

Query Match
Best Local Similarity: 17.0%; Score 474; DB 12; Length 251;
Best Local Similarity: 42.6%; Pred. No. 1, 4e-37;
Matches 107; Conservative 37; Mismatches 83; Indels 24; Gaps 5;

QY 9 THQTEYFRITLLADYSSGSFSNIEPLLRQSTIPVSDAQRFVLYELINQGSISITA 68
DB 9 THQTEYFRITLLADYSSGSFSNIEPLLRQSTIPVSDAQRFVLYELINQGSISITA 68
QY 69 AIDVTNLVYVAYAGDSYFLRDAFRGAETHLFTGTRSSILPNSSYPLER 127
DB 69 AIDVTNLVYVAYAGDSYFLRDAFRGAETHLFTGTRSSILPNSSYPLER 126
QY 128 IEGIDILQSVYALRFGSGSTRQARSILILQWISBAARFVILMARQYINSGASFL 187
DB 127 IEGIDILQSVYALRFGSGSTRQARSILILQWISBAARFVILMARQYINSGASFL 186
QY 188 PDVYMLEETSMQGSQVQVSHTDGVFNPRILAIPEGVYTLINRVIASI 240
DB 187 PDVYMLEETSMQGSQVQVSHTDGVFNPRILAIPEGVYTLINRVIASI 236
QY 237 VAVIALMLFVC 247
DB 237 VAVIALMLFVC 247

Thu Dec 11 16:09:54 2003

US-09-601-667c-4.rapb

Page 6

APPLICANT: Better, Marc D.
Cartoll, Stephen F.
Stundika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Agents
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM: Paper, copy, disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 23-Apr-2002
APPLICATION NUMBER: US/10/127,890
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-May-1998 US94/05348
APPLICATION NUMBER: 1994
FILING DATE: 12-May-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-Dec-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-Jun-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-Nov-1991
ATTORNEY/AGENT INFORMATION:
NAME: McAndrews, Held & Malloy, Ltd.
REFERENCE/DOCKET NUMBER: 200-70, P4
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR WEIGHT: 26521
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-127-890-6
Query Match 11.4%; Score 324; DB 12; Length 247;
Best Local Similarity 35.6%; Pred. No. 5,4e-23;
Matches 85; Conservative 54; Mismatches 86; Indels 14; Gaps 9;
Db
13 TGEYFPFTLLADYVSSGFSNRIPLRQSTTPVSDAQFVYVELTNGGDSITAIIV 72
10 TSSGYVFISNLRALPNERKLDIPLLR-SGLPGS--QRYALHLNVADEFTISVAIV 66
QY 73 TNYVVAQNGQGYFLRDA-FRGAEHLPTGTRS-SLPNGSYPLDERVAGH-RDQIF 129
Db 67 TNYVWGRAGDTSYFNRBSALEAKYVFDKMRKVTLPYSGNVERLTQAGKIRENIF 126
QY 130 LGIDQLQSVTALRPGSGSTFQASILLIQMTSAPAEFNLPMARQYINGASFLPD 189
Db 127 LGIPALDASITITFLY--YNASASALAMVLIQSTSEAAKFKIRBOIGKVDK--TFLPS 182
QY 190 VYALLETISMGQSTVOQ--HSTDCYFNNFRLAIPGNFVTLNVRD--VIASLAIHL 244
Db 183 LATISLNSMSALSKQIOASINNGQFESPVVLIINQCVATITNVDAQVTSNALL 241

RESULT 13
US-10-280-679b-4
Sequence 4; Application US/102806798
Publication No. US20030150019A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
FILE REFERENCE: LSBC-0109-0503
CURRENT FILING DATE: US/10/280,679b
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 02/557,941
PRIOR APPLICATION NUMBER: 08/484,341
PRIOR APPLICATION NUMBER: 1995-06-07
PRIOR FILING DATE: 1992-07-31
PRIOR APPLICATION NUMBER: 07/923,692
PRIOR FILING DATE: 1992-07-31
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR FILING DATE: 1991-01-16
PRIOR APPLICATION NUMBER: 07/737,899
PRIOR FILING DATE: 1991-07-26 739,143
PRIOR APPLICATION NUMBER: 601
PRIOR FILING DATE: 1989-02-17
PRIOR APPLICATION NUMBER: 07/310,881
PRIOR FILING DATE: 1989-02-17
PRIOR APPLICATION NUMBER: 07/160,766
PRIOR FILING DATE: 1988-02-26
PRIOR APPLICATION NUMBER: 07/160,771
PRIOR FILING DATE: 1988-02-26
Remaining Prior Application data removed - See File Wrapper of PLM.
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patent version 3.1
SEQ ID NO 389
TYPE: PRT
ORGANISM: Chinese cucumber protein alpha-tiricosanthin
US-10-280-679b-4
Query Match 11.4%; Score 319; DB 12; Length 289;
Best Local Similarity 35.6%; Pred. No. 2.1e-22;
Matches 85; Conservative 53; Mismatches 87; Indels 14; Gaps 9;
Db
13 TGEYFPFTLLADYVSSGFSNRIPLRQSTTPVSDAQFVYVELTNGGDSITAIIV 72
10 TSSGYVFISNLRALPNERKLDIPLLR-SGLPGS--QRYALHLNVADEFTISVAIV 69
QY 73 TNYVVAQNGQGYFLRDA-FRGAEHLPTGTRS-SLPNGSYPLDERVAGH-RDQIF 129
Db 90 TNYVWGRAGDTSYFNRBSALEAKYVFDKMRKVTLPYSGNVERLTQAGKIRENIF 149
QY 130 LGIDQLQSVTALRPGSGSTFQASILLIQMTSAPAEFNLPMARQYINGASFLPD 189
Db 150 LGIPALDASITITFLY--YNASASALAMVLIQSTSEAAKFKIRBOIGKVDK--TFLPS 205
QY 190 VYALLETISMGQSTVOQ--HSTDCYFNNFRLAIPGNFVTLNVRD--VIASLAIHL 244
Db 206 LATISLNSMSALSKQIOASINNGQFESPVVLIINQCVATITNVDAQVTSNALL 284
RESULT 14
US-10-127-890-111
Sequence 111; Application US/10127890
Publication No. US2003016196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Stundika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Agents
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

Thu Dec 11 16:09:54 2003

us-09-601-667c-4.rapb

Page 7

```

101 STREET: 500 West Madison Street, 34th floor
102 CITY: Chicago
103 STATE: Illinois
104 COUNTRY: USA
105 ZIP: 60661
106 COMPUTER MODEL: PCOM:
107 MEDIUM TYPE: floppy disk
108 OPERATING SYSTEM: PC-DOS/MS-DOS
109 SOFTWARE: Patent In Release #1.0, Version #1.25
110 CURRENT APPLICATION DATA:
111   APPLICATION NUMBER: US/10/127,890
112   FILING DATE: 23-Apr-2002
113   CLASSIFICATION: unknown
114   PRIORITY:
115     APPLICATION NUMBER: US/08/054,360
116     FILING DATE: 13-MAY-1995
117     APPLICATION NUMBER: PCT/US94/05348
118     FILING DATE: 12-MAY-1994
119     APPLICATION NUMBER: US 08/064,691
120     FILING DATE: 12-MAY-1993
121     APPLICATION NUMBER: US 07/989,430
122     FILING DATE: 09-DEC-1992
123     APPLICATION NUMBER: US 07/901,707
124     FILING DATE: 08-DEC-1990
125     APPLICATION NUMBER: US 70
126     FILING DATE: 04-NOV-1991
127   ATTORNEY/AGENT INFORMATION:
128     NAME: NICHOLAS, Janet M.
129     REGISTRATION NUMBER: 32,918
130     REFERENCE/DOCKET NUMBER: 200-70-P4
131     TELECOMMUNICATION INFORMATION:
132     TELEPHONE: 312/707-8889
133     TELEFAX: 312/707-9155
134     FAX: 312/707-9155
135   INFORMATION FOR SEQ ID NO: 111:
136     SEQUENCE CHARACTERISTICS:
137       LENGTH: 251 amino acids
138       TYPE: amino acid
139       TOPOLOGY: linear
140     MOLECULAR TYPE: protein
141     SEQUENCE DESCRIPTION: SEQ ID NO: 111:
142 US-10-127-890-111
143
144 Query Match      114% Score 317.5 DB 12; length 251;
145 Best local similarity 35.2% Pct 12; 14822;
146 Matches 87; Conservative 37; Mismatches 112; Indels 11; Gaps 5;
147
148 Db      Qy      8 VHQHTGHEPPFTLLDLY--VSGSPFNRPFLPGSTIPVSDAPRFLVLEINQGD 64
149      5 VASSTSCATYITVYVNLRLVRLFKGNSHRHPIRLKKADPGKA--FLVLAISNDQ 62
150
151 Qy      65 STIAIDVNLVYVAYQGDGYFLRDPAPGAEHLFTGTSSLPFNQSYDPLERVGH 124
152      63 LAELIVDITVSYVGVQVNRNSISFIPGAPVIAISLFEKVIKTRLHGSGSYSLERAY 122
153      125 RODIPIIDH--TQSYTLAPRPGSGTRQKSGIILIQITSEAPRFLMAQCTIN 161
154      123 RETDPLDIEPRKIDIKEDLNDAIDVYKPELISLAVIVQVSEKAAFFIENQIN--N 180
155
156 Qy      162 SGASLPVDVYKLEIETNSGQGSQVQVHS--TDGVNRPFLRLAIPGNVFLINWADVIASL 240
157      161 FQGRIRPANNNTISLEHKGKSLFQIRTSGANQMPSEVALEKRNKXYIVAVQVYKRI 240
158
159 Qy      241 AAGIR 247
160      Db      241 AATKTC 247
161
162 RESULT 15
163 US-10-127-890-102
164 Sequence 102, Application US/10127890
165 Publication No. US20030166196A1

```

```

1      GENERAL INFORMATION:
2      APPLICANT: Better, Marc D.
3      Caroli, Stephen F.
4      Studinka, Gary M.
5
6      TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
7      Proteins
8
9      NUMBER OF SEQUENCES: 173
10     CORRESPONDENCE ADDRESS:
11     ORGANIZATION: Pharmacia, Held & Malloy, Ltd.
12     STREET: 500 West Madison Street, 9th floor
13     CITY: Chicago
14     STATE: Illinois
15     COUNTRY: USA
16     ZIP: 60661
17
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: floppy disk
20     OPERATING SYSTEM: compatible
21     SOFTWARE: Protein Release #1.0, Version #1.25
22
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/10/127,890
25     FILING DATE: 23-Apr-2002
26
27     CLASSIFICATION DATA:
28     APPLICATION DATA:
29     PRIOR APPLICATION NUMBER: US/08/646,360
30     FILING DATE: 13-May-1996
31     APPLICATION NUMBER: PCT/US94/05348
32     FILING DATE: 13-May-1994
33     APPLICATION NUMBER: US 08/064,691
34     FILING DATE: 12-May-1993
35     APPLICATION NUMBER: US 07/988,430
36     FILING DATE: 09-DEC-1992
37     APPLICATION NUMBER: US 07/901,707
38     FILING DATE: 19-JUN-1992
39     APPLICATION NUMBER: US 07/187,567
40     FILING DATE: 04-NOV-1991
41
42     ATTORNEY/AGENCY INFORMATION:
43     NAME: Kohn, David M.
44     REGISTRATION NUMBER: 32,518
45     REFERENCE/DOCKET NUMBER: 200-70,74
46
47     TELECOMMUNICATION INFORMATION:
48     TELEPHONE: 312/707-8889
49     TELEFAX: 312/707-9155
50     TELEX: 650 388-1248
51
52     INFORMATION FOR SEQ ID NO: 102:
53     SEQUENCE CHARACTERISTICS:
54     LENGTH: 251 amino acids
55     MOLECULE TYPE: protein
56     TOPOLOGY: linear
57
58     SEQUENCE DESCRIPTION: SEQ ID NO: 102:
59
60     US-10-127-890-102
61
62     Query Match      11.2%; Score 313.5; DB 12; Length 251;
63     Best Local Similarity 34.8%; Pctd. No. 5,86-22;
64     Matches 86; Conservative 36; Mismatches 112; Indels 11; Gaps 5
65
66     1  YHQTGTEYRRTPLTLDV--VSQSGNSNEPIINQSTIPSPDAPRNLVEITWGQD 64
67     2  VSRSTKATQITVYNNLAEIRVAKPEKSGHIDLRKK--DPEKGVYVALSDNQ 62
68     3  5
69     4  8
70     5  STAIADIVNNYVAAGQSGVPRADAPRAGAEHNFCTGTRSLSPNSQSYDLEKVAH 124
71     6  LAELADIVSVVVGQYRRRSRSPFKADDAVYGIFQNIKTRHFGSGYSLEEKRY 122
72     7  123
73     8  KETDLDISFLKGLGKIDENALQNIYETELRSLSLVYQVSEKAPFLIENQIR--N 180
74     9  181
75     10 125 KQDLDIDQL--ISVTLAFPSGSTRQARSILILQWISSEAPNPLIMARQYN 181
76     11 182
77     12 123 SASAPSPVWVLELFGSGGQSTQHS--DQYNNPRLALIPGNTVTLTYRDIYASL 240
78     13 182
79     14 181 PQGRIPRANNTISLEWKGSLSPQIRSGANQNSFSALEBRANKRYVTVVQGVKPI 240

```

Thu Dec 11 16:09:54 2003

us-09-601-667c-4.rapb

Page 8

QY 241 ALMKFVC 247
DB 241 ALMKFVC 247

Search completed: December 11, 2003, 14:48:47
OOD time : 35.2191 secs

Thu Dec 11 16:09:53 2003

us-09-601-667c-4.ra1

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 18.3844 Seconds
(without alignments) 1222.073 Million cell updates/sec

Title: US-09-601-667C-4
Perfect score: 2791
Sequence: 1 YERLRLVHTQGTGEYERF.....RIIIPYANGKQWMLPVP 531

Scoring table: BLOSUM62 0, Gapext 0.5
Gapop 10.0, Gapext 0.5

Searched: 326717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 326717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents RA.*
1: /cgm2_6/p/odata/1/aa/55 COMB pep.*
2: /cgm2_6/p/odata/1/aa/55 COMB pep.*
3: /cgm2_6/p/odata/1/aa/65 COMB pep.*
4: /cgm2_6/p/odata/1/aa/65 COMB pep.*
5: /cgm2_6/p/odata/1/aa/PC/US COMB pep.*
6: /cgm2_6/p/odata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Match	Length	DB ID	Description
1	2770	99.2	564	3	US-08-776-059-35 Sequence 35, Appl
2	1406	50.4	263	3	US-08-776-059-43 Sequence 43, Appl
3	1406	50.4	264	3	US-08-776-059-33 Sequence 33, Appl
4	1285	46.0	253	3	US-08-776-059-31 Sequence 31, Appl
5	1157	42.9	235	3	US-08-776-059-39 Sequence 39, Appl
6	1151.5	42.7	540	1	US-08-776-651-77 Sequence 77, Appl
7	1151.5	42.7	540	1	US-08-485-286-77 Sequence 77, Appl
8	467.4	17.0	251	1	US-08-378-573-71 Sequence 71, Appl
9	467.4	16.7	250	1	US-08-485-286-71 Sequence 71, Appl
10	466.5	16.7	250	1	US-08-485-286-71 Sequence 71, Appl
11	418	15.0	534	2	US-08-485-286-10 Sequence 10, Appl
12	387	13.9	267	1	US-07-901-707-1 Sequence 1, Appl
13	387	13.9	267	1	US-07-988-430-1 Sequence 1, Appl
14	387	13.9	267	1	US-08-425-336-1 Sequence 1, Appl
15	387	13.9	267	1	US-08-425-336-1 Sequence 1, Appl
16	387	13.9	267	1	US-08-488-1138-1 Sequence 1, Appl
17	387	13.9	267	1	US-08-477-1848-1 Sequence 1, Appl
18	387	13.9	267	2	US-08-464-360-1 Sequence 1, Appl
19	387	13.9	267	2	US-08-328-7290-61 Sequence 61, Appl
20	387	13.9	267	3	US-09-135-389-1 Sequence 1, Appl
21	387	13.9	267	4	US-09-135-389-1 Sequence 1, Appl
22	387	13.9	267	4	US-09-538-873-1 Sequence 1, Appl
23	387	13.9	267	5	PCR-US92-09487-1 Sequence 1, Appl
24	387	13.9	268	2	US-08-356-786-8 Sequence 8, Appl
25	387	13.9	290	1	US-08-378-7618-27 Sequence 27, Appl
26	383	13.7	290	1	US-08-485-286-27 Sequence 27, Appl
27	383	13.7	290	1	US-08-485-286-27 Sequence 27, Appl

28	383	13.7	290	6	5248606-4 Patent No. 5248606
29	350	12.5	282	1	US-08-324-301-15 Sequence 15, Appl
30	344.5	12.3	263	1	US-07-901-707-4 Sequence 4, Appl
31	344.5	12.3	263	1	US-07-988-430-4 Sequence 4, Appl
32	344.5	12.3	263	1	US-08-425-336-4 Sequence 4, Appl
33	344.5	12.3	263	1	US-08-488-1138-4 Sequence 4, Appl
34	344.5	12.3	263	1	US-08-464-360-4 Sequence 4, Appl
35	344.5	12.3	263	3	US-08-839-785-4 Sequence 4, Appl
36	344.5	12.3	263	3	US-09-135-389-4 Sequence 4, Appl
37	344.5	12.3	263	3	US-09-538-873-4 Sequence 4, Appl
38	344.5	12.3	263	5	PCR-US92-09487-4 Sequence 4, Appl
39	344.5	12.2	286	1	US-08-324-301-13 Sequence 13, Appl
40	340.5	12.2	267	1	US-08-378-7618-74 Sequence 74, Appl
41	326	11.7	267	1	US-08-485-286-74 Sequence 74, Appl
42	326	11.6	247	1	US-08-477-1848-6 Sequence 6, Appl
43	324	11.6	247	1	US-08-477-1848-6 Sequence 6, Appl
44	324	11.6	247	2	US-08-846-300-6 Sequence 6, Appl
45	324	11.6	247	2	US-08-846-300-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-776-059-35
Sequence 35, Application US/087760599
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LANTIER, Hans
INVENTOR: LANTIER, Hans
APPLICANT: BNP, BNP
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (HML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 0599
CURRENT FILING DATE: 1999-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
INVENTOR: LANTIER, Hans
INVENTOR: BNP, BNP
SEQ ID NO: 35
SEQ ID NO: 35
LENGTH: 564
TYPE: PRT
ORGANISM: Vicia album
US-08-776-059-35
Query Match 99.2%; Score 2770; DB 3; Length 564;
Best Local Similarity 99.1%; Pred. No. 1.6e-259;
Matches 526; Conserved: 4; Mismatches 1; Indels 0; Gaps 0;
1 YERLRLVHTQGTGEYERF...RIIIPYANGKQWMLPVP 531
34 YERLRLVHTQGTGEYERF...RIIIPYANGKQWMLPVP 531
61 OGGSDFRPAIDVNLVVA...YAGDSDYFPAAPGAE...FTGTRRS...LPVGSYDLE 120
94 OGGSDFRPAIDVNLVVA...YAGDSDYFPAAPGAE...FTGTRRS...LPVGSYDLE 153
121 YAGSDDFRPAIDVNLVVA...YAGDSDYFPAAPGAE...FTGTRRS...LPVGSYDLE 180
134 YAGSDDFRPAIDVNLVVA...YAGDSDYFPAAPGAE...FTGTRRS...LPVGSYDLE 213
181 NSGAEFEPVWMELETSWQSG...TGVCHTGVVNNP...FRAIPDGNVTL...INWADIASL 240
214 NSGAEFEPVWMELETSWQSG...TGVCHTGVVNNP...FRAIPDGNVTL...INWADIASL 273
241 AMLVTCGRPSSEVYRWELV...RVVADVTCGAEZETVRI...VGNMCMVDV...RDDFRG 300
274 AMLVTCGRPSSEVYRWELV...RVVADVTCGAEZETVRI...VGNMCMVDV...RDDFRG 333
301 NGTQMPSSKNNP...DNLWTKR...DGTISNGSLCTV...GTAGVYVIM...EDCNVATW 360

Thu Dec 11 16:09:53 2003

us-09-601-667c-4.1a1

Page 2

Db 334 NOTCLPESKNDPNOJLTIKROTIHNSGCLTITGTAAGYVMIPECNIAVEALTMQ 393
QY 361 IMNGTIINPRSNVLAASGIGKTLTVOITDYLQOGLAANDTAAREVITIGREDIC 420
Db 394 IMNGTIINPRSNVLAASGIGKTLTVOITDYLQOGLAANDTAAREVITIGREDIC 453
QY 421 MESNGSYWVETCVSSQONQMALVGDGSIKRONODCLTCGRDSVTVINIVCSAGS 480
Db 454 MESNGSYWVETCVSSQONQMALVGDGSIKRONODCLTCGRDSVTVINIVCSAGS 513
QY 481 SCORWFTNEGAILINNGTANPQAPLRIIIPATCKPQOMLPPV 531
Db 514 SCORWFTNEGAILINNGTANPQAPLRIIIPATCKPQOMLPPV 564

RESULT 2
US-08-776-059-43
Sequence 43, Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: ZINKE, Axel
APPLICANT: HOLGER
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 059B
EARLIER FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 263
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-43

Query Match 50.4%; Score 1406; DB 3; Length 263;
Best Local Similarity 98.9%; Pred. No. 6, 1e-128;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 269 DMYTCSSEPTVRIYGRNMCVDVDDPDDPQOICLWPSKSNDDPQJLTIKEDGTRS 328
Db 1 DMYTCSSEPTVRIYGRNMCVDVDDPDDPQOICLWPSKSNDDPQJLTIKEDGTRS 60
QY 329 NSCLTITGTAAGYVMIPECNIAVEALTMQIMNGTIINPRSNVLAASGIGKTLT 388
Db 61 NSCLTITGTAAGYVMIPECNIAVEALTMQIMNGTIINPRSNVLAASGIGKTLT 120
QY 389 VQITDYLQOGLAANDTAAREVITIGREDICMESNGSYWVETCVSSQONQMALVGDG 448
Db 121 VQITDYLQOGLAANDTAAREVITIGREDICMESNGSYWVETCVSSQONQMALVGDG 180
QY 449 SIRPKONODCLTCGRDSVTVINIVCSAGSQQWVFTNEGAILINNGTANPQAPLRII 508
Db 181 SIRPKONODCLTCGRDSVTVINIVCSAGSQQWVFTNEGAILINNGTANPQAPLRII 240
QY 509 PKLRRIIIPATCKPQOMLPPV 531
Db 241 PKLRRIIIPATCKPQOMLPPV 263

RESULT 3
US-08-776-059-33
Sequence 33, Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen

APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 059B
EARLIER FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 264
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-33

Query Match 50.4%; Score 1406; DB 3; Length 264;
Best Local Similarity 98.9%; Pred. No. 6, 1e-128;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 269 DMYTCSSEPTVRIYGRNMCVDVDDPDDPQOICLWPSKSNDDPQJLTIKEDGTRS 328
Db 2 DMYTCSSEPTVRIYGRNMCVDVDDPDDPQOICLWPSKSNDDPQJLTIKEDGTRS 61
QY 329 NSCLTITGTAAGYVMIPECNIAVEALTMQIMNGTIINPRSNVLAASGIGKTLT 388
Db 62 NSCLTITGTAAGYVMIPECNIAVEALTMQIMNGTIINPRSNVLAASGIGKTLT 121
QY 389 VQITDYLQOGLAANDTAAREVITIGREDICMESNGSYWVETCVSSQONQMALVGDG 448
Db 122 VQITDYLQOGLAANDTAAREVITIGREDICMESNGSYWVETCVSSQONQMALVGDG 181
QY 449 SIRPKONODCLTCGRDSVTVINIVCSAGSQQWVFTNEGAILINNGTANPQAPLRII 508
Db 182 SIRPKONODCLTCGRDSVTVINIVCSAGSQQWVFTNEGAILINNGTANPQAPLRII 241
QY 509 PKLRRIIIPATCKPQOMLPPV 531
Db 242 PKLRRIIIPATCKPQOMLPPV 264

RESULT 4
US-08-776-059-31
Sequence 31, Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: ZINKE, Axel
APPLICANT: HOLGER
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 059B
EARLIER FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 263
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-31

Query Match 46.0%; Score 1285; DB 3; Length 253;
Best Local Similarity 99.6%; Pred. No. 3e-116;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YERLALVHTQTEBSEFFITLADYSSGSFNEIFLQSTIFVSDQSFVLYELIN 60

Db 2 YERIRLKVHTQVGEYFFRTLLARDVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSI 61
Qy 61 QGGDSITLADITVNLVYVAYOGDSYFLKADAPRGATMLFTGTSSLPFGSYDPLER 120
Db 62 QGGDSITLADITVNLVYVAYOGDSYFLKADAPRGATMLFTGTSSLPFGSYDPLER 121
Qy 121 YAGHRDQIPGIDILQSVYTLARPGSGSTRQASILLIQMISEAARFPIIMRAQYI 180
Db 122 YAGHRDQIPGIDILQSVYTLARPGSGSTRQASILLIQMISEAARFPIIMRAQYI 181
Qy 181 NSGASLFDVYMLBLETSMGQOSTVOYHSTGVFNNPILAIIPGPFVLTNVDVIAEL 240
Db 182 NSGASLFDVYMLBLETSMGQOSTVOYHSTGVFNNPILAIIPGPFVLTNVDVIAEL 241
Qy 241 AMLFVCGERS 252
Db 242 AMLFVCGERS 253

RESULT 5

US-08-776-059-39
Sequence 39, Application US/08776059B
Patent No. 6272368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
INVENTOR: LENTZEN, Hans
APPLICANT: BUCH, Jürgen
APPLICANT: ZINKS, Holger
TITLE OF INVENTION: RECOMBINANT NISTLENOB LECTIN (NML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
INVENTOR: SBO ID NOS: 56
INVENTOR: SBO ID NOS: 56
SBO ID NO: 31
SBO ID NO: 31
LENGTH: 235
TYPES: PRT
ORGANISM: Viscum album
US-08-776-059-39

Query Match 42.9%; Score 1197; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 8.9e-108;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 FRTLLADVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSITAIIVTNLV 77
Db 1 FRTLLADVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSITAIIVTNLV 60
Qy 78 VAYOGDSYFLKADAPRGATMLFTGTSSLPFGSYDPLER 137
Db 61 VAYOGDSYFLKADAPRGATMLFTGTSSLPFGSYDPLER 120
Qy 138 SVYTLARPGSGSTRQASILLIQMISEAARFPIIMRAQYI 180
Db 121 SVYTLARPGSGSTRQASILLIQMISEAARFPIIMRAQYI 180
Qy 198 SWGQOSTVOYHSTGVFNNPILAIIPGPFVLTNVDVIAEL 240
Db 181 SWGQOSTVOYHSTGVFNNPILAIIPGPFVLTNVDVIAEL 241

RESULT 6

US-08-378-761A-77
Sequence 77, Application US/08378761A
Patent No. 5635394
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HAY, TIMOTHY D

APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESS: ANDREA T. BORUCKI
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/378,761A
FILING DATE: 2003-08-19
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 382728
TELEPHONE: (317) 337-4846
INFORMATION FOR SBO ID NO: 77
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
STRANDS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-761A-77

Query Match 42.7%; Score 1191.5; DB 1; Length 540;
Best Local Similarity 47.6%; Pred. No. 1.2e-106;

Matches 254; Conservative 84; Mismatches 177; Indels 19; Gaps 10;

Qy 9 THTGTGEYFFRTLLARDVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSI 66
Db 13 THTGTGEYFFRTLLARDVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSI 70
Qy 67 THTGTGEYFFRTLLARDVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSI 122
Db 71 THTGTGEYFFRTLLARDVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSI 130
Qy 123 GRDIDILQSVYTLARPGSGSTRQASILLIQMISEAARFPIIMRAQYI 179
Db 121 GRDIDILQSVYTLARPGSGSTRQASILLIQMISEAARFPIIMRAQYI 180
Qy 180 NSGASLFDVYMLBLETSMGQOSTVOYHSTGVFNNPILAIIPGPFVLTNVDVIAEL 240
Db 181 NSGASLFDVYMLBLETSMGQOSTVOYHSTGVFNNPILAIIPGPFVLTNVDVIAEL 241
Qy 241 AMLFVCGERS 252
Db 242 AMLFVCGERS 253
Qy 357 THTGTGEYFFRTLLARDVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSI 66
Db 356 THTGTGEYFFRTLLARDVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSI 70
Qy 417 THTGTGEYFFRTLLARDVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSI 66
Db 426 THTGTGEYFFRTLLARDVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSI 70
Qy 477 THTGTGEYFFRTLLARDVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSI 66
Db 478 THTGTGEYFFRTLLARDVYSSGSFSENFILROSTIPVSDAQRFVLTNVOGDSI 70

Thu Dec 11 16:09:53 2003

us-09-601-667c-4.xai

Page 5

APPLICANT: WALSH, TERENCE A
 APPLICANT: HEY, TIMOTHY D
 APPLICANT: MORGAN, ALICE ER
 TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
 TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
 NUMBER OF SEQUENCE: USING
 CORRESPONDENCE ADDRESS: 31
 ADDRESSER: ANDREA T. BORUCKI
 STREET: 9330 ZIONSVILLE ROAD
 CITY: INDIANAPOLIS
 STATE: IN
 COUNTRY: US
 ZIP: 46268
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/378,761A
 FILING DATE: 26-JAN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BORUCKI, ANDREA T
 REGISTRATION NUMBER: 33651
 REFERENCE/DOCKET NUMBER: 38272B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (317) 337-4846
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 STANDARDS: single
 TOPOLOGY: linear
 IS-08-378-761A-71
 MOLECULE TYPE: protein

Query Match	16.7%	Score 466.5	DB 1	Length 250
Best Local Similarity	42.6%	Pred. No. 5.7e-37		
Matches 107	Conservative 37	Mismatches 82	Indels 25	Gaps 6
Qy	1	THQTGKEFRATLTPLETPYSGFSSSENFRLKSGTIPSPDNRQVLYELNQGSQSLTA	68	
Db	9	TEBANSQSKQFIALLRNL-RGCHIDIPVLPPT-TLGRNRYIVLSSDTSIEIV	66	
Qy	69	AIDVYNLYVAAQKQSGSYFENRANRAEHLFGTGTASSLPENQSYVDLEEVGK-RNQ	127	
Db	67	GIDVNAVYVARRKGSSTFLKRASSASDYFLTGDDHSLPEYGVGLDEMHQSRQ	126	
Qy	128	IFPGIDQLQSYLTPFGSGTQTQTSITLIIOMSEANRPLFLNARQINSQSL	187	
Db	127	IFPGIDQLTHGISFSSGADNEERATLIVIGMAEAAFRYSINRYSIGTDRQ	186	
Qy	188	PDVYMLELFGSGQSYGVSHDQVFNPNFILAIPQNGEYTVITVVD		
Db	187	PDAMNISNNH-DNIRGVDSYQDTFPGQ-----VTLVIRNEEYIVDSLSHTP	235	
Qy	237	IASLAIATLTPVC	247	
Db	236	VAVIALMLTPVC	246	

US-08-465-286-71
Sequence 71, Application US/08465286
Patent No. 5646026
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME RNA

1 TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
2
3 TITLE OF INVENTION: USING
4
5 NUMBER OF SEQUENCES: 81
6
7 NUMBER OF SEQUENCES: 81
8
9 ADDRESSER/AGENT: BOWUCKI
10
11 ADDRESSER/AGENT: BOWUCKI
12
13 STREET: 5130 ZIONSVILLE ROAD
14
15 CITY: INDIANAPOLIS
16
17 STATE: IN
18
19 COUNTRY: US
20
21 ZIP: 46268
22
23 COMPUTER READABLE FORM:
24
25 MEDIUM TYPE: floppy disk
26
27 COMPUTER: IBM PC compatible
28
29 OPERATING SYSTEM: PC-DOS/MS-DOS
30
31 SOFTWARE: PatentIn Release #1.0, Version #1.25
32
33 CURRENT APPLICATION DATA:
34
35 APPLICATION NUMBER: US/08/485,286
36
37 FILING DATE:
38
39 CLASSIFICATION: 435
40
41 PRIORITY APPLICATION DATA:
42
43 APPLICATION NUMBER: US 08/378761
44
45 FILING DATE: 05-21-1992
46
47 ATTORNEY/AGENT INFORMATION:
48
49 NAME: BOWUCKI
50
51 ADDRESSER/AGENT: BOWUCKI
52
53 REGISTRATION NUMBER: 336451
54
55 REFERENCE/DOCKET NUMBER: 382728
56
57 TELECOMMUNICATION INFORMATION:
58
59 TELEPHONE: (317) 337-4946
60
61 INFORMATION FOR SEQ ID NO: 71:
62
63 SEQUENCE CHARACTERISTICS:
64
65 LENGTH: 250 amino acids
66
67 TYPE: amino acid
68
69 STRANDEDNESS: single
70
71 TOPOLOGY: linear
72
73 MOLECULE TYPE: protein
74
75 IS-08-485-286-71

	Query Match	Best Local Similarity	16.7%; Score 466.5; DB 1; Length 250;
	Matches	107; Conservative	42.6%; Pred. No. 5.7e-37; Mismatches 82; Indels 25; Gaps 6
Qy	THQTGKEKPEPTLILAPYVSSSPSSPILPAGTIVSQVAPVYELTQSGQSTTA	68	
Db	9 TEATGSSKQPIFALNRFL-RGLIHIDIPVLPDPT-FLQENRYVELNSQTSISIV	66	
Qy	69 AIDVNLVYVQAQDSYELTADPAKGAFTLPTGTSSILSPNSQSPLELRYAGR-RDQ	127	
Db	67 GIDVNLVYVQAQDSYELTADPAKGAFTLPTGTSSILSPNSQSPLELRYAGR-RDQ	126	
Qy	128 IFPGIDQGSVTLAPFGSGRRDASITLILQMSAARAPVILPAPKQVINSASFL	187	
Db	127 IFPGIDQGSVTLAPFGSGRRDASITLILQMSAARAPVILPAPKQVINSASFL	186	
Qy	188 EDVYLELTSMQSGSYVSHSDYENNPRIALAPENAPVILINVAQD-----V	236	
Db	187 EDVYLELTSMQSGSYVSHSDYENNPRIALAPENAPVILINVAQD-----V	235	
Qy	237 ISALTIAPVPC 247		
Db	236 VAVATLAPVPC 246		

RESULT 11
 US-08-356-786-10
 Sequence 10, Application US/08356786
 Patent No. 5677305
 INVENTOR: GERSHBERG, JONATHAN;
 APPLICANT: Oppenheimer, James S.
 APPLICANT: Oppenheimer, Herman
 APPLICANT: Houscor, U. I.
 APPLICANT: Ring, David B.
 TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
 TYPE OF INVENTION: Marker

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Plichter, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIORITY INFORMATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Plichter, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRF-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-10

Query Match 15.0%; Score 418; DB 2; Length 534;
Best Local Similarity 27.8%; Pred. No. 9,6e-32;
Matches 149; Conservative 76; Mismatches 171; Indels 140; Gaps 20;
9 THQTGEEFRPITLLADYVSSGS-ESNEIPL-ROSTIPVSDAPFVVELTNGGDSI 66
16 TQATVQSTNFIKAVKRLTGADVHEIPLVPRVGLPIN-QEFLVLSNHAESV 73
67 TTAIDVTNLVVAQKQSYPLR-DAPRGA-THLFTGR-FRESLFRNGSYDLERYA 122
74 TLAIDVTNAVVGRAAGNSAYPHPDQEDBAITLFTDVQRXYTAFQGNIDRLQA 133
123 GR-RDQIPLGIDQIGSYPLR-FGASTRQASILLIOMISPAAREPILMARQ 178
134 GMLKEMIELANGPLEKIASLYVSGTQPLFLASRFITICQWISBAFQYIEGEMT 193
179 YNSGASFLPVYMLELTSNGQSTQVQSTHSDGVFNNPRLALPGRFVTLNVDYA 238
194 KIRNRSAPDPISVITLNSWKLSTIQSNQGFASPIQDORNSKFSYVDSILIP 253
239 SLALNLFVCGERSSDQVYMYTIRPY-AD-----DY 271
254 IIALVYRCAPRESSQ-FSLIRPVVPRNADVCMBELQVQSGFELKXRGETVXI 309
272 TCSASEPFAIVGRNGV-----CDVRDDPDHNGQIQAMPKX-- 310
310 SCASGTFPAVGMWKAQAPKQLRMGMINTYQSTVADPKERFASLETATYH 369
311 ---NNDPMQMTIKDQSTRNSG---CLTYGTAGVYVAFPCNTANRATIMQNG 363
370 LQIN-----LNRDSATYFOARERGA-----YNG 395
364 KNTIIPRSLVLAASGILK-----TLITVQLIDYTLQO----- 398
396 QSLVVSASISSSGSGSGGSGGSGGSDIQWTQSSSLASIGRPVSLTCSADQION 455
399 --GMLAGNUTAPREVITYGFRLL-----CHESNGQSVWVETVSSQGNRMALY 445

Db 456 SLNMGQEDPDGRIELIATVATSSLDGVPRKSGSGSDVSLT-LSLSSEDPFVY 510
RESULT 12
US-07-901-707-1
Sequence 1, Application US/07901707
Patent No. 5376546
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Bernhardt, Susan F.
APPLICANT: Carroll, Steve F.
TITLE OF INVENTION: Materials Comprising and Methods of
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIORITY INFORMATION DATA: US 07/787,567
APPLICATION NUMBER: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greca E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
LENGTH: 267 amino acids
TYPE: amino acid
SEQUENCE CHARACTERISTICS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-901-707-1
Query Match 13.9%; Score 387; DB 1; Length 267;
Best Local Similarity 40.0%; Pred. No. 3.2e-29;
Matches 102; Conservative 45; Mismatches 96; Indels 12; Gaps 8;
9 THQTGEEFRPITLLADYVSSGS-ESNEIPL-ROSTIPVSDAPFVVELTNGGDSI 66
13 TQATVQSTNFIKAVKRLTGADVHEIPLVPRVGLPIN-QEFLVLSNHAESV 70
67 TTAIDVTNLVVAQKQSYPLR-DAPRGA-THLFTGR-FRESLFRNGSYDLERYA 122
71 TLAIDVTNAVVGRAAGNSAYPHPDQEDBAITLFTDVQRXYTAFQGNIDRLQA 130
123 GR-RDQIPLGIDQIGSYPLR-FGASTRQASILLIOMISPAAREPILMARQ 178
131 GMLKEMIELANGPLEKIASLYVSGTQPLFLASRFITICQWISBAFQYIEGEMT 190
179 YNSGASFLPVYMLELTSNGQSTQVQSTHSDGVFNNPRLALPGRFVTLNVDYA 238
191 KIRNRSAPDPISVITLNSWKLSTIQSNQGFASPIQDORNSKFSYVDSILIP 250
239 SLALNLFVCGERSS 253

Thu Dec 11 16:09:53 2003

us-09-C01-667c-4.ral

QY 239 SLALMPCGCRPSS 253
Db 251 IIALWYRCAPPPSS 265

RESULT 15

US-08-425-336-1
Sequence 1, Application US/08425336
Patent No. 5,210,628
GENERAL INFORMATION:
APPLICANT: Bettef, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS: O'Toole, Gerstein, Murray & Borun
FIRM: 6300 Sears Tower, 233 South Wacker Drive
CHICAGO, ILLINOIS 60606-6402
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425/336
CLASSIFICATION: 18-24R-1995
PRIORITY NUMBER: 08/064,691
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 13-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
FIRM: 1800 Summit St.
REFERENCE/DOCKET NUMBER: 1-36,988
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
SOURCE: cDNA library
MOLECULE TYPE: protein
US-08-425-336-1

Query Match 13.9%; Score 387; DB 1; Length 267;

Best Local Similarity 40.0%; Pred. No. 3.2e-29; Mismatches 96; Indels 12; Gaps 8;

Matches 102; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

QY 9 TQOTGEYFRITLNDYSSGS-FSEIPL-ROSTIPVSDQRFVLINQCGDSI 66

Db 13 TQAKTVOSTINEIARGLTADVAHSEIPLVEMVGLPIN-QEFLVLSHAELSV 70

QY 67 TAAIDVYNLYTAKQDQGRFIR-DARGAR-TLFTGT-TRESIPNNSIPDIEVIA 122

Db 71 TIALDVYNLYTAKQDQGRFIR-DARGAR-TLFTGT-TRESIPNNSIPDIEVIA 130

QY 123 GH-ADQIFGIDILQSVYALRF--PGSTRIOASITLTIOMISSEARFPIIMBARQ 178

Db 131 GUNRENIEIAGNPISAEISALVYVSTGTOTLPTANSPICIOMISSEARFQYIEGEMT 190

QY 179 YINSGASFLPYVMELETSNGCOSTOVQNSTDQVFNNRILALPFGFVTLNNRDVYA 238
Db 191 RIRYNNRSDPDSVITLNSMGRSLTALQSNQAFASIDLCRRNSKSTVYDVSILIP 250
QY 239 SLALMPCGCRPSS 253
Db 251 IIALWYRCAPPPSS 265

Search completed: December 11, 2003, 14:11:32
Job time: 19.3644 secs

Thu Dec 11 16:10:02 2003

us-09-601-667c-6.rpr

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 8.17513 Seconds
(without alignments)
3093.817 Million cell updates/sec

Title: US-09-601-667c-6

Perfect score: 1420

Sequence: 1 DVTGASAEPTVRIYGRNGM.....RRIIVYATGRKPMQMLPVP 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 283308 seqs, 9616862 residues

283308

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting first 45 summaries

Database:

1: pir76.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1339.5	94.3	264	2	PD0019	mistletoe lectin I
2	1329	93.6	265	2	JM0090	lectin I B chain - ricin d precursor
3	913	64.3	576	1	RLCSD	ricin E - calicor b
4	891.5	62.8	263	2	S06330	agglutinin precus
5	779.7	56.1	564	1	RLCSAG	abrin-a precursor
6	773.5	54.5	528	1	TLZLSA	abrin-b precursor
7	759.5	53.8	527	2	S12430	adrian-g precursor
8	758.5	53.4	528	2	S12431	adrian-g precursor
9	558.5	39.3	570	2	SG6627	endo-1,4-beta-xylanase B (EC 3.2.2)
10	558.5	39.3	477	1	DS0589	chitinase (EC 3.2.2)
11	149.5	10.5	383	2	T34603	arabinofuranosidase
12	146.5	10.3	383	2	T34603	glucan endo-1,3-beta
13	145.5	10.2	377	2	UC7535	protease RFI - R
14	130	9.2	525	2	T35697	arabinofuranosidase
15	124	8.7	475	2	T35697	glucan endo-1,3-beta
16	119	8.4	475	2	T35697	protease RFI - R
17	107.5	7.6	553	2	A88515	probable polypepti
18	107.5	7.4	553	2	A88515	actinobiovin precu
19	104.5	7.4	464	2	T35943	probable hydrolyti
20	104.5	7.4	464	2	T35943	probable polypepti
21	99.5	7.0	451	2	T34988	beta transducin-11
22	99.5	7.0	451	2	T34988	hypothetical prote
23	97.5	6.9	1633	2	S76086	mosaicocidal toxic
24	95.5	6.7	386	2	AE1996	hypothetical prote
25	95.5	6.7	870	2	S27514	cyclostin vrbha pre
26	94.5	6.7	471	2	A41478	hypothetical prote
27	94	6.6	357	2	T21152	hypothetical prote
28	92	6.5	1067	2	T28663	polypeptide N-acet
29	91	6.4	571	2	I37405	

30	90.5	6.4	545	2	S21582	alpha-galactosidase
31	90	6.3	2229	2	T61919	hypothetical prote
32	90	6.3	4180	2	G83559	hypothetical prote
33	89	6.3	542	2	A49114	protein-tyrosine k
34	89	6.3	1708	2	AE1866	WD-40 repeat prote
35	88.5	6.2	1773	2	A47666	structural polypep
36	88.5	6.2	1008	2	T32986	hypothetical prote
37	87	6.1	1526	2	A69222	hypothetical prote
38	86.5	6.1	1526	2	AC2239	WD-40 repeat prote
39	86.5	6.1	1526	2	H83452	probable short-cha
40	86.5	6.1	1526	2	AE0930	probable bacteriop
41	86.5	6.1	1526	2	AE0930	probable bacteriop
42	86.5	6.1	1526	2	AE0930	probable bacteriop
43	85.5	6.0	1032	2	T43287	beta-1,3 exoglucan
44	85	6.0	157	2	H70902	hypothetical prote
45	84.5	6.0	292	2	S58857	botulinum neurotox

ALIGNMENTS

RESULT 1

PD0019

mistletoe lectin I B chain - Viscum album (fragment)

C/Species: Viscum album

C/Accession: PD0019

C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999

R/Eschschburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, B.

Biochem. Biophys. Res. Commun. 247, 367-372, 1998

A/Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum

A/Reference number: PD0019, MIM:96308123, PMID:9642133

A/Accession: PD0019

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A/Module type: protein

A:Molecule type: Protein	
A:Residues: 1-265 <SOL>	
C:Superfamily: ricin; rRNA: rRNA: N-glycosylase homology	
E:Keywords: glycoprotein	
F:1,6,19:Binding site: carbohydrate (asn) (covalent) #status experimental	
Query Match	39.6% Score 129; DB 2
Best Local Similarity	95.5% Pred. No. 1.1e-104
Matches 252; Conservative 2; Mismatches 8; Indels 2; Gaps 2	

Qy	1	DVDTGASAESEPTAIVKSNMCVYDDDFHDDNIOIOLMPSKSNPNPQWLTIKSDGRTS	60
Db	1	DVDTGASAESEPTAIVKSNMCVYDDDFHDDNIOIOLMPSKSNPNPQWLTIKSDGRTS	60
Qy	61	NSGCLTGYTAGYVYVIFDNCNVAEAKITWQIMQNCITINPSKNIYLAASGIGITLT	120
Db	61	NSGCLTGYTAGYVYVIFDNCNVAEAKITWQIMQNCITINPSKNIYLAASGIGITLT	120
Qy	121	VQTLDTLTCGMLANDNPHEITLIGFRDLCHSNKSGSVAWITCVSSQND-FMALYED	179
Db	121	VQTLDTLTCGMLANDNPHEITLIGFRDLCHSNKSGSVAWITCVSSQNDKMAIYED	180
Qy	180	GSIRPKNOPOCLTCGDSVETVINYINVCASSGQWFMTEGALINLKNGLANDVQA	239
Db	181	GSIRPKNOPOCLTCGDSVETVINYINVCASSGQWFMTEGALINLKNGLANDVQA	240
Qy	240	NPGLRRRIIPATKRNQW-LPY 262	
Db	241	NPGLRRRIIPATKRNQW-LPY 264	

RESULT 3

Ric1in D precursor - castor bean
 N:contains: rRNA N-glycosidase (EC 3.2.2.22)
 C:species: Ricinus communis (castor bean)
 C:place: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 16-Jul-1999
 A:accession: A24041, S20513, A24641, A033172, A24014, A03374, S10903
 A:author: A. Chailion, A. C. Murray, B. S. Ladin, B. F. Houston, L. L. Weaver, R. F. Nusslein-Volhard
 A:title: Genomic cloning and characterization of a ricin gene from *Ricinus communis*.
 A:feature: genomic number: A24041, MUID:186067214, PMID:2999712
 A:molecule type: DNA
 A:residues: 1-576 (<HML>)
 A:cross-references: GB:X03179, NID:g21082; PIND:CA26936.1; PID:g21083
 R:legat: J. M. Roberts, L. M.
 A:publ: Mol. Biol. Cell, 1992, 3, 515-525, 1992
 A:publ: Mol. Biol. Cell, 1992, 3, 515-525, 1992
 A:reference number: S20513, MUID:92163016, PMID:1371405
 A:accession: S20513
 A:molecule type: DNA
 A:residues: 1-576 (<RFB>)
 A:cross-references: EMBL:X52908, NID:g21084; PIND:CA37095.1; PID:g21085
 R:lamh, P. I. Roberts, L. M.; Lord, J. M.
 A:publ: Biochem. J., 1989, 265-270, 1989
 A:publ: Biochem. J., 1989, 265-270, 1989
 A:feature: Nucleotide sequence of cloned cDNA coding for preproprotein.
 A:accession: A24614, MUID:85179479, PMID:3838723
 A:molecule type: mRNA
 A:residues: 13-75, 'D', 77-550, 'R', 552-576, <LHM>
 A:cross-references: GB:X02388, NID:921077; PIND:CA26230.1; PID:g21078
 R:oshaltke, S.; Pumatnu, G.; Pumatnu, M.
 A:publ: Agric. Biol. Chem. 42, 1267-1274, 1978
 A:publ: Agric. Biol. Chem. 42, 1267-1274, 1978
 A:title: Isolation and sequences of peptic peptides, and the complete sequence of Ile ch
 A:feature: genomic number: A03372
 A:accession: A03372
 A:molecule type: protein
 A:residues: 35-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'V', 286-288, 290-302, <YOS>
 A:note: T. Pumatnu cites the others in the series providing experimental details for the
 R:shaltke, S.; Pumatnu, G.
 A:publ: EMS Lett. 191, 121-124, 1985
 A:publ: EMS Lett. 191, 121-124, 1985
 A:title: Isolated amino acid sequence of the B-chain of ricin D due to loss of tryptophan

[illegible]

Thu Dec 11 16:10:02 2003

us-09-601-667c-6.rpt

Page 4

A>Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A.Reference number: A39761; PMID:91201329; PMID:2016300
A.Accession: A39761
A.Molecule type: protein
A.Cross-references: GB:581872
A.Residues: 187, 2-251 <EVR>
A>Note: residues 1-9 were derived from the synthesized primer
R:Klimza, M.; Sumiizawa, T.; Funatsu, G.
A>Title: Bioelectron. Biochem. 57, 165-169, 1993
A>Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic lectins from *Canavalia maritima*
A.Reference number: JCI398; PMID:93169023; PMID:7763422
A.Content: seeds
A.Molecule type: protein
A.Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-358 <INV>
A.Experimental source: seed
R:Evensen, G.; Mathiesen, A.; Sundan, A.
A>Description: Direct molecular cloning of two distinct abrin A-chains.
A.Reference number: S14471
A.Accession: S14472
A.Molecule type: protein
A.Molecule type: DNA
A.Residues: 'ME', 2-221 <EV2>
A>Cross-references: EMBL:X54873; NID:G16090; PIDN:CA38655.1; EID:gi16091
R:Chen, Y.L.; Chow, L.P.; Tseng, A.; Lin, J.Y.
EMBL Lett. 309, 115-118, 1992
A>Title: The complete primary structure of abrin-a, B chain.
A.Reference number: S24133; PMID:92371656; PMID:1505674
A.Molecule type: protein
A.Accession: S24133
R:Lin, S.H.; Chow, L.P.; Chen, Y.C.; Chen, J.K.; Lin, J.Y.
Eur. J. Biochem. 240, 564-569, 1996
A>Title: Probing the domain structure of abrin-a by tryptic digestion.
A.Reference number: S74110; PMID:97009345; PMID:8856055
A.Accession: S74110
A.Molecule type: protein
A.Residues: 83-108,154-172 <LIN>
A.Cross-references: EMBL:X54873
A.Accession: S74111
A.Molecule type: protein
A.Residues: 262-276, 'X', 278-280,329-348,369-388,399-418 <INV>
A.Experimental source: seed
C>Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inflicts damage on the cell surface. The A and B chains are linked by a single disulfide bond.
C>Superfamily: ricin; rRNA_N-glycosidase homology
C>Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid; protein
F:7-216/Domestic: rRNA_N-chain A #status experimental <KCH>
F:261-558/Product: abrin-a-chain B #status experimental <KCH>
F:283-325,336-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
F:2/Modified site: pyrroloindane carboxylic acid (Gln) #status experimental
F:4,113,193,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:164,167/Active site: Glu, Arg #status predicted
F:247-249,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
F:368-412/Binding site: B-acetylglucosamine (Asp, Asn) #status predicted
F:368-412/Binding site: B-acetylglucosamine (Asn) (covariant) #status experimental
F:500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 54.5% Score 773.5; DB 1; Length 528;
Best Local Similarity 54.9%; Pred. No. 1.8e-57;
Matches 14; Conservative 45; Mismatches 70; Indels 1; Gaps 1;

OY CSAS: BFTVATVBNKACVAVXDDEPHQNOGLAPSSKNPDVQMLTRRQDTRIRNS 63
Db CSARHRYVAKIGCDNRCKQCVVDVYDGNHNNKIKKCDLSENLQVATLSTRTIRNR 328
64 CLTVGTAGVAVVIDDQNAFVATVQVIMQNGKGVNIPNSVVAALSSGIRKTLT 123
Db CLTVGARGSVVVIDQTSAAVAVRYVINDQGITINPESLVLLVASSSGVGRITV 386

[illegible]

Thu Dec 11 16:10:02 2003

us-09-601-667c-6.rpr

Page 5

RESULT 8
Abn-4 precursor - Indian 11cortic
N/Contains: RNA N-glycosidase homology
C/Species: Abn-4 precursor (Indian 11cortic)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1997
C/Accession: S16022
R/Wood, K.A.; Lord, J.M.; Nawrzymiak, E.T.; Patlak, M.
A/Title: Preproabrin: genomic cloning, characterization and the expression of the A-chain
A/Reference number: S16022; PMID:9166957; PMID:2050149
A/Accession: S16022
A/Status: preliminary
A/Residues: 562 amino acids
A/Cross-references: EMBL:X55667; NID:q16084; PIDN:CA32902.1; PID:q16085
C/Comment: Abn-4 consists of an A chain, which inhibits protein synthesis by inactivating
C/Superfamily: ricin; RNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid
F/35-265/Product: abn-4 chain A status predicted <ACH>
F/41-280/Domain: RNA N-glycosidase homology <RNG>
F/295-562/Product: abn-4 chain B status predicted <RCH>
F/31-253/360-400/403-441/448-483/487-528/529-562/Region: 40-residue repeats
F/108-147/259-310/313-359/363-400/403-441/448-483/487-528/Region: 40-residue repeats
F/198-201/Active site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/234-287/395-435-436/Binding site: carbonyl (Asn) (covalent) #status predicted
F/281-303/320-339/363-380/451-464/490-507/Diisulfide bonds: #status predicted
F/322/346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/534/555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 53.5%; Score 759.5; DB 2; Length 562;
Best Local Similarity 54.1%; Pred. No. 2.9e-56;
Matches 139; Conservative 45; Mismatches 72; Indels 1; Gaps 1;

QY 5 CSAS-EPTVIVGRNGKCVDDDFDNDQIQLPKSKNDPQWLTIRKDGTRNSG 63
DB 303 CSREYEVYIGDGRKQCVDDDFDNDQIQLPKSKNDPQWLTIRKDGTRNSG 362
QY 64 CLTGYVAGVYVWFEDQNTVARENTVQNGGTTINPSTVLAASGIGTTLTVOT 123
DB 363 CLTGYVAGVYVWFEDQNTVARENTVQNGGTTINPSTVLAASGIGTTLTVOT 422
QY 124 LDYTLGGQMLAGNDTAREVTVYGRDLQMGESGVVETCVSQNGQRMALYDCDSIR 183
DB 423 NDTLMRGKRGKNTSPVTSISGYSIDLCMQAGSNVWALDDCNKKRQGMALYDCDSIR 482
QY 184 PRQNDQDQITCGRSVSTVIVYSGAGSGQGVTFNKGALNLKGLAMVQANPFL 243
DB 483 SVQTNNDQLTSKGRQGSFVLAASGQVTFNKGALNLKGLAMVQANPFL 542
QY 244 RRTIIVPARGKQWML 260
DB 543 KQILLMPYRQKQWML 559

RESULT 9
Abn-4 precursor - Indian 11cortic (fragment)
N/Contains: RNA N-glycosidase homology
C/Species: Abn-4 precursor (Indian 11cortic)
C/Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
C/Accession: S32431; S34408
R/Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
A/Title: Primary structure of three distinct isoabirins determined by cDNA sequencing. C
A/Reference number: S32431; PMID:8421313
A/Accession: S32431
A/Molecule type: mRNA
A/Residues: 1528 amino acids

A/Cross-references: GB:M98346
R/Hung, C.; Lee, M.; Lee, T.; Lin, J.
A/Title: Primary structure of three distinct isoabirins determined by cDNA sequencing. C
A/Reference number: S34408
A/Accession: S34408
A/Molecule type: mRNA
A/Residues: 1528 amino acids
A/Cross-references: GB:M98346
C/Comment: Abn-4 consists of an A chain, which inhibits protein synthesis by inactivating
C/Superfamily: ricin; RNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid
F/35-265/Product: abn-4 chain A status predicted <ACH>
F/41-280/Domain: RNA N-glycosidase homology <RNG>
F/295-562/Product: abn-4 chain B status predicted <RCH>
F/31-253/360-400/403-441/448-483/487-528/529-562/Region: 40-residue repeats
F/108-147/259-310/313-359/363-400/403-441/448-483/487-528/Region: 40-residue repeats
F/198-201/Active site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/234-287/395-435-436/Binding site: carbonyl (Asn) (covalent) #status predicted
F/281-303/320-339/363-380/451-464/490-507/Diisulfide bonds: #status predicted
F/322/346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/534/555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 53.4%; Score 758.5; DB 2; Length 528;
Best Local Similarity 54.1%; Pred. No. 3.2e-56;
Matches 139; Conservative 46; Mismatches 71; Indels 1; Gaps 1;

QY 5 CSAS-EPTVIVGRNGKCVDDDFDNDQIQLPKSKNDPQWLTIRKDGTRNSG 63
DB 269 CSREYEVYIGDGRKQCVDDDFDNDQIQLPKSKNDPQWLTIRKDGTRNSG 328
QY 64 CLTGYVAGVYVWFEDQNTVARENTVQNGGTTINPSTVLAASGIGTTLTVOT 123
DB 329 CLTGYVAGVYVWFEDQNTVARENTVQNGGTTINPSTVLAASGIGTTLTVOT 388
QY 124 LDYTLGGQMLAGNDTAREVTVYGRDLQMGESGVVETCVSQNGQRMALYDCDSIR 183
DB 389 NDTLMRGKRGKNTSPVTSISGYSIDLCMQAGSNVWALDDCNKKRQGMALYDCDSIR 446
QY 184 PRQNDQDQITCGRSVSTVIVYSGAGSGQGVTFNKGALNLKGLAMVQANPFL 243
DB 449 SVQTNNDQLTSKGRQGSFVLAASGQVTFNKGALNLKGLAMVQANPFL 508
QY 244 RRTIIVPARGKQWML 260
DB 509 KQILLMPYRQKQWML 525

RESULT 10
Abn-4 precursor - European elder
N/Contains: RNA N-glycosidase homology
C/Species: Abn-4 precursor (European elder)
C/Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1997
C/Accession: S62627
R/Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
A/Title: The NeuAc(alpha-2-6)-Gal/GalNAc-binding lectin from elderberry (Sambucus r
A/Reference number: S62627; PMID:9620226; PMID:8631113
A/Accession: S62627
A/Status: preliminary
A/Residues: 529 amino acids
A/Cross-references: EMBL:U71122; NID:q141772; PIDN:AAQ9158.1; PID:q141773
A/Molecule type: mRNA
A/Residues: 1-570 <VNA>
A/Cross-references: GB:M98346
C/Comment: Abn-4 consists of an A chain, which inhibits protein synthesis by inactivating
C/Superfamily: ricin; RNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid
F/35-265/Product: abn-4 chain A status predicted <ACH>
F/41-280/Domain: RNA N-glycosidase homology <RNG>
F/295-562/Product: abn-4 chain B status predicted <RCH>
F/31-253/360-400/403-441/448-483/487-528/529-562/Region: 40-residue repeats
F/108-147/259-310/313-359/363-400/403-441/448-483/487-528/Region: 40-residue repeats
F/198-201/Active site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/234-287/395-435-436/Binding site: carbonyl (Asn) (covalent) #status predicted
F/281-303/320-339/363-380/451-464/490-507/Diisulfide bonds: #status predicted
F/322/346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/534/555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 39.3%; Score 558.5; DB 2; Length 570;
Best Local Similarity 46.1%; Pred. No. 2.6e-39;

Thu Dec 11 16:10:02 2003

us-09-601-667c-6.rpr

A45053
protease RPI - *Ratobacter faecitabidus*

C:Species: *Ratobacter faecitabidus*

C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 22-Oct-1999

C:Accession: A45053

C:SHIMOL, H.; Iimura, Y.; Ohtsuka, T.; Tadenuma, M.

C:Ref: J. Biol. Chem. 267, 25189-25192, 1992

C:Ref: J. Biol. Chem. 267, 25189-25192, 1992

C:Reference number: A45053; PMID:93094225; PMID:1339445

A:Accession: A45053

A:Status: preliminary

A:Molecule type: DNA, protein

A:Residues: 1-525 <SH1>

A:Cross-references: GB:010753; NID:9216923; PIDN:BA01585.1; PID:d1002060; PID:g912440

A:Experimental source: YIM-50

A>Note: sequence extracted from NCBI backbone (NCBIN:120149, NCBI:120151)

Query Match 9 24; Score 130; DB 2; Length 525;

Best local similarity 33.04; Pred. No. 0.0032;

Matches 35; Conservative 17; Mismatches 42; Indels 12; Gaps 5;

QY 2 DVTCSASPTVAIVGSMGCVDRDDPHDNOIQLPMSKANDPNQIWTIRKGTIRSN 61

DB 399 DVT-----TSYVGQNNCIDVPSDFTEKQIQVWNCNGTN--AQKVSFPDGTIRIN 450

QY 62 GSCL-TTYGT-AGYVMIPTCQVAREATIMQWENGITIRSN 105

DB 451 GKLDLRWMTIRNGEVQVQNCNHI--AQKFTLNAGDIDVYHAN 494

RESULT 15

arabinofuranosidase - *Streptomyces coelicolor*

C:Species: *Streptomyces coelicolor*

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Dec-1999

C:Accession: T35697

R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, January 1998

A:Reference number: Z21548

A:Accession: T35697

A:Status: preliminary; translated from GB/EMBL/DDB3

A:Residues: 12475 <MUR>

A:Cross-references: EMBL:AL021411; PIDN:CA16189.1; GSPDB:GN00070; SCODEB:SC7H1.02

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: abfB; SCODEB:SC7H1.02

Query Match 8.74; Score 124; DB 2; Length 475;

Best local similarity 24.14; Pred. No. 0.0091;

Matches 65; Conservative 33; Mismatches 116; Indels 56; Gaps 13;

QY 6 SASPTVAIVGSMGCVDRDDPHDNOIQLPMSKANDPNQIWTIRKGTIRSN-SC 64

DB 37 ASGSLAGNSN-RCIDVLAGSGDDGALQLVDKMGKT--NQWSTDTGRLTYVGDIC 93

QY 65 LTTVGYTA--GYVWIFDNTVAEATIMQWENGITIRSNLYV--AASSG-IGTTLT 120

DB 94 LDVSGATAPRTVQVSCSGANQO--WRNSDITVVGESGLCEAAGAGTANGTAVQ 151

QY 121 VQIDVTLGGWLAGNDIPAREVTI-----YGFRLCMESNGSSVWETCVSQNOR 173

DB 152 LWTGNGSNQWNGIATGPTDGCALPSTYRSGTVAIAQPSGVNVLKQFTVYTROR 211

QY 174 NALVGGGIRPKQNDQCLTGRDSYIVINIVSCAGSSGGRVY---FTMBEALINLN 230

DB 212 HLTVG-----STSSGSSGVSVSPFTNWDASAGQ 243

QY 231 GLADVAQANPKLRIIYIPATKPNQML 260

DB 244 N-ANQANAVPTL---FYFA---PKITIV 265

Search completed: December 11, 2003, 13:55:42
Job time: 9.17513 secs

FT VARIANT 231 231 N -> S OR T.
 FT VARIANT 231 233 NGL -> KGP.
 FT VARIANT 232 235 GLAM -> SLAM.
 SO SEQUENCE 264 AA: 28981 WM; 7D0DC326CFCF5A4 CRC64;

Query Match 94.3%; Score 1339.5; DB 1; Length 264;
 Best Local Similarity 95.8%; Pred. No. 2.9e-110;
 Matches 292; Conservative 27; Mismatches 9; Indels 1; Gaps 1;

DB 1 DPVTCASSEPTVRIYVGNKQVYDDDFHDQNGICLTPSKSNMDPQGLTIKDDTIS 60
 QY 1 DPVTCASSEPTVRIYVGNKQVYDDDFHDQNGICLTPSKSNMDPQGLTIKDDTIS 60
 DB 61 NSCLTGYGTAGYVMIIPDQNAVRENTIMQWNGITIPRSNLVLAASGKGTTLT 130
 QY 61 NSCLTGYGTAGYVMIIPDQNAVRENTIMQWNGITIPRSNLVLAASGKGTTLT 130
 DB 121 VQTLDTYLGQMLAGNDTAPREVTYGFHDLCMESGSAWVETCSQQNQ-RMALYGD 179
 QY 121 VQTLDTYLGQMLAGNDTAPREVTYGFHDLCMESGSAWVETCSQQNQ-RMALYGD 179
 DB 61 NSCLTGYGTAGYVMIIPDQNAVRENTIMQWNGITIPRSNLVLAASGKGTTLT 130
 QY 61 NSCLTGYGTAGYVMIIPDQNAVRENTIMQWNGITIPRSNLVLAASGKGTTLT 130
 DB 121 VQTLDTYLGQMLAGNDTAPREVTYGFHDLCMESGSAWVETCSQQNQ-RMALYGD 179
 QY 121 VQTLDTYLGQMLAGNDTAPREVTYGFHDLCMESGSAWVETCSQQNQ-RMALYGD 179
 DB 180 GSIRPKMDQCTISRUSVSTVINYSCGASGSRVFTNEGALLNLKGLMDVMA 240
 QY 180 GSIRPKMDQCTISRUSVSTVINYSCGASGSRVFTNEGALLNLKGLMDVMA 240
 DB 240 NPPLARRITTPATCKPMOMLTPV 262
 QY 240 NPPLARRITTPATCKPMOMLTPV 262
 DB 241 NPLARRITTPATCKPMOMLTPV 263

RESULT 2
 RCT_RICCO STANDARD; PRT; 576 AA.
 AC P02879; P02880;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ricin precursor [Contains: Ricin A chain (RNA N-glycosidase)]
 DB (EC 3.2.2.22); Ricin B chain)
 OS Ricinus communis (Castor bean)
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Cornales; Malvales; Euphorbiales; Euphorbiaceae; Ricinus.
 CX NCBL_14610=3989;
 CO NCBL_14610=3989;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86067214; PubMed=2999712;
 RA Halling K.C., Halling A.C., Murray E.R., Ladin B.F., Houston L.L.,
 RA Weaver R.F.;
 RA "Genomic cloning and characterization of a ricin gene from Ricinus
 ricinus";
 RL Nucleic Acids Res. 13:8019-8033(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92163016; PubMed=1371405;
 RA Tregear J.W., Roberts L.M.;
 RA "The lectin gene family of Ricinus communis: cloning of a functional
 ricin gene and three lectin pseudogenes";
 RL Plant Mol. Biol. 18:515-525(1992).
 RN [3]
 RP SEQUENCE OF 12-576 FROM N.A.
 RA MEDLINE=85179479; PubMed=3838723;
 RA Lamb A., Roberts L.M., Lord J.M.;
 RA "Nucleotide sequence of cloned cDNA coding for preproricin";
 RL Eur. J. Biochem. 181:265-270(1989).
 RN [4]
 RP SEQUENCE OF 36-302.
 RA Yoshitake S., Funatsu G., Funatsu M.;
 RA "Isolation and sequences of peptic peptides, and the complete
 sequence of the chain of ricin-D.";
 RL Agric. Biol. Chem. 42:1267-1274(1978).
 RN [5]
 RP SEQUENCE OF 315-576.

RA Funatsu G., Kimura M., Funatsu M.;
 RA "Primary structure of A1a chain of ricin D.",
 RL Agric. Biol. Chem. 43:2221-2224(1979).
 RN [6]
 RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
 RA MEDLINE=90344223; PubMed=1368517;
 RA Kimura Y., Kusuda H., Tada M., Takagi S., Funatsu G.;
 RA "Structural analysis of sugar chains from ricin A-chain variant";
 RL Agric. Biol. Chem. 54:157-162(1990).
 RN [7]
 RP MEDLINE=21480122; PubMed=11595934;
 RA Olines S., Kozlov J.V.;
 RA "Ricin";
 RL Toxicon 39:1723-1728(2001).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RA MEDLINE=87165993; PubMed=3558397;
 RA Montfort M., Villafraña J.E., Monzinger A.F., Ernst S.R., Katzin B.,
 RA Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.;
 RA "The three-dimensional structure of ricin at 2.8 A";
 RL J. Biol. Chem. 262:5398-5403(1987).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RA MEDLINE=91352004; PubMed=1681891;
 RA Katzin B.J., Collins B.J., Robertus J.D.;
 RA "Structure of ricin A-chain at 2.5 A";
 RL Proteins 10:251-259(1991).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
 RA MEDLINE=91352005; PubMed=1681892;
 RA Rutenber E., Robertus J.D.;
 RA "Structure of ricin B-chain at 2.5-A resolution";
 RL Proteins 10:260-269(1991).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
 RA MEDLINE=95082010; PubMed=7990130;
 RA Mason S.A., Tucker A.D., Thatcher D.R., Dedyshire D.J.,
 RA Pauplit R.A.;
 RA "X-ray structure of recombinant ricin A-chain at 1.8-A resolution";
 RL J. Mol. Biol. 244:410-422(1994).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
 RA MEDLINE=95714222; PubMed=8780513;
 RA Day P.J., Ernst S.R., Palmer A.E., Monzinger A.F., Pascal J.M.,
 RA Rutenber E., Robertus J.D.;
 RA "Structure and activity of an active site substitution of ricin A
 chain";
 RL Biochemistry 35:11098-11103(1996).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RA MEDLINE=97240820; PubMed=9086290;
 RA Yan X., Hollis T., Svinch N., Day P., Monzinger A.F., Milne G.W.,
 RA Robertus J.D.;
 RA "Structure-based identification of a ricin inhibitor";
 RL J. Mol. Biol. 266:1043-1049(1997).
 RN [14]
 RP MUTAGENESIS.
 RA MEDLINE=93166632; PubMed=1287657;
 RA Kin Y., Robertus J.D.;
 RA "Analysis of several key active site residues of ricin A chain by
 mutagenesis and X-ray crystallography";
 RL Protein Eng. 5:175-179(1992).
 RN [15]
 RP FUNCTION: Ricin is highly toxic to animal cells and to a less
 extent to plant cells. The A chain is responsible for inhibiting
 protein synthesis through the catalytic inactivation of 60S
 ribosomal subunits. It acts as a glycosylase that removes a
 specific adenine residue from an exposed loop of 28S ribosomal
 RNA. This modification is irreversible and prevents the support protein
 synthesis. The modified ribosomes are unable to support protein
 synthesis. The A chain can inactivate a few thousand ribosomes
 per minute, thus inactivating faster than the cell can make
 new ones. A single A-chain molecule can therefore kill an animal

FT	DISULFID	281	303		INTERCHAIN (BY SIMILARITY).
FT	DISULFID	320	339		BY SIMILARITY.
FT	DISULFID	363	380		BY SIMILARITY.
FT	DISULFID	451	464		BY SIMILARITY.
FT	DISULFID	490	507		BY SIMILARITY.
FT	MOL RES	35	35		PYROLIDONE CARBOXYLIC ACID
FT	CARBOND	234	234		(BY SIMILARITY)
FT	CARBOND	335	335		N-LINKED GLYCOC.
FT	CARBOND	435	435		N-LINKED GLYCOC.
SQ	SEQUENCE	562 AA;	62817 MW;	IPDAB067B7BA6278 C6C64,	POTENTIAL.

Query Match	53.5%;	Score 759.5;	DB 1;	Length 562;
Best Local Similarity	54.1%;	Pred.No. 4; e-59;		
Matches 133;	Conservative 45;	Mismatches 72;	Indels 1;	Gaps 1.

Dy	5	CSAS-EPTVATVERAKNCVDVADDDPHGDCIOLMPSKSNNDPQMLTFIKEDGTIRASGS	63
Dy	303	CSRLRIETVRICSGSDGVCLVHDIQDSNNTIAMCKDLREQLWLTLSKDSKTINSGK	362
Qy	64	CLITGYTGYGVYVHPDQAVARETNQINGNGCTINPSNLTAASSGIKRTGLTQ	123
Dy	363	CLITEGYARGNYVIYDCTSAVAAYETWINDGTTINPSNLTVLSSMSMGTLTQ	422
Qy	124	LVTLLQGQGLMAGMDLPPEVETTYTGRLCEKNSGSVWFCTVSQGDONPAALYGDSIR	183
Dy	423	NEYLMRGMRGNRNNSTSPFTVTSISGSLDLOMACGSRWALADDNNKKKEQMALYTDGSH	482
Qy	184	PYQNDQCCLTGKRDVSIVTSCBASSSQSQRWFTNEGAILNLKNGLANDVAQAANKFI	243
Dy	483	SYQNVLCVLTKGRDSCSPLVYLALCNQMGACGMFLNKDSDITVLDWDVWDVXNSDFSL	542
Qy	244	RLLTYTPAEGEPQOMLT	260
Dy	543	KELLHYHGPNQIMLT	559

RESULT 7
 TIGES SANMI STANDARD; PRT; 563 AA.
 TIGES SANMI

RN	SEQUENCE FROM N.A.
RX	TISSUE-Bark;
RX	MEDLINE=662151449; PubMed=6647092;
RA	Van Damme A.J., Barre A.J., Rouge P., Van Leuven F., Pennaux W.G.J.;
RT	"Characterization and molecular cloning of Sambucus nigra agglutinin V
RT	(nigrin B), a GalNAc-specific type-2 ribosome-inactivating protein
RT	from the bark of elderberry (Sambucus nigra).";
RT	[2]. J. Biochem. 237:505-513(1996).
RP	SEQUENCE OF 26-49 AND 298-321.
RX	TISSUE-Bark;
RX	MEDLINE=9403077; PubMed=9400155;
RA	Galbes T., Cloteres L., Ferreira J.M., Rojo M.A., Iglesias R.,
RA	Munoz R., Arias P.O., Calonge M., Garcia J.R., Mendez E.;
RT	"Isolation and partial characterization of nigrin B, a non-toxic
RT	novel type 2 ribosome-inactivating protein from the bark of Sambucus
RT	nigra L." Biol. 22:1181-1186(1993).
RT	Faint function, non-toxic, inhibits strongly inhibits mammalian
CC	PROTEIN SYNTHESIS BUT DOES NOT AFFECT PROTEIN INTRINSIC PROTEIN
CC	SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITION


```

CC CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE
CC B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
CC BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
CC KNOXOCYTOSIS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC end of the N-glycan on the 28S RNA. A AND B CHAINS
CC -1- SUBUNIT: DISULFID-BINDING
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION BELONGS THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY TYPE 2 RIP SUPERFAMILY
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: U41299; AA83475.1;
DR PIR: S37382; S37382.1;
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00356; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00466; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; Signal.
FT SIGNAL 1 25
FT CHAIN 26 297
FT CHAIN 305 563
FT DOMAIN 305 431
FT DOMAIN 434 559
FT REPEAT 316 356
FT REPEAT 357 397
FT REPEAT 400 432
FT REPEAT 445 482
FT REPEAT 483 524
FT REPEAT 527 563
FT ACT_SITE 168 188
FT DISULFID 274 302
FT DISULFID 319 338
FT DISULFID 360 377
FT DISULFID 448 463
FT DISULFID 489 506
FT CARBOHYD 221 221
FT CARBOHYD 358 368
FT CARBOHYD 430 430
FT CARBOHYD 492 492
FT CARBOHYD 537 537
FT CONFLICT 39 39
SQ SEQUENCE 563 AA; 62300 MW; P250CHB24621B714 CRC64;
Query Match 38.0%; Score 539; DB 1; Length 563;
Best Local Similarity 41.4%; Pred. No. 1e-39;
Matches 109; Conservative 43; Mismatches 105; Indels 6; Gaps 4;
OY 1 DDTYCSASEPTVR IYGNENACVDPDDPDHNGNOIOLMSKSNDDNOIWTIRKQCTIR 59
DB 298 DSGITLRTSFTKNTVGRSGICADVDRNGVDTGFGQLQPGQGR-NQRPVPSDDIR 355
OY 60 SNGSGITRTYAGTATWIPRCNVAETIQTQWKGITLNSNTVYLAASGIRGTL 119
DB 356 SNGKCTPANGLNNSIVIFNCSPTAENAKIKVPIIDSLINSGLVWTFAPASRTIL 415
OY 120 TVQTLDTYTGQGTAGNDTAPREVIYIGRDIQCSNSG-SGYWYECVSSQDQPMALY 177
DB 416 LLENDITVAGSGMTVNVNVIIVASIVGYKEMCLQNGENNGVWMECEATSLQQOMALY 475

```

```

DR InterPro: IPR000772; Ricin B lectin.
DR Pfam: PF00331; Glyco_hydro_10; 1.
DR Pfam: PF00652; Ricin B lectin; 3.
DR PRINTS: PR00134; GHYDRLASE10.
DR SMART: SM00633; Glyco_10; 1.
DR SMART: SM00633; Ricin B lectin; 1.
DR PROSITE: PS00654; RYCINOLY_HYDROL_F10; 1.
DR PROSITE: PS00231; Ricin B lectin; 1.
DR Kxan degradation; Hydrolase; glycosidase; signal; lectin;
KM 3D-structure.
FT SIGNAL 1 41
FT CHAIN 42 477 ENDO-1,4-BETA-XYLANASE A.
FT DOMAIN 361 477 RICIN B-TYPE LECTIN.
FT ACT_SITE 169 169 PROTON DONOR.
FT ACT_SITE 277 277 NUCLEOPHILE.
SQ SEQUENCE 477 AA; 51162 MW; 814AF837EDC68CC CRC64;

Query March
Best Local Similarity 10.5%; Score 149.5; DB 1; Length 477;
Matches 49; Conservative 20; Mismatches 54; Indels 51; Gaps 8;

QY 7 ASP-----TVAIVGKMGCVDDPDHFGNQLMPSKSNPDNLTKKDTITSN 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 346 SSEPPADGQDKVG-SGKLDVPASTSTGTQLQMDCHGPT--NQWATADAGELAVY 402
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 62 G-SCLTYGTAGVYVMPDNTAVREKTIQWINGTIPRSLVLAASGKKTITLT 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 403 GDKCLDAAGTSGSKVQLYSGWGDNCK--WELNSGSGVGVSGCLDRA----- 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 VQTLDTLGGMLGNDTPREVTYGRDLCHMSGSGVAVETVSSQGNCR 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 451 -----VGNCH-----NGLIDLYIC-SNSNGNR 474
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
SPL_RARRA STANDARD; PRT; 525 AA.
ID SPL_RARRA
AC 005308;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-1995 (Rel. 41, Last annotation update)
DE Serine protease 1, 41, precursor (SC 3.4.21.-?) (R21).
OS Bacteroides faecitabidus
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Micrococciaceae; Rarobacteriaceae; Rarobacter.
CX NCBI_TaxID=13243;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 212-222; 224-238 AND 240-244.
RC MEDLINE=9218668; PubMed=1778983;
RA Shmool H., Tadenuma M.;
RT "Characterization of Rarobacter faecitabidus protease I, a
RT yeast-lytic serine protease having mannose-binding activity.";
CU J. Biochem. 110:608-613(1991).
CC -1- FUNCTION: MAJOR SERINE PROTEASE EXHIBITING LYTIC ACTIVITY TOWARD
CC FUNGUS AND CELLULOSE.
CC SPECIFICITY AND HAS A HIGH AFFINITY FOR MANNOSE.
CC MANNOSE BINDING MAY BE THE NATURAL SUBSTRATE FOR RPI.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 52A.
CC -1- SIMILARITY: CONTAINS 1 ricin B-type lectin domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D10753; BA01585.1; -.
DR HSRP: P00778; I08A.
DR SMART: SM00633; Glyco_10; 1.
DR SMART: SM00633; Ricin B lectin; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR PROSITE: PS00231; RICIN_B_LECTIN; 1.
DR Hydrolase; serine protease; mannose-binding; signal; Zymogen;
KM 3D-structure.
FT SIGNAL 1 33
FT CHAIN 33 211 POTENTIAL.
FT DOMAIN 112 525 SERINE PROTEASE I.
FT DOMAIN 396 525 RICIN B-TYPE LECTIN.
FT DOMAIN 401 525 ESSENTIAL FOR THE LYTIC ACTIVITY, BUT NOT
FT FOR PROTEASE FUNCTION.
FT DISULFID 223 239 BY SIMILARITY.
FT DISULFID 310 320 BY SIMILARITY.
FT DISULFID 346 376 BY SIMILARITY.
FT DISULFID 412 431 BY SIMILARITY.
FT DISULFID 482 492 BY SIMILARITY.
FT DISULFID 492 514 BY SIMILARITY.
FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 270 270 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 352 352 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 525 AA; 55654 MW; DA28CF7D330EB861 CRC64;

Query March
Best Local Similarity 9.2%; Score 130; DB 1; Length 525;
Matches 35; Conservative 17; Mismatches 42; Indels 12; Gaps 5;

QY 2 DPTGASRPYRIVKMGCVDDPDHFGNQLMPSKSNPDNLTKKDTITSN 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 451 GSKCLDAAGTSGSKVQLYSGWGDNCK--WELNSGSGVGVSGCLDRA----- 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
SPL_RARRA STANDARD; PRT; 475 AA.
ID SPL_RARRA
AC 004151;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-L-arabinofuranosidase precursor (SC 3.2.1.55) (Arabinoxidase).
GN ABPA OR SC05932 OR SC0H1.02.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Streptomycetaceae; Streptomyces.
CX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4102 / M45.
RA MEDLINE=2196410; PubMed=12000953;
RA Bentley S.D., Chater K.P., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieaser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

```

RA Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz B., Rajendran M.A., Rutherford K., Rutter S., Taylor K.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT Complete genome sequence of the model actinomycete Streptomyces
RT Coelicolor A1(2).
RT Nature 417:413-421 (2002)
CC -1- SUBCELLULAR LOCATION: Cytoplasm; nucleus; hydrolase of terminal non-reducing alpha-L-
CC -1- ARABINOFURANOSIDE RESIDUES in alpha-L-arabinosides.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AL939125; CAA16189.1; -
DR PIR: T35697; T35697.
DR InterPro: IPR005193; Glyco_hydro_62.
DR InterPro: IPR007172; Ricin_B_lectin.
DR Pfam: PF03664; Glyco_hydro_62; 1.
DR Pfam: PF00652; Ricin_B_lectin; 3.
DR SMART: SM00458; Ricin; 1.
DR PROSITE: PS0231; Ricin_B_lectin; 1.
DR KX: Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
KM Complete proteome.
FT SIGNAL 37
FT CHAIN 1
FT DOMAIN 39 475
FT DOMAIN 165
FT DOMAIN 475 50045 NM; 47507FE543CA6D CR64;
SQ SEQUENCE 475 AA; 50045 NM; 47507FE543CA6D CR64;
Query Match 8.7%; Score 124; DB 1; Length 475;
Best Local Similarity 24.1%; Pred. No. 0.0019;
Matches 65; Conservative 33; Mismatches 116; Indels 56; Gaps 13;
QY 6 SASPTTAYVGNKNCVTRDDDFDGNQQLMPKSKNNDPNQLMTIKEDGTIRSG-SC 64
DB 37 AAGSGLAKAGSN-RCDLYLGGSDGALQDLDPKGGT-NQOMSTYDTRKRLTVGDK 93
QY 65 LITVGYTA-GYVWTFDQNTVRAETIQTQWNGTIIIPNSWLT-AASGI-IGTTLT 120
DB 94 LDVGHATATGRTVQINSKSGRNOQ-MWVSDGTIVVSGSLCEAAGAGPMTGAVQ 151
QY 121 VQTDYTLGQGLMAGNDTAPREVTI-----YGFEDLCNESNGSVVETCVSSQOQR 173
DB 152 LMTGCGGNGKWTGLTGPFDGCLPSTYRSGTGLAPKSGVWALKPFTVTHNGR 211
QY 174 KALYGGGSIKPKONQDCLTGKDSVSTVINVSCAGSSGGRV--FTNEGALINIKR 230
DB 212 HLYTG-----STSSGSGVSNVSPFTNMDASAGQ 243
QY 231 GLANDVAQNPFLRIIIPATKPNQWL 260
DB 244 N-AMNOAAVAPLT---FFFA---PKNIWV 265
RESUME 11
ID ABB: STRL1
AC P96463; STANDARD; PRT; 475 AA.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (arabinosidase).
GN ABBP.
OS Streptomyces lividans.

OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Streptomyces; Streptomyces; Streptomyces; Streptomyces;
OX NBL_TextId=1316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=66 / 1326;
RX MEDLINE=9720396; PubMed=9148759;
RT Vincent P., Shareck F., Dupont C., Morosoli R., Kluepfel D.,
RT "New alpha-L-arabinofuranosidase produced by Streptomyces lividans:
RT cloning and DNA sequence of the abtB gene and characterization of the
RT "gene". J. 322:845-852 (1997).
RN [2]
RP REVISIONS.
RC STRAIN=66 / 1326;
RA Shareck F.;
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: HAS A SPECIFIC ARABINOFURANOSIDE-BRANCHING ACTIVITY ON
CC XILAN FROM GRAMINAE, ACTS SYNERGISTICALLY WITH THE XYLANASES AND
CC BINDS SPECIFICALLY TO XILAN. FROM SMALL ARABINOXYLO-OLIGOSIDES.
CC IT LIBERATES ARABINOSE AND, AFTER PROLONGED INCUBATION, THE
CC FORMED ENZYME EXHIBITS SOME XYLANOXYLYTIC ACTIVITY AS WELL.
CC -1- SUBCELLULAR LOCATION: Hydrolase of terminal non-reducing alpha-L-
CC -1- ARABINOFURANOSIDE RESIDUES in alpha-L-arabinosides.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M6451; AAC26524.1; -
DR InterPro: IPR005193; Glyco_hydro_62.
DR InterPro: IPR007172; Ricin_B_lectin.
DR Pfam: PF03664; Glyco_hydro_62; 1.
DR Pfam: PF00652; Ricin_B_lectin; 3.
DR SMART: SM00458; Ricin; 1.
DR PROSITE: PS0231; Ricin_B_lectin; 1.
DR KX: Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin.
KM Complete proteome.
FT SIGNAL 37
FT CHAIN 1
FT DOMAIN 39 475
FT DOMAIN 165
FT DOMAIN 475 50369 NM; CCA1AEBTB85RAD CR64;
SQ SEQUENCE 475 AA; 50369 NM; CCA1AEBTB85RAD CR64;
Query Match 8.5%; Score 121; DB 1; Length 475;
Best Local Similarity 24.1%; Pred. No. 0.0024;
Matches 65; Conservative 33; Mismatches 116; Indels 56; Gaps 13;
QY 6 SASPTTAYVGNKNCVTRDDDFDGNQQLMPKSKNNDPNQLMTIKEDGTIRSG-SC 64
DB 37 AAGSGLAKAGSN-RCDLYLGGSDGALQDLDPKGGT-NQOMSTYDTRKRLTVGDK 93
QY 65 LITVGYTA-GYVWTFDQNTVRAETIQTQWNGTIIIPNSWLT-AASGI-IGTTLT 120
DB 94 LDVGHATATGRTVQINSKSGRNOQ-MWVSDGTIVVSGSLCEAAGAGPMTGAVQ 151
QY 121 VQTDYTLGQGLMAGNDTAPREVTI-----YGFEDLCNESNGSVVETCVSSQOQR 173
DB 152 LMTGCGGNGKWTGLTGPFDGCLPSTYRSGTGLAPKSGVWALKPFTVTHNGR 211
QY 174 KALYGGGSIKPKONQDCLTGKDSVSTVINVSCAGSSGGRV--FTNEGALINIKR 230
DB 212 HLYTG-----STSSGSGVSNVSPFTNMDASAGQ 243
QY 231 GLANDVAQNPFLRIIIPATKPNQWL 260
DB 244 N-AMNOAAVAPLT---FFFA---PKNIWV 265

RESULT 12
 ID E13B ORXA STANDARD; PRT; 548 AA.
 AC P22222;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase).
 GN GLCI.
 OS Arthrobacter sp. (strain YCM03).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcales; Micrococcaceae; Arthrobacter.
 RX [1]_taxid:1667;
 RP SEQUENCE FROM N.A.
 RA Watanabe T., Hasegawa H., Tanaka H., Doi A., Doi K.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
 CC IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
 CC in 1,3-beta-D-glucans.
 CC -1- SUBCELLULAR LOCATION: Periplasmic (by similarity).
 CC -1- SIMILARITY: BELONGS TO FAMILY 64 OF GLYCOSYL HYDROLASES.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
 CC This SWISS-PROT entry is copyright. It is produced through collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL laboratory
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL: J23686; BAB4892.1; .
 DR HSS: P28282; BAB00772; Ricin B lectin.
 DR InterPro: IPR000772; Ricin B lectin.
 DR Pfam: PF00652; Ricin B lectin.
 DR SMART: SM00458; RICIN_1.
 DR PROSITE: PS50231; Ricin B lectin; 1.
 DR HydroLase; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.
 KW HydroLase; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.
 FT SIGNAL 1 36
 FT CHAIN 37 548
 FT DOMAIN 422 548
 FT DOMAIN 422 548
 FT SEQUENCE 548 AA; 58164 MW; BD5635435750596 CRC64;
 SQ
 Query Match 8.4%; Score 119; DB 1; Length 548;
 Best Local Similarity 32.0%; Pred. No. 0.0661;
 Matches 39; Conservative 14; Mismatches 53; Indels 16; Gaps 5;
 QY 20 MCVYRDDPFDNGOIGLWPKSKNDPQWLTIRKIDTRNSGCL--TYGYTAGYVW 77
 DB 432 LCLDVPADPTDINQVQL--ATCSGNAQOWTREGTDFRALGKCLDVASGADSTAW 489
 QY 78 IPDONTAVEATWQW---GNGTIIIPNSNVLAAAGSI--KETTIVQITDYLQ 130
 DB 490 IYCN-----GTGAKWTYDSATYALRNPSGKCLDAGAGAPLDQKQVQWNTCNQTAQ 544
 QY 131 GW 132
 DB 545 RM 546

RESULT 14
 ID E13B ORXA STANDARD; PRT; 612 AA.
 AC P22222;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase).
 GN GLCI.
 OS Arthrobacter sp. (strain YCM03).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcales; Micrococcaceae; Arthrobacter.
 RX [1]_taxid:1667;
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 37-63.
 RA Watanabe T., Hasegawa H., Tanaka H., Doi A., Doi K.;
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
 CC IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
 CC in 1,3-beta-D-glucans.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: BELONGS TO FAMILY 64 OF GLYCOSYL HYDROLASES.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
 CC This SWISS-PROT entry is copyright. It is produced through collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL laboratory
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL: J23686; BAB4892.1; .
 DR HSS: P28282; BAB00772; Ricin B lectin.
 DR InterPro: IPR000772; Ricin B lectin.
 DR Pfam: PF00652; Ricin B lectin.
 DR SMART: SM00458; RICIN_1.
 DR PROSITE: PS50231; Ricin B lectin; 1.
 DR HydroLase; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.
 KW HydroLase; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.
 FT SIGNAL 1 36
 FT CHAIN 37 548
 FT DOMAIN 422 548
 FT DOMAIN 422 548
 FT SEQUENCE 548 AA; 58088 MW; 412554A4A2C04D CRC64;
 SQ
 Query Match 8.4%; Score 119; DB 1; Length 548;
 Best Local Similarity 32.0%; Pred. No. 0.0661;
 Matches 39; Conservative 14; Mismatches 53; Indels 16; Gaps 5;
 QY 20 MCVYRDDPFDNGOIGLWPKSKNDPQWLTIRKIDTRNSGCL--TYGYTAGYVW 77
 DB 432 LCLDVPADPTDINQVQL--ATCSGNAQOWTREGTDFRALGKCLDVASGADSTAW 489
 QY 78 IPDONTAVEATWQW---GNGTIIIPNSNVLAAAGSI--KETTIVQITDYLQ 130
 DB 490 IYCN-----GTGAKWTYDSATYALRNPSGKCLDAGAGAPLDQKQVQWNTCNQTAQ 544
 QY 131 GW 132
 DB 545 RM 546


```
FT REPEAT 1596 1616 WD 15.
FT REPEAT 1627 1657 WD 16.
SQ SEQUENCE 1693 AA; 18935 MW; 0977A827A0251CFP CRC64;

Query Match
      Similarity 21.8%; Score 97.5; DB 1; Length 1693;
      Local 57; Conservative 33; Mismatches 92; Indels 79; Gaps 12;
      Matches 57;

QY 3 VTCSASEPTVRIVGRMCQVDV---RDDEP-----DSNQIQLPKSNDEPVLATIK 53
DB 1234 ITSSSDGTARWRHRKCLGLRGRHDHNIHGRFSLDQKIVLY--STDTARLMT-- 1288
QY 54 RDTTRENSSCLTY-GYTAGVYVIMFDCH-----TAVREATIMQINGGI-INPRS 104
DB 1289 KEGLT-----LTLRGQKEVYDADFSDGRFVFTVSAQDTARQMDISQKDIITLCHS 1342
QY 105 NLYLAASSGIKGTTLTVQTLDTYL-----QQGMLAGNDTAPREVTIYGF 149
DB 1343 HWVRHAFNPRKDHLLTVSADKTAALMTTREGCAVALADRGQWVREGQFSP----- 1393
QY 150 DLQMSNGSGVWVETCVSSQONQRMALYDQSIHFQKQNDQCLTGRDSVSTVNI--- 205
DB 1394 -----DQQWIVTGSADKTAQALNWTLG-----KKLTVLRGHQDAVLAWTRFSP 1434
QY 206 --VSCASASSGQRWVFTNBQ 223
DB 1435 DSGYTVTASDGTAFVWNTG 1455
```

Search completed: December 11, 2003, 14:09:04
Job time : 5.60292 secs

Thu Dec 11 16:10:02 2003

us-09-601-667c-6.rpt

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18; Search time 20.2717 Seconds
(without alignments)
3347.915 Million cell updates/sec

Title: US-09-601-667c-6
Perfect score: 1420
Sequence: 1 DDTCSASEPTRIYGRNM.....PRIIYPAKPKMQLFVP 263

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 45 summaries

Database:

1: SP_bacteria*
2: SP_bacteri*
3: SP_fungi*
4: SP_human*
5: SP_invertebrate*
6: SP_mammal*
7: SP_mhc*
8: SP_organelle*
9: SP_phase*
10: SP_plant*
11: SP_protent*
12: SP_vari*
13: SP_viridiplantae*
14: SP_virus*
15: SP_virus*
16: SP_bacteri*
17: SP_archae*
18: SP_archae*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1397	98.4	531	10 Q8RX6	Q8RX6 vicium albu
2	1189	83.7	265	10 Q8RX2	Q8RX2 vicium albu
3	1160	81.7	565	10 Q8RX3	Q8RX3 vicium albu
4	1155	81.3	265	10 Q8RX1	Q8RX1 vicium albu
5	1060.5	74.7	266	10 Q8RX3	Q8RX3 vicium albu
6	915	64.4	541	10 Q41174	Q41174 ricinus com
7	902.5	63.6	580	10 Q948W4	Q948W4 ricinus com
8	895.2	63.1	580	10 Q948W3	Q948W3 ricinus com
9	895.2	63.1	580	10 Q948W3	Q948W3 ricinus com
10	864	60.8	543	10 Q948W5	Q948W5 ricinus com
11	864	60.8	543	10 Q948W5	Q948W5 ricinus com
12	755.5	53.3	528	10 Q96076	Q96076 abrus prec
13	755.5	53.3	547	10 Q96076	Q96076 abrus prec
14	743	52.3	382	10 Q8A43	Q8A43 abrus prec
15	684	48.2	573	10 Q8W28	Q8W28 iris hollan
16	684	48.2	592	10 Q8W27	Q8W27 iris hollan

17	592.5	41.7	570	10 Q22415	Q22415 sambucus n
18	577	40.6	316	10 Q8RT45	Q8RT45 sambucus n
19	576	40.6	316	10 Q93W1	Q93W1 sambucus n
20	575	40.5	316	10 Q94554	Q94554 sambucus n
21	565	39.8	564	10 Q9AVR2	Q9AVR2 sambucus n
22	560.5	39.5	604	10 Q9M654	Q9M654 polyonatum
23	558.5	39.3	570	10 Q41358	Q41358 sambucus n
24	558.5	39.3	570	10 Q41358	Q41358 sambucus n
25	548	38.6	320	10 Q94553	Q94553 sambucus n
26	548	38.6	320	10 Q94553	Q94553 sambucus n
27	545.5	38.4	603	10 Q9M653	Q9M653 polyonatum
28	544.5	38.3	565	10 Q04072	Q04072 sambucus n
29	542.5	38.2	566	10 Q94552	Q94552 sambucus n
30	539	38.0	563	10 Q94566	Q94566 sambucus n
31	538	37.9	320	10 Q94566	Q94566 sambucus n
32	534.5	37.6	307	10 Q8GT46	Q8GT46 sambucus n
33	534.5	37.6	307	10 Q93543	Q93543 sambucus n
34	452.5	31.9	569	10 Q9SV9	Q9SV9 cucumis sat
35	155	13.7	293	10 Q9SV9	Q9SV9 cucumis sat
36	152	11.0	422	10 Q9EVR5	Q9EVR5 streptomyce
37	145.2	10.7	435	2 Q8641	Q8641 streptomyce
38	145.2	10.7	435	2 Q8641	Q8641 streptomyce
39	145.2	10.7	435	2 Q8641	Q8641 streptomyce
40	144.5	9.5	585	16 Q9K438	Q9K438 streptomyce
41	134	9.4	962	16 Q9K473	Q9K473 streptomyce
42	132	9.3	579	16 Q9K473	Q9K473 streptomyce
43	125.5	8.8	476	2 Q9RW45	Q9RW45 streptomyce
44	125.5	8.8	476	2 Q9RW45	Q9RW45 streptomyce
45	116	8.2	1545	16 Q9RDQ1	Q9RDQ1 streptomyce

ALIGNMENTS

RESULT 1
Q8RX6 PRELIMINARY: PRT: 531 AA.
AC Q8RX6;
DT 01-JUN-2002 (TEMBLrel, 21, Created)
DT 01-JUN-2002 (TEMBLrel, 21, Last sequence update)
DT 01-MAR-2003 (TEMBLrel, 23, Last annotation update)
DE Lectin chain A isoform 1 (EC 3.2.2.23) (RNA N-glycosidase)
DE (fragment)...
OS Vicium album (European mistletoe).
OC Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Gnastrophysales; Eudicotyledons; core eudicots;
OC Santalales; Viciales; Viciales.
OX NCBI_TaxID:3972;
RN [1]
RP SOURCE FROM N.A.
RA TRSUS-Leat;
RA Parmasivam M., Misra V., Srinivasan A., Singh T.P.;
RT "vicium album (Indian) mRNA for Mistletoe lectin chain A isoform 1 and
RT chain B.";
RC Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -L- CATALYTIC ACTIVITY: ENDORIBONUCLEASE OF THE 28S RRNA.
CC -L- SPECIFIC ACTIVITY: INACTIVATING PROTEIN FAMILY.
CC EMBL: AY081149; AA087066.1; The RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR InterPro: IPR001572; RIBIN_B_lectin.
DR Pfam: PF00652; RIBIN_B_lectin; 6.
DR Pfam: PF00652; RIBIN_B_lectin; 6.
DR SMART: SM00458; RIBIN_2.
DR PROSITE: PS0231; RIBIN_B_LECTIN; 2.
KW Hydroxylase; Toxin.
FT NDNTER 1
FT CDSNTER 1
FT CHAIN 1
FT CHAIN 1
SQ SEQUENCE 531 AA; 58802 MW; 162448BEEF55422 CRC64;
Query Match 98.4%; Score 1397; DB 10; Length 531;
Best Local Similarity 98.4%; Pred. No. 1.1e-14;

Matches 258; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDVTCASAEPTVATVGNKMCVVDGDDPHDGNQIQIOLMPSKSNNDPNQIWTIKEDGTRS 60
DB 269 DDVTCASAEPTVATVGNKMCVVDGDDPHDGNQIQIOLMPSKSNNDPNQIWTIKEDGTRS 328

QY 61 NSGCLITGTTAGTGMIFDONTAVREATTIWIWNGETINPESNVLAASSGKGTTLT 120
DB 329 NSGCLITGTTAGTGMIFDONTAVREATTIWIWNGETINPESNVLAASSGKGTTLT 388

QY 121 VQTLDYTLGGGWLAGNDTPREVTIYGFRLCNEKSGSVWETCVSSQONRMALYDGG 180
DB 389 VQTLDYTLGGGWLAGNDTPREVTIYGFRLCNEKSGSVWETCVSSQONRMALYDGG 448

QY 181 SIREKQNDQCLTCGRDSVSTVINTVSCSAGSGQRFVFNKGAIIINLKNGLAMVDAQN 240
DB 449 SIREKQNDQCLTCGRDSVSTVINTVSCSAGSGQRFVFNKGAIIINLKNGLAMVDAQN 508

QY 241 PSLRRITITPATCKENQWMLPVP 263
DB 509 PSLRRITITPATCKENQWMLPVP 531

RESULT 2

Q8LKQ2 PRELIMINARY; FRT; 263 AA.

AC 08LKQ2; 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Lactin chain B (Isolated from *Streptococcus*).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159376;
RN [1].
RP SEQUENCE FROM N.A.
RA MEDLINE=2156752; PubMed=11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.-K.,
RA Park C.-H., Song S.-K.,
RA "Cloning and sequence analysis of the lactin genes of the Korean
RT mislabeled *Streptococcus coloratum*."?
RL Mol. Cells 12:215-220(2001).
RN [2].

RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.-K.,
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508918; A046936.1; -
DR InterPro; IPR000772; Rctn_B_Lectin.
DR Pfam; PF00652; Rctn_B_Lectin; 5.
DR Stem; S00052; Rctn_B_Lectin; 2.
DR PROSITE; PS50231; Rctn_B_Lectin; 2.
FT NOY TER 1
FT NOY TER 263
SQ SEQUENCE 263 AA; 29150 MW; B685BCB749C8D1F CRC64;

Query Match 83.7%; Score 1189; DA 10; Length 263;
Best Local Similarity 82.5%; Pred. No. 9,3e-97;

Matches 217; Conservative 20; Mismatches 26; Indels 0; Gaps 0;

QY 1 DDVTCASAEPTVATVGNKMCVVDGDDPHDGNQIQIOLMPSKSNNDPNQIWTIKEDGTRS 60
DB 1 DDVTCASAEPTVATVGNKMCVVDGDDPHDGNQIQIOLMPSKSNNDPNQIWTIKEDGTRS 60

QY 61 NSGCLITGTTAGTGMIFDONTAVREATTIWIWNGETINPESNVLAASSGKGTTLT 120
DB 61 NSGCLITGTTAGTGMIFDONTAVREATTIWIWNGETINPESNVLAASSGKGTTLT 120

QY 121 VQTLDYTLGGGWLAGNDTPREVTIYGFRLCNEKSGSVWETCVSSQONRMALYDGG 180
DB 121 VQTLDYTLGGGWLAGNDTPREVTIYGFRLCNEKSGSVWETCVSSQONRMALYDGG 180

QY 181 SIREKQNDQCLTCGRDSVSTVINTVSCSAGSGQRFVFNKGAIIINLKNGLAMVDAQN 240
DB 181 SIREKQNDQCLTCGRDSVSTVINTVSCSAGSGQRFVFNKGAIIINLKNGLAMVDAQN 240

QY 241 PSLRRITITPATCKENQWMLPVP 263
DB 241 PSLRRITITPATCKENQWMLPVP 263

RESULT 3

Q8W243 PRELIMINARY; FRT; 565 AA.

AC 08W243; 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE VCA precursor (BC 3.2.2.22) (rRNA N-glycosylase).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159376;
RN [1].
RP SEQUENCE FROM N.A.
RA Park W.-S., Lyu S.,
RT "Cloning of Viscum album subsp. coloratum (Korean mistletoe)."
RT Blochm. Biophys. Res. Commun. 0:0-0(2002).
CC -1- CATALYTIC ACTIVITY: ENDHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF369511; A040411.1; -
DR InterPro; IPR001574; Rctn_B_Lectin.
DR Pfam; PF00652; Rctn_B_Lectin; 6.
DR PRINTS; PR00396; SHIGARCTN.
DR SMART; SM00458; Rctn; 2.
DR PROSITE; PS50231; Rctn_B_Lectin; 2.
KW Hydroxylase; signal; toxin.
FT SIGNAL 1
FT CHAIN 23
FT CHAIN 273
FT CHAIN 309
SQ SEQUENCE 565 AA; 62401 MW; 991E33994D05F11 CRC64;

Query Match 81.7%; Score 1160; DA 10; Length 565;
Best Local Similarity 82.5%; Pred. No. 8.8e-94;

Matches 217; Conservative 16; Mismatches 26; Indels 4; Gaps 1;

QY 1 DDVTCASAEPTVATVGNKMCVVDGDDPHDGNQIQIOLMPSKSNNDPNQIWTIKEDGTRS 60
DB 307 DDVTCASAEPTVATVGNKMCVVDGDDPHDGNQIQIOLMPSKSNNDPNQIWTIKEDGTRS 362

QY 61 NSGCLITGTTAGTGMIFDONTAVREATTIWIWNGETINPESNVLAASSGKGTTLT 120
DB 61 NSGCLITGTTAGTGMIFDONTAVREATTIWIWNGETINPESNVLAASSGKGTTLT 120

QY 121 VQTLDYTLGGGWLAGNDTPREVTIYGFRLCNEKSGSVWETCVSSQONRMALYDGG 180
DB 121 VQTLDYTLGGGWLAGNDTPREVTIYGFRLCNEKSGSVWETCVSSQONRMALYDGG 180

QY 181 SIREKQNDQCLTCGRDSVSTVINTVSCSAGSGQRFVFNKGAIIINLKNGLAMVDAQN 240
DB 483 SIREKQNDQCLTCGRDSVSTVINTVSCSAGSGQRFVFNKGAIIINLKNGLAMVDAQN 542

QY 241 PSLRRITITPATCKENQWMLPVP 263
DB 543 PSLRRITITPATCKENQWMLPVP 565

RESULT 4

Q8LKQ1 PRELIMINARY; FRT; 263 AA.

```

AC 081K01;
AT 01-OCT-2002 (TRENBERL. 22, Created)
DT 01-OCT-2002 (TRENBERL. 22, Last sequence update)
RT 01-OCT-2002 (TRENBERL. 22, Last annotation update)
DE Lectin chain subunit 3 (fragment).
OS Viscum album subsp. coloratum.
OC Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Santalales; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2156752; PubMed=1170524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RD Do M.-S., Song S.K.;
RI Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF508919; AAM46937.1;
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
DR NON_TER
FT NON_TER
SQ
SEQUENCE 263 AA; 29071 MW; 359C4AD3A60F6D CRC64;

Query Match 61.3%; Score 1155; DB 10; Length 263;
Best Local Similarity 80.6%; Pred. No. 9.2e-94;
Matches 212; Conservative 21; Mismatches 30; Indels 0; Gaps 0;

QY 1 DDVTGSASEPTVRIYGNMGCVYRDDPDHDCNQIQIMPEKSNNDPQWLTIKEDGITS 60
DB 1 DDVTCTSEPTVRIYGNMGCVYRDDPDHDCNQIQIMPEKSNNDPQWLTIKEDGITS 60
QY 61 NSGCLITVGTAGVYVMEPCNTAVERITWQIMGNQITIPRSNLIVL--AASGIGKT 120
DB 61 NSGCLITVGTAGVYVMEPCNTAVERITWQIMGNQITIPRSNLIVL--AASGIGKT 120
QY 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 180
DB 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 180
QY 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 180
DB 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 180
QY 181 STIRKONQOCLTQSDSVYVINYVSCASSGQWFTNFGAILNLKMLAMVQNA 240
DB 181 STIRKONQOCLTQSDSVYVINYVSCASSGQWFTNFGAILNLKMLAMVQNA 240
QY 241 PCLRRITIIYPATKPNQWMLPYV 263
DB 241 PCLRRITIIYPATKPNQWMLPYV 263
DB 241 PCLRRITIIYPATKPNQWMLPYV 263

RESULT 5
ID 081K03 PRELIMINARY; PRT; 266 AA.
AC 081K03
AT 01-OCT-2002 (TRENBERL. 22, Created)
DT 01-OCT-2002 (TRENBERL. 22, Last sequence update)
RT 01-OCT-2002 (TRENBERL. 22, Last annotation update)
DE Lectin chain B isoform 1 (fragment).
OS Viscum album subsp. coloratum.
OC Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Santalales; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2156752; PubMed=1170524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RD Do M.-S., Song S.K.;
RI Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF508919; AAM46937.1;
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
DR NON_TER
FT NON_TER
SQ
SEQUENCE 263 AA; 29071 MW; 359C4AD3A60F6D CRC64;

Query Match 61.3%; Score 1155; DB 10; Length 263;
Best Local Similarity 80.6%; Pred. No. 9.2e-94;
Matches 212; Conservative 21; Mismatches 30; Indels 0; Gaps 0;

QY 1 DDVTGSASEPTVRIYGNMGCVYRDDPDHDCNQIQIMPEKSNNDPQWLTIKEDGITS 60
DB 1 DDVTCTSEPTVRIYGNMGCVYRDDPDHDCNQIQIMPEKSNNDPQWLTIKEDGITS 60
QY 61 NSGCLITVGTAGVYVMEPCNTAVERITWQIMGNQITIPRSNLIVL--AASGIGKT 120
DB 61 NSGCLITVGTAGVYVMEPCNTAVERITWQIMGNQITIPRSNLIVL--AASGIGKT 120
QY 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 180
DB 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 180
QY 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 180
DB 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 180
QY 181 STIRKONQOCLTQSDSVYVINYVSCASSGQWFTNFGAILNLKMLAMVQNA 240
DB 181 STIRKONQOCLTQSDSVYVINYVSCASSGQWFTNFGAILNLKMLAMVQNA 240
QY 241 PCLRRITIIYPATKPNQWMLPYV 263
DB 241 PCLRRITIIYPATKPNQWMLPYV 263
DB 241 PCLRRITIIYPATKPNQWMLPYV 263

RESULT 6
ID 041174 PRELIMINARY; PRT; 541 AA.
AC 041174
AT 01-NOV-1996 (TRENBERL. 01, Created)
DT 01-NOV-1996 (TRENBERL. 01, Last sequence update)
RT 01-NOV-1996 (TRENBERL. 01, Last annotation update)
DE Pycnidia A chain (EC 3.2.2.22) (rRNA N-glycosidase)
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Euphorbiales; Euphorbiaceae; Euphorbia.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9238377; PubMed=163311;
RA Roberts L.M., Tregear J.W., Lord J.M.;
RD "Molecular cloning of ricin."
RT Targeted Diagn. Ther. 7:81-97(1992).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
-1- SERINE RESIDUE IN THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; P02879; 1BR6
DR InterPro; IPR000772; Ricin_B_lectin.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
DR NON_TER
FT NON_TER
SQ
SEQUENCE 266 AA; 29537 MW; 4A51473C37B94C73 CRC64;

Query Match 74.7%; Score 1060.5; DB 10; Length 266;
Best Local Similarity 72.6%; Pred. No. 2e-85;
Matches 153; Conservative 29; Mismatches 41; Indels 3; Gaps 1;

QY 1 DDVTGSASEPTVRIYGNMGCVYRDDPDHDCNQIQIMPEKSNNDPQWLTIKEDGITS 60
DB 1 DDVTCTSEPTVRIYGNMGCVYRDDPDHDCNQIQIMPEKSNNDPQWLTIKEDGITS 60
QY 61 NSGCLITVGTAGVYVMEPCNTAVERITWQIMGNQITIPRSNLIVL--AASGIGKT 117
DB 61 NSGCLITVGTAGVYVMEPCNTAVERITWQIMGNQITIPRSNLIVL--AASGIGKT 117
QY 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 177
DB 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 177
QY 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 177
DB 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 177
QY 178 GDSIRFPKQOCLTQSDSVYVINYVSCASSGQWFTNFGAILNLKMLAMVQNA 237
DB 178 GDSIRFPKQOCLTQSDSVYVINYVSCASSGQWFTNFGAILNLKMLAMVQNA 237
QY 238 QANPKRLRIIYPATKPNQWMLPYV 263
DB 238 QANPKRLRIIYPATKPNQWMLPYV 263
QY 241 PCLRRITIIYPATKPNQWMLPYV 266
DB 241 PCLRRITIIYPATKPNQWMLPYV 266
DB 241 PCLRRITIIYPATKPNQWMLPYV 266

RESULT 7
ID 041174 PRELIMINARY; PRT; 541 AA.
AC 041174
AT 01-NOV-1996 (TRENBERL. 01, Created)
DT 01-NOV-1996 (TRENBERL. 01, Last sequence update)
RT 01-NOV-1996 (TRENBERL. 01, Last annotation update)
DE Pycnidia A chain (EC 3.2.2.22) (rRNA N-glycosidase)
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Euphorbiales; Euphorbiaceae; Euphorbia.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9238377; PubMed=163311;
RA Roberts L.M., Tregear J.W., Lord J.M.;
RD "Molecular cloning of ricin."
RT Targeted Diagn. Ther. 7:81-97(1992).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
-1- SERINE RESIDUE IN THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; P02879; 1BR6
DR InterPro; IPR000772; Ricin_B_lectin.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
DR NON_TER
FT NON_TER
SQ
SEQUENCE 266 AA; 29537 MW; 4A51473C37B94C73 CRC64;

Query Match 74.7%; Score 1060.5; DB 10; Length 266;
Best Local Similarity 72.6%; Pred. No. 2e-85;
Matches 153; Conservative 29; Mismatches 41; Indels 3; Gaps 1;

QY 1 DDVTGSASEPTVRIYGNMGCVYRDDPDHDCNQIQIMPEKSNNDPQWLTIKEDGITS 60
DB 1 DDVTCTSEPTVRIYGNMGCVYRDDPDHDCNQIQIMPEKSNNDPQWLTIKEDGITS 60
QY 61 NSGCLITVGTAGVYVMEPCNTAVERITWQIMGNQITIPRSNLIVL--AASGIGKT 117
DB 61 NSGCLITVGTAGVYVMEPCNTAVERITWQIMGNQITIPRSNLIVL--AASGIGKT 117
QY 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 177
DB 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 177
QY 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 177
DB 121 VOTLDYTLGQMLAGNDTAPREVTIYGFNDLCMESNGSVWETCVSSQONQWALY 177
QY 178 GDSIRFPKQOCLTQSDSVYVINYVSCASSGQWFTNFGAILNLKMLAMVQNA 237
DB 178 GDSIRFPKQOCLTQSDSVYVINYVSCASSGQWFTNFGAILNLKMLAMVQNA 237
QY 238 QANPKRLRIIYPATKPNQWMLPYV 263
DB 238 QANPKRLRIIYPATKPNQWMLPYV 263
QY 241 PCLRRITIIYPATKPNQWMLPYV 266
DB 241 PCLRRITIIYPATKPNQWMLPYV 266
DB 241 PCLRRITIIYPATKPNQWMLPYV 266

```

Thu Dec 11 16:10:02 2003

us-09-601-667c-6.rsp

Page 4

DR	Pfam: PF00161; RIP; 1.
DR	PRINTS: PR00396; SHIGALICIN.
DR	SMART: SMO0458; RICIN; 2.
DR	PROSITE: PS50231; RICIN_B_LECTIN; 2.
DR	PROSITE: PS00275; SHIGA_RICIN; 1.
DR	PROSITE: PS00338; SOMATOCTROPIN_2; 1.
KM	Hypocistae; Toxin.
SC	SEQUENCE 541 AA; 60281 MW; 2/BZBDSEFIIEE9D9 CACC4;
QY	Query Match 64.4%; Score 915; DB 10; Length 541;
DB	Best Local Similarity 63.6%; Pred. No.3,28-72;
	Matches 164; Conservative 33; Mismatches 61; Indels 0; Gaps 0
Df	5 CSASPPVRIYVERGNKCVDVDDDPHDNDQILPAPSRKMDPNQMLTIRKDTIKRSNGC 64
Oy	283 CMPEPIETRIYVRNKGCDVADDDRHRNSNAIDLPFCSSKATNQALDKLTKITRISGEC 342
Oy	65 LTTNYGRVGVYVMFPGCTANREATTQKNGKITIPRSYVLAAAGCVKTLLAYCL 124
Df	343 LTVGYSPGVLYMTDNTAATAIRWQINDNGKITIPRSSYLTAANSGETLLAYCN 402
Oy	123 DYLLCGGLAKGNDIAPAEPTLYTFRLDMESGSGVAVTCVSQQDNFMALYGCSGISP 184
Df	403 IYVSGSWLVLTNRTPPVITIVELGCLDAASGVVIDESSERKACQVALYADSIHP 462
Oy	185 KKNQDCQLTGSDSVSTVINIVSCASSSQRRVFNEGALIMLKNGLANDVAAPKR 244
Df	463 QNNPDHEDIDENIRETYVLIICGPASQGMFRMRNDQILMDISGLVLPKRSDESLK 522
Oy	245 RIITYPANPKGPNQMLNV 262
Df	523 GIILYPLHDPNQMLLEP 540
RESULT 7	
Oy+EMBL	PRELIMINARY; PRT; 560 AA.
AC	034B#4;
DT	01-DEC-2001 (TREMBLrel. 1), Created)
DT	01-DEC-2001 (TREMBLrel. 1), Last update)
DT	01-MAR-2003 (TREMBLrel. 2), Last annotation update)
DE	Type 2 ribosome-inactivating protein cinanomom II precursor
DE	(EC 3.2.2.22) (cinn X-N-glycosylase).
OC	Cinanomom camphora (camphor tree).
OC	Bakarioca Viaticiana (camphor); Streptophyta; Embryophyta; Tracheophyta;
OC	Phenanthopyta; Magnoliophyta; Laurales; Lauraceae; Cinanomum.
ON	[1] _taxid=19429;
RP	SEQUENCE FROM N.A.
RA	Yang O., Gong Z.Z., Liu W.Y.;
RT	"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT	genes encoding cinanomom proteins and study of their expression
RT	patterns";
RT	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC	CC-BY-NC-ND 4.0 International license
CC	- - SWIMINARTY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC	EMBL: A0309802; AA882459.1; TREMBL: P0000772; Ricin_B_Lectin.
DR	InferPro: IP0000772; Ricin_B_Lectin.
DR	InferPro: IP00652; Ricin_B_Lectin; 6.
DR	Pfam: PF00161; RIP; 1..
DR	PRINTS: PR00396; SHIGALICIN.
DR	SMART: SMO0458; RICIN; 2.
DR	PROSITE: PS50231; RICIN_B_LECTIN; 2.
KM	Hypocistae; Signal; toxin.
FT	SIGNAL 33
FT	POTENTIAL TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN II.
SO	SEQUENCE 580 AA; 64265 MW; 37EA289CECECPFP CRC64;
Query Match	63.6%; Score 903.5; DB 10; Length 580.

Query Match	Best Local Similarity	63.9%	Pred. No. 3.6e-71	Matches 169	Conservative 32	Mismatches 62	Indels 1	Gaps 1									
Db	1	DDVCSASPEFVIVIVRNMKCVDDDDPHQNGQIQIOLWPSKANDPNOLMTIKEDQITRS	60														
Db	317	NBDVDAPEFVIVSRNGICVDVADKXNNGNPLQIPLCKNSDVQIOLTRSDITRS	376														
Qy	61	NSGCLITVITAGVYVNIPECTAYREATIQIWMKGTIINPRSLVLAASGIKGTIT	120														
Db	121	VQDLDYTLQSQMLAGNDARFVITVYPPDDCKENSIGSVYVETCVSSQOQVRLAYDGD	180														
Db	377	NKCLITVYSAGDYVNIHCTGTVPASISQPMNGNIIINQSLVLSASGNPTLT	436														
Qy	437	VQANVYASQOQMLAGNTEPFVTSIVQPDICQANQGMATVVESSSACQKMLAYDGD	496														
Qy	161	SIRPKQDOCLTICGRSVSTVINIVSCNSGSSQGRVETNEGAILNIRKGLAMDVAQA	239														
Db	497	SIRPKQDOCLTIDNHSQGLISCSQSSQSGQGRVETNEGAILNIRKGLAMDVAQA	556														
Qy	240	NSGCLITVITAGVYVNIPECTAYREATIQIWMKGTIINPRSLVLAASGIKGTIT	262														
Db	557	NSGCLITVITAGVYVNIPECTAYREATIQIWMKGTIINPRSLVLAASGIKGTIT	579														
RESULT 8																	
ID	Q94BM3	PRELIMINARY	ERT	580 AA													
Db	Q94BM3	PRELIMINARY	ERT	580 AA													
DT	01-DEC-2001 (TrEMBL)	19	Crystall														
DT	01-DEC-2001 (TrEMBL)	23	Last annotation update														
DT	01-MAR-2003 (TrEMBL)	23	Last annotation update														
Db	Type 2 ribosome-inactivating protein cinmamom III precursor																
Db	(EC 3.2.2.22) (rRNA N-glycosidase)																
OC	Cinmamomun campohra (Camphor tree)																
OC	Cinmamoyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;																
OC	Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum																
OC	NCBI_TaxID=13429;																
CC	SEQUENCE FROM N.A.																
CC	Yang Q. Gong Z.Z. Liu M.Y.																
RT	"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)																
RT	genes encoding cinmamom proteins and study of their expression																
RT	patterns"																
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.																
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE																
CC	SPECIFIC ADENOSINE ON THE 28S RRNA.																
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.																
Db	EMBL:AF031803.2; GenBank:AF031803.1; B																
Db	EMBL:AF031803.2; GenBank:AF031803.1; B																
DR	InterPro: IPR001574; RIP																
DR	Pfam: PF00652; Ricin B_lectin; 6																
DR	Pfam: PF00161; RIP; 1																
DR	PRINTS: PR00396; SHIGARICIN																
DR	SMART: SMO0458; RICIN; 2																
DR	PROSITE: PS50231; Ricin B_lectin; 2																
FM	Hydrophobic; Signal; Toxin																
FM	Hydrophobic; Signal; Toxin																
FM	Hydrophobic; Signal; Toxin																
FM	Hydrophobic; Signal; Toxin																
FM	Hydrophobic; Signal; Toxin																

QY 121 VOTLDYTLGGMLAGNDTAPREVITYGFDLCMESNGSVWVCVSSQONKMLVQDD 180
DB 437 VQADIVASRQGMALGNTEPPTVSIVGFNDLCQONADAMVVCBSKAEQKMLVQDD 496
QY 181 STRKONQOCLT-CGRDSVSTVINIVSCASGSSGQRWTFNEGAILNKGLAMVQAQ 239
DB 497 STRKONQOCLTSDNHSQSLIISCSFSSGQRWTFNDGILINKGLAMVQVKS 556
QY 240 NPGKRLIIVPATGKPNOMLVP 262
DB 557 DPLHQLIIVPATGKPNOMLVP 579

RESULT 9

ID Q41143 PRELIMINARY; PRT; 263 AA.
DT 01-NOV-1996 (TRENBERG) 01. Created.
DT 01-NOV-1996 (TRENBERG) 01. Last annotation update.
DT 01-MAR-2003 (TRENBERG) 23. Last annotation update.
DE Rictin B beta chain (Fragment).
GN RICTIN B BETA CHAIN.
OS Rictinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids 1; Malpighiales; Euphorbiaceae; Rictinus.
OX NCBI_TaxID=3983;
RN [1]
RF SEQUENCE FROM N.A.
RA Xie L., Liu W.-Y., Wang E.-D.;
RA "Molecular cloning of cinnamomin A-, B-chain and the expression,
RT purification, characterization and mutagenesis of the A-chain";
RT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOTHELIALYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- STRUKTUR: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR HSSP; P02879; 2A1.
DR Interpro: IPR000772; Rictin_B_lectin.
DR Pfam: PF00652; Rictin_B_lectin; 5.
DR PRINTS; PR00161; RIP; 1.
DR SMART; SM00458; RICTIN.
DR PROSITE; PS0231; RICTIN_B_LECTIN; 2.
KW HYDROLASE; TOXIN.
FT NON_TER 1.
SQ SEQUENCE 549 AA; 60648 MW; 02607FE607C44B0 CRC64;

Query Match 62.8%; Score 891.5; DB 10; Length 263;
Best Local Similarity 62.5%; Pred. No. 1, 5e-70;
Matches 162; Conservative 34; Mismatches 62; Indels 1; Gaps 1;

QY 5 CSASEPTVAVIRGNKCVDRDDPHDQNOIOLMPSKSNDDPNQWTLIRGDTIRNSGC 64
DB 4 CNDPEPTVAVIRGNKCVDRDORFHNGNALQIMPCKSNDDNQLWTLIRGDTIRNSGC 63
QY 65 LTTVGTAQVYVAFPCQNTANRELTWQNGFTINPRSNVLASGIGKTLTQVT 124
DB 64 LTTVGISPVYVAVYDQNTADPDRQNGFTINPRSNVLASGIGKTLTQVT 123
QY 125 DYTLAGQMLAGNDTAPREVITYGFDLCMESNGSVWVCVSSQONKMLVQDDGIRP 184
DB 124 IYAVSQGMALGNTEPPTVSIVGFNDLCQONADAMVVCBSKAEQKMLVQDDGIRP 183
QY 185 KQNDQCLTGRDSVSTVINIVSCASGSSGQRWTFNEGAILNKGLAMVQAQNP-KI 243
DB 184 QKRRNCLTIDNANKGIVAKLSICAPVSSGQRWTFNDGILINKGLAMVQVRSPESL 243
QY 244 RLLIIVPATGKPNOMLVP 262
DB 244 KQIIVHPFQNLQIMLVP 262

RESULT 10

ID Q9FV22 PRELIMINARY; PRT; 549 AA.
Q9FV22

AC Q9FV22;
DT 01-MAR-2001 (TRENBERG) 16. Created.
DT 01-MAR-2001 (TRENBERG) 16. Last sequence update.
DT 01-OCT-2002 (TRENBERG) 22. Last annotation update.
DE Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (rRNA
DE N-glycosidase) (Fragment).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RF SEQUENCE FROM N.A.
RA Xie L., Liu W.-Y., Wang E.-D.;
RA "Molecular cloning of cinnamomin A-, B-chain and the expression,
RT purification, characterization and mutagenesis of the A-chain";
RT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOTHELIALYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- STRUKTUR: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR HSSP; P02879; 2A1.
DR Interpro: IPR000772; Rictin_B_lectin.
DR Pfam: PF00652; Rictin_B_lectin; 5.
DR PRINTS; PR00161; RIP; 1.
DR SMART; SM00458; SHIGARICIN.
DR PROSITE; PS0231; RICTIN_B_LECTIN; 2.
KW HYDROLASE; TOXIN.
FT NON_TER 1.
SQ SEQUENCE 549 AA; 60648 MW; 02607FE607C44B0 CRC64;

Query Match 60.8%; Score 864; DB 10; Length 549;
Best Local Similarity 61.0%; Pred. No. 1e-67;
Matches 161; Conservative 32; Mismatches 69; Indels 2; Gaps 1;

QY 1 DDTVCASEPTVAVIRGNKCVDRDDPHDQNOIOLMPSKSNDDPNQWTLIRGDTIRNSGC 60
DB 285 NDVDCADDEPTVAVIRGNKCVDRDORFHNGNALQIMPCKSNDDNQLWTLIRGDTIRNSGC 344
QY 61 NSCLTLYGTAGVYVAFPCQNTANRELTWQNGFTINPRSNVLASGIGKTLT 120
DB 345 NSCLTLYGTAGVYVAFPCQNTANRELTWQNGFTINPRSNVLASGIGKTLT 119
QY 121 VOTLDYTLGGMLAGNDTAPREVITYGFDLCMESNGSVWVCVSSQONKMLVQDD 180
DB 405 VQADIVASRQGMALGNTEPPTVSIVGFNDLCQONADAMVVCBSKAEQKMLVQDD 464
QY 181 STRKONQOCLT-CGRDSVSTVINIVSCASGSSGQRWTFNEGAILNKGLAMVQAQ 238
DB 465 STRKONQOCLTSDNHSQSLIISCSFSSGQRWTFNDGILINKGLAMVQVKS 524
QY 239 NPGKRLIIVPATGKPNOMLVP 262
DB 525 DPLHQLIIVPATGKPNOMLVP 548

RESULT 11

ID Q94BMS PRELIMINARY; PRT; 581 AA.
Q94BMS;
DT 01-DEC-2001 (TRENBERG) 19. Created.
DT 01-DEC-2001 (TRENBERG) 19. Last sequence update.
DT 01-MAR-2003 (TRENBERG) 23. Last annotation update.
DE Type 2 ribosome-inactivating protein cinnamomin I precursor
DE (EC 3.2.2.22) (rRNA N-glycosidase).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RF SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.-Y.;

RT	"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)	
RT	genes encoding cinnamon proteins and study of their expression	
RT	patterns.";	
RL	Submitted (JUN-2001) to the EMBL/Genbank/DBJ databass.	
CC	-1- CATALYTIC ACTIVITY: ENOHPHOSPHATIS OF THE N-GLYCOSIDIC BOND AT ONE	
CC	SPECIFIC ADENOSINE ON THE 28S RNA.	
CC	EMBL: AY039801; AKK9458.1; THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
DR	InterPro: IPR000772; RcinB_lectin.	
DR	Pfam: PF00652; RcinB_lectin_5.	
DR	PRINTS: PR00396; SHIGALICIN.	
DR	SMART: SM00458; RCIN; 2.	
DR	PROSITE: PS02031; RCIN_B_LECTIN; 2.	
DR	Kinase: Kinase; Signal; Toxin.	
FT	CHAIN	
FT	33	
FT	581	
FT	TYR 272	
FT	CINNAMOMI 1	
FT	SEQUENCE 581 AA; 64215 MW; 6885F8B9A3AD196 CCK64;	
QY	Query Match 60.8%; Score 864; DB 10; Length 581;	
QY	Best Local Similarity 61.0%; Pred. No. 1.1e-67;	
Db	Matches 161; Conservative 32; Mismatches 69; Indels 2; Gaps 1;	
QY	1 DVTGCSASEPTVAVGNKQCVADDDPDHDSQGLQPLPSKSNDDPQMTKIDGTTSS 60	
Db	317 NOTDQDPEPTVAVSNKGLCVADVDKNNKNNLIDLPKQNSQVQVQMLTRIDALRS 376	
QY	61 NSSCLITVTVGVYVYVPCNVAPEATITQIKNGKITINPSVTLAASGIGKETT 120	
Db	437 VQNTATVSSQKGLANNPEPTVAVFENDLQWAGQAGVAEESSVAREKALYEDG 496	
QY	121 VQHDYTLQSGMLANDAPREVTYGFEDLCESNGSVAVETVSSQGNRMALYDGG 180	
Db	457 VQNTATVSSQKGLANNPEPTVAVFENDLQWAGQAGVAEESSVAREKALYEDG 496	
QY	161 STEPQNN-QCLTQDSSTVYNNVSSGSGQGVFNIGAILIKNGALNDVQA 238	
Db	497 STRPDQPPAPACFLYDNDHQSGIILSSCSGSEBRKPPMDQVTLNKGALNDVQG 556	
QY	239 ANPKRLRIITVYVAPGVNQMLPV 262	
Db	557 SNPSLHQIIMVAPGVNHEMLP 580	
RESULT 12		
ID	Q06076 PRELMINARY; PRT; 528 AA.	
CC	Q06076;	
DT	01-NOV-1996 (TRENDEL, 01, Created)	
DT	01-NOV-1996 (TRENDEL, 01, Last sequence update)	
DT	01-MAR-2003 (TRENDEL, 23, Last annotation update)	
DE	Abtin-d (EC 3.2.2.22) (ZMA N-glycosidase) (Pigment).	
OS	Abtin precatorius (Indian Ixorida) (Crah's eye).	
CC	Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
CC	Magnoliophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;	
CC	NCHL; Fabales; Fabaceae; Fupliimolidae; Abreae; Abnns.	
CC	[1] Textid:5816;	
RX	SEQUENCE FROM N.A.	
RX	MEDLINE=3132798; PubMed=8421313;	
RA	Rang C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;	
RA	"Primary structure of three distinct isoforms determined by cDNA	
RL	sequencing: conservation and significance";	
RL	J. Mol. Biol. 229:263-267(1993).	
CC	-1- SPECIFIC ACTIVITY: ENOHPHOSPHATIS OF THE N-GLYCOSIDIC BOND AT ONE	
CC	SPECIFIC ADENOSINE ON THE 28S RNA.	
CC	-1- SIMILARITY RELATIONS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
CC	EMBL: M93346; AA32666.1; "	
DR	HMRP. P11340; IABR.	
DR	InterPro: IPR000772; RcinB_lectin.	
DR	InterPro: IPR001574; RIP.	

DR	Pfam: PF00652; Ricin_B_lectin; 6.
DR	Pfam: PF00161; RIP; 1.
DR	PRINTS: PR00366; SHIGARICIN.
DR	SMART: SMO0458; RICIN; 2.
DR	PROSITE: PS50231; RICIN_B_LECTIN; 2.
DR	PROSITE: PS00275; SHIGA_RICIN; 1.
KM	Hydrolase; Toxin.
FM	NON-TERMINAL
FT	520..521
SC	SEQUENCE 528 AA; 58970 MW; 62ED42BDFE60F8 CRC64;
	Query Match 53.1%; Score 756.5; DB 10; Length 528;
	Best Local Similarity 5.1%; Pred.No.2.ee-58;
	Matches 139; Conservative 46; Mismatches 71; Indels 1; Gaps 1;
Oy	CSAS-BPPTATVSRNMCVCVEDDPDQNDQILNPSSNNDPQNLTIKEDTIRSGS 63
Dd	5 GSAS-BPPTATVSRNMCVCVEDDPDQNDQILNPSSNNDPQNLTIKEDTIRSGS 63
Oy	CLTFYTGAYGVYVPCDMQVRELTQNTQNGCTIIPNSVLTAASGLKETLTYQC 123
Dd	269 CSASBPPTATVSRNMCVCVEDDPDQNDQILNPSSNNDPQNLTIKEDTIRSGS 328
Oy	CLTEGYAGQVYVYIDGTSAAVAATYWEINDGTIIPEASLVLSAESSMSGTLTYQC 388
Dd	339 CLTEGYAGQVYVYIDGTSAAVAATYWEINDGTIIPEASLVLSAESSMSGTLTYQC 388
Oy	LDTYGCGWLQMDTPAPEETLYSPFDLCMSNGSVWATEVSQQDNRFALVGGSGIR 183
Dd	124 LDTYGCGWLQMDTPAPEETLYSPFDLCMSNGSVWATEVSQQDNRFALVGGSGIR 183
Oy	NELMARGRMGKRGNNSTPVTYSISGSDLCQDAQSNWMLADDNNKKRQDAVALYTDSIR 448
Dd	389 NELMARGRMGKRGNNSTPVTYSISGSDLCQDAQSNWMLADDNNKKRQDAVALYTDSIR 448
Oy	PRONODCITCGRDSTVTVNVCSAGSGSQGMVITREBALIKRLANDPAQNAFLX 243
Dd	184 PRONODCITCGRDSTVTVNVCSAGSGSQGMVITREBALIKRLANDPAQNAFLX 243
Oy	SQNUNNCITCKKHQSGPIVLACNSMGQAQMPLFDDISTYSIVDWMDVYGSDBSL 508
Dd	449 SQNUNNCITCKKHQSGPIVLACNSMGQAQMPLFDDISTYSIVDWMDVYGSDBSL 508
Oy	RRIITYPAPGEPQNMFL 260
Dd	244 RRIITYPAPGEPQNMFL 260
Oy	PRELMINARY; FR; 547 AA.
ID	096659 PRELMINARY; FR; 547 AA.
EX	096659 PRELMINARY; FR; 547 AA.
RT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DR	Proteoglycanin (EC 3.2.2.2) (rRNA-N-glycosylase).
AKA:	Amino precatator (Indian locosid) (Graby's eno)
OC	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophytes; Magnoliophyta; Eudicotyledons; core eudicots; Rosidae;
OC	eucrois I; Fabales; Fabaceae; Papilionoidae; Abreae; Abrus.
OX	NCBI_TaxID=3816;
AX	[1]
RP	SEQUENCE FROM N.A.
EX	MEDLINE=20102702; PubMed=1063690;
FA	Liu C.T., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Huang M.J.,
LA	Liu C.T., Structure and Function Analysis of the Abrus precatorius
RT	proteinase A from the seed coat of the legume Abrus precatorius
RT	alpha-helix H imparts protein synthesis inhibitory activity.?
RL	J. Biol. Chem. 275:18971-19011(2000)
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOCIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR	EMBL: AF190173; AACF8309.1. ?.
DR	HSSP: P1140; IMR.
DR	Inesecio: INES01572; Ricin_A_lectin.
DR	Inesecio: INES01572; Ricin_B_lectin.
DR	Pfam: PF00652; Ricin_B_lectin; 6.
DR	Pfam: PF00161; RIP; 1.
DR	PRINTS: PR00366; SHIGARICIN.
DR	SMART: SMO0458; RICIN; 2.
DR	PROSITE: PS50231; RICIN_B_LECTIN; 2.
DR	PROSITE: PS00275; SHIGA_RICIN; 1.
FM	Hydrolase; Toxin.

SEQUENCE 547 AA; 61248 MW; 355A25C354A1BD CRC64;
Query Match
Best Local Similarity 53.1%; Score 753.5; DB 10; Length 547;
Matches 138; Conservative 41; Mismatches 76; Indels 1; Gaps 1;
QY 5 CSAS-EPTVAIVGNKVCVDRDDPDHNGNOIQIAMSNSKNDNDOLMTIRKGTIRSGNSGLTYV 63
DB 288 CSAS-EPTVAIVGNKVCVDRDDPDHNGNOIQIAMSNSKNDNDOLMTIRKGTIRSGNSGLTYV 63
QY 64 CLTYGYTAGVYVIMFDGNCNVAERATYVQNGNTIIPRSNVLAAASGKLTLYVOT 123
DB 348 CLTYGYTAGVYVIMFDGNCNVAERATYVQNGNTIIPRSNVLAAASGKLTLYVOT 123
QY 124 LDYTLGGWLAGNDTAPREVTIYGFRLDQESNCSQSWVETVSSQONQPMALYDGSIR 183
DB 408 NDTRNRQSGMRTGNDISPEVTISLNGFPLDCHRNQSNMVLVDYDIKESQMAVYDPSIR 467
QY 184 PRONDOCTCGRDSVTYVIVNVCASGSGQWTFMEGALINLNGLADYVQANPEL 243
DB 468 PRONDOCTCGRDSVTYVIVNVCASGSGQWTFMEGALINLNGLADYVQANPEL 243
QY 244 RLIIYVATGKKNQW 259
DB 528 KOIIMPYTGANQW 543
RESULT 14
QY 085N43 PRELIMINARY; PRT; 382 AA.
AC 085N43;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Abirin isoform G (EC 3.2.2.22) (tRNA N-glycosidase)
DB (Fragment).
OS Abirus precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotids I; Fabales; Fabaceae; Papilionoideae; Abraceae; Abirus.
CC NCBI_TaxID=3816;
RN 111; TaxID=3816;
RS 111; SOURCE FROM N.A.
RA Cook J.P., Roberts L.M., Lord M.;
RT "New isoform of Abirin - Abirin G";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF479828; AAL7744.1; -;
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00452; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIB_1_lectin; 1.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00231; RICIN B LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Toxin.
FT NON_TER 1
FT CHAIN 1 >105 ABRIN A CHAIN.
FT NON_TER 382 >382 ABRIN B CHAIN.
FT CHAIN 382
SQ SSQDENCE 382 AA; 42743 MW; B08AB341813AD2EE CRC64;
Query Match
Best Local Similarity 53.2%; Score 743; DB 10; Length 382;
Matches 135; Conservative 43; Mismatches 74; Indels 0; Gaps 0;
QY 9 EPTVAIVGNKVCVDRDDPDHNGNOIQIAMSNSKNDNDOLMTIRKGTIRSGNSGLTYV 68
DB 128 EPTVAIVGNKVCVDRDDPDHNGNOIQIAMSNSKNDNDOLMTIRKGTIRSGNSGLTYV 187

QY 69 GTVAGVYVIMFDGNCNVAERATYVQNGNTIIPRSNVLAAASGKLTLYVOTLYTL 128
DB 186 GTVAGVYVIMFDGNCNVAERATYVQNGNTIIPRSNVLAAASGKLTLYVOTLYTL 128
QY 129 GQWLAGNDTAPREVTIYGFRLDQESNCSQSWVETVSSQONQPMALYDGSIRPQNQ 188
DB 246 GQWLAGNDTAPREVTIYGFRLDQESNCSQSWVETVSSQONQPMALYDGSIRPQNQ 188
QY 189 DQCTICGRDSVTYVIVNVCASGSGQWTFMEGALINLNGLADYVQANPELRII 248
DB 306 DQCTICGRDSVTYVIVNVCASGSGQWTFMEGALINLNGLADYVQANPELRII 248
QY 249 YPATGKPNQWML 260
DB 368 WPTGKPNQWML 379
RESULT 15
QY 08W28 PRELIMINARY; PRT; 573 AA.
AC 08W28;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Ribosome-inactivating protein IPAR (EC 3.2.2.22) (tRNA N-glycosidase)
DB (Fragment).
OS Iris hollandica (Dutch iris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
CC NCBI_TaxID=35876;
RN 111; TaxID=35876;
RS 111; SOURCE FROM N.A.
RA Van Damme E.J.M., Peumans W.J.;
RT "Iris (iris hollandica var. Professor Blaauw) plants express both type
1 and type 2 ribosome-inactivating proteins in bulb tissue";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF35084; AAL5093.1; -;
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00452; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIB_1_lectin; 1.
DR SMART: SM00458; SHIGA_RICIN.
DR PROSITE: PS00231; RICIN B LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Toxin.
FT NON_TER 1
SQ SSQDENCE 573 AA; 63759 MW; 141A3B9ACD4F5C CRC64;
Query Match
Best Local Similarity 48.2%; Score 684; DB 10; Length 573;
Matches 130; Conservative 42; Mismatches 86; Indels 2; Gaps 2;
QY 1 DPTVCASEPPTVAIVGNKVCVDRDDPDHNGNOIQIAMSNSKNDNDOLMTIRKGTIRSG 60
DB 311 DPTVCASEPPTVAIVGNKVCVDRDDPDHNGNOIQIAMSNSKNDNDOLMTIRKGTIRSG 60
QY 61 NSGLTYGYTAGVYVIMFDGNCNVAERATYVQNGNTIIPRSNVLAAASGKLTLYVOT 120
DB 371 NSGLTYGYTAGVYVIMFDGNCNVAERATYVQNGNTIIPRSNVLAAASGKLTLYVOT 120
QY 121 VQTLVYTAGVYVIMFDGNCNVAERATYVQNGNTIIPRSNVLAAASGKLTLYVOT 179
DB 430 VQTLVYTAGVYVIMFDGNCNVAERATYVQNGNTIIPRSNVLAAASGKLTLYVOT 179
QY 180 GSIRPNQWQOQCTCGRDSVTYVIVNVCASGSGQWTFMEGALINLNGLADYVQANPEL 239
DB 490 GSIRPNQWQOQCTCGRDSVTYVIVNVCASGSGQWTFMEGALINLNGLADYVQANPEL 239

Thu Dec 11 17:00:23 2003

US-09-601-667C-6.rag

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 16:56:51, Search time 43 seconds

Title: US-09-601-667C-6
Sequence: 1 DVTCSASEPTWRIYGRNM.....RRITVATKPNQWLPVP 263

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A:Geneseq_1901003.*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1406	100.0	263	20	AAW90127	Mistletoe lectin B
2	1406	100.0	263	20	AAW90127	Mistletoe lectin B
3	1420	100.0	531	20	AAW25982	Mistletoe lectin B
4	1420	100.0	531	20	AAW25982	Mistletoe lectin B
5	1406	99.0	263	19	AAW64662	Mistletoe lectin B
6	1406	99.0	263	19	AAW64662	Mistletoe lectin B
7	1406	99.0	263	20	AAW90126	Mistletoe lectin B
8	1406	99.0	263	19	AAW64660	Mistletoe lectin B
9	1406	99.0	564	18	AAW10021	Prepro mistletoe 1

10	1406	99.0	564	20	AAW90127	Mistletoe lectin B
11	1339.5	94.3	264	20	AAW25986	Mistletoe lectin B
12	1339.5	94.3	265	20	AAW25992	Mistletoe lectin B
13	1333.5	93.9	264	20	AAW25988	Mistletoe lectin B
14	1333.5	93.9	265	20	AAW25994	Mistletoe lectin B
15	1332	93.8	267	19	AAW64667	Mistletoe lectin B
16	1326.5	93.4	264	20	AAW25985	Mistletoe lectin B
17	1326.5	93.4	265	20	AAW25990	Mistletoe lectin B
18	1324.5	93.3	265	20	AAW25996	Mistletoe lectin B
19	1324.5	93.3	264	20	AAW25987	Mistletoe lectin B
20	1306.5	92.0	264	20	AAW25989	Mistletoe lectin B
21	1306.5	92.0	265	20	AAW25993	Mistletoe lectin B
22	1277.5	90.0	264	20	AAW25978	Mistletoe lectin B
23	1277.5	90.0	264	20	AAW25972	Mistletoe lectin B
24	1277.5	90.0	264	20	AAW25975	Mistletoe lectin B
25	1277.5	90.0	533	20	AAW25970	Mistletoe lectin B
26	1277.5	90.0	533	20	AAW25973	Mistletoe lectin B
27	1277.5	90.0	533	20	AAW25976	Mistletoe lectin B
28	1189	83.7	263	22	AAW47095	B-chain isoform to
29	1189	83.7	263	22	AAW47095	B-chain isoform to
30	1189	83.7	263	22	AAW47095	B-chain isoform to
31	1061.5	78.7	261	23	AAW47093	Sequence of prepro
32	915	64.4	565	6	AAW50166	Castor bean prepro
33	915	64.4	565	22	AAW78300	Modified castor be
34	913	64.3	574	8	AAW78304	Sequence of Ricinu
35	913	64.3	574	10	AAW94793	Castor bean ricin
36	913	64.3	576	18	AAW25877	Castor bean ricin
37	913	64.3	576	20	AAW25892	Ricinus communis r
38	913	64.3	576	21	AAW78502	Castor bean prepro
39	913	64.3	576	22	AAW78502	Castor bean prepro
40	913	64.3	576	7	AAW78502	Sequence of Ricinu
41	913	64.3	576	7	AAW78502	Sequence of Ricinu
42	907	63.9	262	10	AAW90020	B chain of ricin D
43	905	63.7	576	6	AAW70326	Sequence of Ricinu
44	904	63.7	262	9	AAW92896	Ricin B subunit wit

PT Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 9, Fig 7B, 78pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to and activates T-cells and
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cells and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC derived from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B protein.
 XX
 SQ Sequence 263 AA:
 Query Match 100.0%; Score 1420; DB 20; Length 263;
 Best Local Similarity 100.0%; Pred. No. 5,4e-130;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 DDVTGASAEPTVAVKNNKCVADDDPHDNGQIQLPKSKNDPQQLMTTKRGGTIR 60
 QY 1 DDVTGASAEPTVAVKNNKCVADDDPHDNGQIQLPKSKNDPQQLMTTKRGGTIR 60
 DB 61 NSGLTGYGTAGVYVAFPCNNAVREATTQWNGNTINPSSNLVLAASGIGKTTT 120
 QY 61 NSGLTGYGTAGVYVAFPCNNAVREATTQWNGNTINPSSNLVLAASGIGKTTT 120
 DB 61 NSGLTGYGTAGVYVAFPCNNAVREATTQWNGNTINPSSNLVLAASGIGKTTT 120
 QY 121 VQTLDDYTLGGWLAGNDTPREVTIYGFRLCMBSNGSGVWVETCVSQONRMALYGDG 180
 DB 121 VQTLDDYTLGGWLAGNDTPREVTIYGFRLCMBSNGSGVWVETCVSQONRMALYGDG 180
 QY 181 SIFPKQNDQCLTGKDSVSTVINIVSCAGSSGQWVFTNEGALINLKNGLAMDVAQAN 240
 DB 181 SIFPKQNDQCLTGKDSVSTVINIVSCAGSSGQWVFTNEGALINLKNGLAMDVAQAN 240
 QY 241 PKLRRIITYPATGKRNQMLFVP 263
 DB 241 PKLRRIITYPATGKRNQMLFVP 263
 XX
 RESULT 2
 AA125991
 ID AA125991 standard; Protein: 264 AA.
 XX
 AC AA125991;
 XX
 DT 18-OCT-1999 (first entry)
 XX
 DE Mistletoe lectin B variant protein fragment.
 XX
 KW Mistletoe lectin; antitumor; immunostimulant; A-chain; MA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B.
 XX
 CS Viscum album.
 PN DE19804210-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 03-FEB-1998; 98DE-1004210.
 XX
 PR 03-FEB-1998; 98DE-1004210.
 XX
 FX (BIOS-) BIOSIS ARZNEIMITTEL GMBH.
 XX

PT Morris P, Stiefel T, Voelker W, Walters P;
 XX WPI; 1999-44535/38.
 DR N-PDB; AA09115.
 XX
 CC Preparation of mistletoe lectins in heterologous systems,
 CC particularly for use as anticancer agents and immunostimulants
 CC
 CC Disclosure, Fig 13b, 78pp; German.
 CC
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The B-chain (MA)
 CC of the mistletoe lectin binds to and inactivates T-cells and
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cells and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC derived from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B protein.
 XX
 SQ Sequence 264 AA:
 Query Match 100.0%; Score 1420; DB 20; Length 264;
 Best Local Similarity 100.0%; Pred. No. 5,5e-130;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 DDVTGASAEPTVAVKNNKCVADDDPHDNGQIQLPKSKNDPQQLMTTKRGGTIR 60
 QY 1 DDVTGASAEPTVAVKNNKCVADDDPHDNGQIQLPKSKNDPQQLMTTKRGGTIR 60
 DB 1 DDVTGASAEPTVAVKNNKCVADDDPHDNGQIQLPKSKNDPQQLMTTKRGGTIR 60
 QY 61 NSGLTGYGTAGVYVAFPCNNAVREATTQWNGNTINPSSNLVLAASGIGKTTT 120
 DB 61 NSGLTGYGTAGVYVAFPCNNAVREATTQWNGNTINPSSNLVLAASGIGKTTT 120
 QY 61 NSGLTGYGTAGVYVAFPCNNAVREATTQWNGNTINPSSNLVLAASGIGKTTT 120
 DB 61 NSGLTGYGTAGVYVAFPCNNAVREATTQWNGNTINPSSNLVLAASGIGKTTT 120
 QY 121 VQTLDDYTLGGWLAGNDTPREVTIYGFRLCMBSNGSGVWVETCVSQONRMALYGDG 180
 DB 121 VQTLDDYTLGGWLAGNDTPREVTIYGFRLCMBSNGSGVWVETCVSQONRMALYGDG 180
 QY 181 SIFPKQNDQCLTGKDSVSTVINIVSCAGSSGQWVFTNEGALINLKNGLAMDVAQAN 240
 DB 181 SIFPKQNDQCLTGKDSVSTVINIVSCAGSSGQWVFTNEGALINLKNGLAMDVAQAN 240
 QY 241 PKLRRIITYPATGKRNQMLFVP 263
 DB 241 PKLRRIITYPATGKRNQMLFVP 263
 XX
 RESULT 3
 AA125979
 ID AA125979 standard; Protein: 531 AA.
 XX
 AC AA125979;
 XX
 DT 18-OCT-1999 (first entry)
 XX
 DE Mistletoe lectin I protein fragment.
 XX
 KW Mistletoe lectin; antitumor; immunostimulant; A-chain; MA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin I.
 XX
 CS Viscum album.
 PN DE19804210-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 03-FEB-1998; 98DE-1004210.
 XX
 PR 03-FEB-1998; 98DE-1004210.
 XX
 FX (BIOS-) BIOSIS ARZNEIMITTEL GMBH.
 XX

Thu Dec 11 17:00:23 2003

us-09-601-667c-6.rag

Page 4

NW		Internal disease; treatment; disorder; cell proliferation; activation;
KX		autoimmune disease; allergy; tumour; ricin; translocation.
OS	Viscum album.	
XX		
PN	M09829540-A2.	
PD	09-JUL-1998.	
PF	02-JAN-1998; 38NO-BP00009.	
PR	02-JAN-1997; 97EB-0100012.	
PX	(BRAT) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.	
PI	Eck J, Schmidt A, Zinke H.	
DR	Wfi; 1998-388122/33.	
NR	N-PSDB; AAIV51344.	
CC	Nucleic acid encoding fusion protein containing mistletoe lectin A chain - useful for treatment of proliferative and autoimmune diseases, allergies and tumours	
PS	Disclosure; Fig 11b'; 11sep; German.	
XX	This sequence represents a variant mistletoe lectin B-chain, mLB. This sequence can be used in the construction of a fusion protein which comprises an effector module that is cytotoxic intracellularly, a processing module covalently bonded to the effector module and containing a protease recognition sequence, and a targeting module covalently bonded to the processing module, able to bind specifically to the surface of a cell so as to mediate internalisation of the fusion protein. Such a fusion protein can be used for treating disorders involving immunodeficiency and elevated activation of cells, especially autoimmune disease, allergy and leukaemia. The proteins can be administered e.g. by injection or topically, but especially by intravenous infusion at 1 mg to 500 mg/g/day, or for ex vivo use at 1 pg to 500 ng/ml.	
CC	Fusion proteins can develop toxic activity in a wide range of target cells. The processing module prevents extracellular dissociation, and fusion proteins based on mistletoe lectin A-chain are far more active than those based on ricin and do have the associated problems of low-specific toxicity. The protein may be expressed in a non-glycosylated form.	
CC	Long half-life in the blood stream. Mistletoe lectin B-chain is used, it actively resists in translation of the Nd A-chain from the endoplasmic reticulum to the cytoplasm.	
SQ	Sequence 263 AA:	
XX		
Query Match:	99.0%; Score 1406; DB 19; Length 263;	
Best Local Similarity:	98.9%; Pred. No. 1,3e+128;	
Matches 260:	Conservative 2; Mismatches 1; Indels 0; Gaps 0	
Dy	1 DDTGSAASEPTTAYRGNMCKVYDPDHDNDQIQIMSGKSNDDPGCTITREGGTIRS 60	
Qy	1 DDTGSAASEPTTAYRGNMCKVYDPDHDNDQIQIMSGKSNDDPGCTITREGGTIRS 60	
Dx	1 DDVTGSASEPTTAYRGNMCKVYDMDPDFDNDQIQIMSPSKNNDDPGTITKHDDGIS 60	
Dz	61 NSGCITTYGTAGTVGVVYVFDNNANVAEKLTIWGNGTIFNPSNVLVAASGIGKITLT 120	
Qz	61 NSGCITTYGTAGTVGVVYVFDNNANVAEKLTIWGNGTIFNPSNVLVAASGIGKITLT 120	
Dd	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Df	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Dg	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Dh	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qd	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qf	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qg	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qh	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qi	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qj	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qk	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Ql	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qm	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qn	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qo	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qp	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qq	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qr	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qs	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qt	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qu	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qv	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qw	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qx	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qy	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Qz	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rd	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rf	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rg	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rh	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Ri	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rj	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rk	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rl	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rm	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rn	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Ro	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rp	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rq	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rr	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rs	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rt	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Ru	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rv	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rw	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rx	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Ry	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Rz	121 VQIDLYTLTGGMALKNVDTPHETLTYGRDLCHESNGSVMVFETYSQQSQNFALYVG 180	
Sd	1	

[illegible]

RESULT 7

AAM90126
 ID AAM90126 standard; Protein; 264 AA.
 XX
 AC AAM90126;
 XX
 XX 20-MAR-2003 (updated)
 XX 30-MAR-1999 (first entry)
 XX
 DE Mistletoe ML B-chain protein.
 XX
 XX ML; mistletoe; lectin; MLB; B-chain; transgenic plant; glycosylation;
 KW dimer; immunotoxin; large-scale production; diagnosis; therapeutic;
 KW cancer.
 XX
 OS Viscum album.
 XX
 XX EP984388-A1.
 XX
 PD 16-DEC-1998.
 XX
 PF 26-JUN-1995; 98EP-0105660.
 XX
 PR 26-JUN-1995; 95EP-0109949.
 PR 26-JUN-1995; 98EP-0105660.
 XX
 XX (NADU) MADRUS KOEIN AG.
 XX
 PA Baur A, Eck J, Lentzen H, Zinke H;
 PT WPI; 1999-026582/03.
 DR N-PSDB; AAV74181.
 XX
 XX New transgenic plant expressing mistletoe lectin - useful for
 PT producing recombinant lectin in e.g. cancer diagnosis and therapy
 XX
 XX Disclosure; Fig 4b; 30pp; German.
 PS
 XX This invention describes a novel transgenic plant transformed with a
 CC vector capable of encoding a mistletoe (Viscum album) lectin
 CC preproprotein or a biologically active fragment. The specification
 CC describes a polypeptide produced by a plant where the polypeptide
 CC exhibits a specific sequence at the N-terminus, a fusion protein
 CC that occurs in Viscum album or the polypeptide is a fusion protein
 CC mistletoe lectin polypeptide dimer and an immunotoxin comprising the
 CC polypeptide or the polypeptide dimer. The plants are used for large-scale
 CC production of mistletoe lectin for diagnostic or therapeutic purposes
 CC (e.g. in cancer therapy). This sequence represents the mistletoe lectin
 CC B-chain which is contained in expression vector pT7MB.
 CC (Updated on 20-MAR-2003 to correct PF field.)
 XX
 XX
 SQ Sequence 264 AA;
 Query Match 99.0%; Score 1406; DB 20; Length 264;
 Best Local Similarity 98.9%; Pred. NO. 1,35-128;
 Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DDTVCASAEPTVIVGKMGKCVVDDDFHGNQIQIOLMPSKSNNDPNQMLATIKRGGTIRS 60
 DB 2 DDTVCASAEPTVIVGKMGKCVVDDDFHGNQIQIOLMPSKSNNDPNQMLATIKRGGTIRS 61
 QY 61 NSGCLTGYTGAGYVMIIPDONTAVRRLTIQIWGNTINPNSMLVLAASGGIKGTTLT 120
 DB 62 NSGCLTGYTGAGYVMIIPDONTAVRRLTIQIWGNTINPNSMLVLAASGGIKGTTLT 121
 QY 121 VQTLDTYTLGGWLGMDTNPRLTVYGRPLQNSGSGWTFVTSQQNQRLHVGK 180
 DB 122 VQTLDTYTLGGWLGMDTNPRLTVYGRPLQNSGSGWTFVTSQQNQRLHVGK 181
 QY 181 SIIPKQNDQCLTCGRDSVTYNTIVSCASGSGQKRWTFNEGATILNKGILMDVDAQAN 240
 DB 182 SIIPKQNDQCLTCGRDSVTYNTIVSCASGSGQKRWTFNEGATILNKGILMDVDAQAN 241
 QY 241 PKLRRIIVPATGKNQMLPVP 263

DB 242 PKLRRIIVPATGKNQMLPVP 264
 RESULT 8
 XX AAM64660
 XX AAM64660 standard; Protein; 267 AA.
 XX
 XX AAM64660;
 XX
 XX 23-OCT-1998 (first entry)
 XX
 DE Mistletoe TMB protein.
 XX
 XX Lectin B-chain; mistletoe; TMB; fusion protein; effector; cytotoxic;
 KW intracellular; processing module; protease recognition; targeting module;
 KW internalisation; treatment; disorder; cell proliferation; activation;
 KW autoimmune disease; allergy; tumour; feline; translocation.
 XX
 OS Viscum album.
 XX
 XX WO9823540-A2.
 XX
 PD 09-JUN-1998.
 XX
 PF 02-JAN-1998; 98WO-EP00009.
 XX
 PR 02-JAN-1997; 97EP-0100012.
 PR (BR/1-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.
 XX
 XX Eck J, Schmidt A, Zinke H;
 PT WPI; 1998-388122/33.
 DR N-PSDB; AAV51342.
 XX
 XX Nucleic acid encoding fusion protein containing mistletoe lectin A
 PT chain - useful for treatment of proliferative and autoimmune
 PT diseases, allergies and tumours
 XX
 XX Disclosure; Fig 11b; 115pp; German.
 PS
 XX This sequence represents a lectin B-chain, TMB, isolated from mistletoe.
 CC This sequence can be used in the construction of a fusion protein which
 CC comprises an effector module that is cytotoxic intracellularly, a
 CC processing module covalently bonded to the effector module and
 CC containing a protease recognition sequence, and a targeting module
 CC covalently bonded to the processing module, able to bind specifically to
 CC the surface of a cell so as to mediate internalisation of the fusion
 CC protein. Such a fusion protein can be used for treating disorders
 CC involving proliferation and/or elevated activation of cells, especially
 CC autoimmune disease, allergy and tumours. The proteins can be administered
 CC e.g. by injection or topically but especially by intravenous infusion.
 CC at a dose of 500 mg/kg/day, or for ex vivo use at 1 pg to 500 ng/ml.
 CC cells. The processing module prevents extracellular dissociation and
 CC fusion proteins based on mistletoe lectin A-chain are far more active
 CC than those based on ricin and do have the associated problems of
 CC non-specific toxicity. The protein may be expressed in a non-glycosylated
 CC form that does not bind to sugar receptors in the liver, and which has a
 CC long half-life in the blood. Where the mistletoe lectin B-chain is used,
 CC it actively assists in translocation of the ML A-chain from the
 CC endoplasmic reticulum to the cytoplasm.
 XX
 XX
 SQ Sequence 267 AA;
 Query Match 99.0%; Score 1406; DB 19; Length 267;
 Best Local Similarity 98.9%; Pred. NO. 1,35-128;
 Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DDTVCASAEPTVIVGKMGKCVVDDDFHGNQIQIOLMPSKSNNDPNQMLATIKRGGTIRS 60
 DB 1 DDTVCASAEPTVIVGKMGKCVVDDDFHGNQIQIOLMPSKSNNDPNQMLATIKRGGTIRS 60

QY 61 NSGCLTYGTAGAGVYMFDCNTAVREATTIWIWNGITIIIPRSNVLVAASSGIKGTTT 120
 DB 61 NSGCLTYGTAGAGVYMFDCNTAVREATTIWIWNGITIIIPRSNVLVAASSGIKGTTT 120
 QY 121 VQTLDTYTLGGMLAGNDTARREVTIYGFRLCHESNGSVWERTCVSQQRNALYGDG 180
 DB 121 VQTLDTYTLGGMLAGNDTARREVTIYGFRLCHESNGSVWERTCVSQQRNALYGDG 180
 QY 181 SIRPKONODCLTCGRDSVSTIVINIVSCASSGQGRVFTNEGALINAGLAMDVAQN 240
 DB 181 SIRPKONODCLTCGRDSVSTIVINIVSCASSGQGRVFTNEGALINAGLAMDVAQN 240
 QY 241 PKLRRIIYPATGKPKQMWLPVP 263
 DB 241 PKLRRIIYPATGKPKQMWLPVP 263

RESULT 9
 ID AAM10021 standard; Protein: 564 AA.
 AC AAM10021;
 DT 18-DEC-1997 (first entry)
 XX
 DE Prepro mistletoe lectin.
 XX
 KM Mistletoe; lectin; cytotoxic; A chain; B chain; dimer.
 XX
 OS Viscum album.
 XX
 PN EP751221-A1.
 XX
 PD 02-JAN-1997.
 XX
 PF 26-JUN-1995; 95EP-0109949.
 XX
 PR 26-JUN-1995; 95EP-0109949.
 XX
 PA (MADU) MADUS KOELEN AG.
 XX
 PI Baur A, Eck J, Lentzen H, Zinke H;
 XX
 DR WPI; 1997-054678/06.
 DR N-PSDB; AAT70473.
 XX

XX Nucleic acid encoding prepro form of mistletoe lectin - for
 PT therapeutic or diagnostic use
 XX
 PS Claim 12; Fig 4c; 30pp; German.
 XX
 CC Mistletoe lectin is a cytotoxic agent that has been used for tumour
 CC chemotherapy. It can be used as a cytotoxic and medicament. Nucleic
 CC acid fragments can be used in diagnostic and therapeutic purposes.
 CC AAT70473) comprises an A chain (AAT70473) and a B chain (AAT70473).
 XX
 SQ Sequence 564 AA;

Query Match 99.0%; Score 1406; DB 18; Length 564;
 Best Local Similarity 98.9%; Pred. No. 3.8e-128;
 Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPTGCSAEPPTVIRGNKCTVDVDDPHDSQGLQIMPSKANDNQMTTKEDGTTIS 60
 DB 302 DPTGCSAEPPTVIRGNKCTVDVDDPHDSQGLQIMPSKANDNQMTTKEDGTTIS 60
 QY 61 NSGCLTYGTAGAGVYMFDCNTAVREATTIWIWNGITIIIPRSNVLVAASSGIKGTTT 120
 DB 61 NSGCLTYGTAGAGVYMFDCNTAVREATTIWIWNGITIIIPRSNVLVAASSGIKGTTT 120
 QY 362 NSGCLTYGTAGAGVYMFDCNTAVREATTIWIWNGITIIIPRSNVLVAASSGIKGTTT 421
 DB 362 NSGCLTYGTAGAGVYMFDCNTAVREATTIWIWNGITIIIPRSNVLVAASSGIKGTTT 421
 QY 121 VQTLDTYTLGGMLAGNDTARREVTIYGFRLCHESNGSVWERTCVSQQRNALYGDG 180
 DB 121 VQTLDTYTLGGMLAGNDTARREVTIYGFRLCHESNGSVWERTCVSQQRNALYGDG 180

DB 422 VQTLDTYTLGGMLAGNDTARREVTIYGFRLCHESNGSVWERTCVSQQRNALYGDG 481
 QY 181 SIRPKONODCLTCGRDSVSTIVINIVSCASSGQGRVFTNEGALINAGLAMDVAQN 240
 DB 482 SIRPKONODCLTCGRDSVSTIVINIVSCASSGQGRVFTNEGALINAGLAMDVAQN 541
 QY 241 PKLRRIIYPATGKPKQMWLPVP 263
 DB 542 PKLRRIIYPATGKPKQMWLPVP 564

RESULT 10
 ID AAM90127 standard; Protein: 564 AA.
 AC AAM90127;
 DT 20-MAR-2003 (updated)
 DT 30-APR-1999 (first entry)
 XX
 DE Mistletoe lectin prepro-protein.
 XX
 KM Mistletoe; lectin; ML; transgenic plant; glycosylation;
 XX
 OS Viscum album.
 XX
 PN EP884388-A1.
 XX
 PD 16-DEC-1998.
 XX
 PF 26-JUN-1995; 98EP-0105660.
 XX
 PR 26-JUN-1995; 98EP-0109949.
 XX
 PA (MADU) MADUS KOELEN AG.
 XX
 PI Baur A, Eck J, Lentzen H, Zinke H;
 XX
 DR WPI; 1999-026582/03.
 DR N-PSDB; AAM74182.
 XX

XX New transgenic plant expressing mistletoe lectin - useful for
 PT producing recombinant lectin in e.g. cancer diagnosis and therapy
 XX
 PS Claim 1a; Fig 4c; 30pp; German.
 XX
 CC This invention describes a novel transgenic plant transformed with a
 CC vector capable of encoding a mistletoe (Viscum album) lectin
 CC preproprotein or a biologically active fragment. The specification
 CC also describes a polypeptide produced by a plant where the polypeptide
 CC exhibits at least one enzymatic modification other than the glycosylation
 CC that occurs in Viscum album or the polypeptide is a fusion protein, a
 CC mistletoe lectin polypeptide dimer and an immunotoxin comprising the
 CC polypeptide or the polypeptide dimer. The plants are used for large-scale
 CC production of mistletoe lectin for diagnostic or therapeutic purposes
 CC (e.g. in cancer therapy). This sequence represents the mistletoe lectin
 CC used in the method of the invention (pf field.1)
 XX
 SQ Sequence 564 AA;

Query Match 99.0%; Score 1406; DB 20; Length 564;
 Best Local Similarity 98.9%; Pred. No. 3.8e-128;
 Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPTGCSAEPPTVIRGNKCTVDVDDPHDSQGLQIMPSKANDNQMTTKEDGTTIS 60
 DB 302 DPTGCSAEPPTVIRGNKCTVDVDDPHDSQGLQIMPSKANDNQMTTKEDGTTIS 60
 QY 61 NSGCLTYGTAGAGVYMFDCNTAVREATTIWIWNGITIIIPRSNVLVAASSGIKGTTT 120
 DB 61 NSGCLTYGTAGAGVYMFDCNTAVREATTIWIWNGITIIIPRSNVLVAASSGIKGTTT 120

DB 362 NSCLCTTGYAGVYVMIEDCNVAREATIMQIMONGTIIIPRSNLVLAASSGIGKTTLT 421
QY 121 VQTLDTYTLGGQMLAGNDTAPREVTIYGRDLCMESNGSVMWETCVSSQONQRMALYGDG 180
DB 422 VQTLDTYTLGGQMLAGNDTAPREVTIYGRDLCMESNGSVMWETCVSSQONQRMALYGDG 481
QY 181 SIREKONODQCTLCGRDSVSTVINIVSCAGSSGQRWVFTNEGAILNLKGLAMDVAQA 240
DB 482 SIREKONODQCTLCGRDSVSTVINIVSCAGSSGQRWVFTNEGAILNLKGLAMDVAQA 541
QY 241 PMLRRIIITYPATGKPNQMLPVP 263
DB 542 PMLRRIIITYPATGKPNQMLPVP 564

RESULT 11

AAZ5986
ID AAZ5986 standard; Protein; 264 AA.

AAZ5986;
18-OCT-1999 (first entry)

DB Mistletoe lectin B1 protein fragment.

KM Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
KX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KV cancer; cytotoxicity; antigen; isoform; lectin B1.

OS Viscum album.

PN DE19804210-A1.

PD 12-AUG-1999.

PE 03-FEB-1998; 98DE-1004210.

PF 03-FEB-1998; 98DE-1004210.

PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

PI Morris P. Stiefel T. Voelter W. Walters P;

DR WPI; 1999-44535/38.

DN N-PSDB; AA209110.

PT Preparation of mistletoe lectins in heterologous systems,
particularly for use as anticancer agents and immunostimulants

Claim 9; Fig 8b; 78pp; German.

CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a mistletoe lectin B1 protein.

Sequence 264 AA;

Query Match 94.3%; Score 1339.5; DB 20; Length 264;
Best Local Similarity 95.8%; Pred. No. 3.8e-122;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 DVTCSASBPFTVRIYGRNKGKVDVEDDDPHDNOIQIMPSKSNQNPQNLTKDGTIRS 60
DB 1 DVTCSASBPFTVRIYGRNKGKVDVEDDDPHDNOIQIMPSKSNQNPQNLTKDGTIRS 60
QY 61 NSCLCTTGYAGVYVMIEDCNVAREATIMQIMONGTIIIPRSNLVLAASSGIGKTTLT 120
DB 61 NSCLCTTGYAGVYVMIEDCNVAREATIMQIMONGTIIIPRSNLVLAASSGIGKTTLT 120
QY 121 VQTLDTYTLGGQMLAGNDTAPREVTIYGRDLCMESNGSVMWETCVSSQONQRMALYGD 179
DB 121 VQTLDTYTLGGQMLAGNDTAPREVTIYGRDLCMESNGSVMWETCVSSQONQRMALYGD 180
QY 180 GSIREKONODQCTLCGRDSVSTVINIVSCAGSSGQRWVFTNEGAILNLKGLAMDVAQA 239
DB 181 GSIREKONODQCTLCGRDSVSTVINIVSCAGSSGQRWVFTNEGAILNLKGLAMDVAQA 240
QY 240 PMLRRIIITYPATGKPNQMLPVP 262
DB 241 PMLRRIIITYPATGKPNQMLPVP 263

RESULT 12

AAZ5992
ID AAZ5992 standard; Protein; 265 AA.

AAZ5992;
18-OCT-1999 (first entry)

DB Mistletoe lectin B1 variant protein fragment.

KM Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
KX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KV cancer; cytotoxicity; antigen; isoform; lectin B1.

OS Viscum album.

PN DE19804210-A1.

PD 12-AUG-1999.

PE 03-FEB-1998; 98DE-1004210.

PF 03-FEB-1998; 98DE-1004210.

PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

PI Morris P. Stiefel T. Voelter W. Walters P;

DR WPI; 1999-44535/38.

DN N-PSDB; AA209116.

PT Preparation of mistletoe lectins in heterologous systems,
particularly for use as anticancer agents and immunostimulants

Disclosure; Fig 14b; 78pp; German.

CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a variant mistletoe lectin B1 protein.

Sequence 265 AA;

Query Match 94.3%; Score 1339.5; DB 20; Length 265;
 Best Local Similarity 95.8%; Pred. No. 3.9e-122;
 Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 DDTVCASAEPTVRIYVGNKQCVVDDDPHDNQIQLPMSKSNNDPNQMTTKEDGTRIS 60
 DB 1 DDTVCASAEPTVRIYVGNKQCVVDDDPHDNQIQLPMSKSNNDPNQMTTKEDGTRIS 60
 QY 61 NSGCLTGYGTAGVYVIMFDQNTAVRENTIWIQNGNIIIPRSNLYVLAASGIGKFTLT 120
 DB 61 NSGCLTGYGTAGVYVIMFDQNTAVRENTIWIQNGNIIIPRSNLYVLAASGIGKFTLT 120
 QY 121 VQTLDTYTLGGQMLAGNDTAVRENTIWIQNGNIIIPRSNLYVLAASGIGKFTLT 179
 DB 121 VQTLDTYTLGGQMLAGNDTAVRENTIWIQNGNIIIPRSNLYVLAASGIGKFTLT 180
 QY 180 GSIRPKNOQDCLTSGRDSVSTVINIVSGASGSGRWFTNKGALINLKGALMDVDAQ 239
 DB 181 GSIRPKNOQDCLTSGRDSVSTVINIVSGASGSGRWFTNKGALINLKGALMDVDAQ 240
 QY 240 NPKLRRIIYFATGKPNQMLPV 262
 DB 241 NPKLRRIIYFATGKPNQMLPV 263

RESULT 13

AAZ5988
 ID AAZ5988 standard; Protein: 264 AA.

XX AAZ5988;
 AC AAZ5988;

DT 18-OCT-1999 (first entry)
 XX

DE Mistletoe lectin B3 protein fragment.
 XX

KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KM ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;

KM cancer; cytotoxicity; antigen; isoform; lectin B3.
 XX

OS Viscum album.
 XX

PN DE19804210-AL.
 XX

PD 12-AUG-1999.
 XX

PE 03-FEB-1998; 98DE-1004210.
 XX

PR 03-FEB-1998; 98DE-1004210.
 XX

PK (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX

PI Morris P, Stiefel T, Voelter W, Welters P;
 XX

DR WPI; 1999-44535/38.
 XX

DR N-PSDB; AAZ09112.
 XX

PT Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants

PS Claim 9; Fig 10B; 78pp; German.
 XX

CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)

CC of the mistletoe lectin binds to and inactivates the 268 subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and

CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly

CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms

CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B3 protein.
 XX

Sequence 264 AA;
 Query Match 93.9%; Score 1339.5; DB 20; Length 264;
 Best Local Similarity 95.4%; Pred. No. 3.9e-122;
 Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DDTVCASAEPTVRIYVGNKQCVVDDDPHDNQIQLPMSKSNNDPNQMTTKEDGTRIS 60
 DB 1 DDTVCASAEPTVRIYVGNKQCVVDDDPHDNQIQLPMSKSNNDPNQMTTKEDGTRIS 60
 QY 61 NSGCLTGYGTAGVYVIMFDQNTAVRENTIWIQNGNIIIPRSNLYVLAASGIGKFTLT 120
 DB 61 NSGCLTGYGTAGVYVIMFDQNTAVRENTIWIQNGNIIIPRSNLYVLAASGIGKFTLT 120
 QY 121 VQTLDTYTLGGQMLAGNDTAVRENTIWIQNGNIIIPRSNLYVLAASGIGKFTLT 179
 DB 121 VQTLDTYTLGGQMLAGNDTAVRENTIWIQNGNIIIPRSNLYVLAASGIGKFTLT 180
 QY 180 GSIRPKNOQDCLTSGRDSVSTVINIVSGASGSGRWFTNKGALINLKGALMDVDAQ 239
 DB 181 GSIRPKNOQDCLTSGRDSVSTVINIVSGASGSGRWFTNKGALINLKGALMDVDAQ 240
 QY 240 NPKLRRIIYFATGKPNQMLPV 262
 DB 241 NPKLRRIIYFATGKPNQMLPV 263

RESULT 14

AAZ5994
 ID AAZ5994 standard; Protein: 265 AA.

XX AAZ5994;
 AC AAZ5994;

DT 18-OCT-1999 (first entry)
 XX

DE Mistletoe lectin B3 variant protein fragment.
 XX

KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KM ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;

KM cancer; cytotoxicity; antigen; isoform; lectin B3.
 XX

OS Viscum album.
 XX

PN DE19804210-AL.
 XX

PD 12-AUG-1999.
 XX

PE 03-FEB-1998; 98DE-1004210.
 XX

PR 03-FEB-1998; 98DE-1004210.
 XX

PK (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX

PI Morris P, Stiefel T, Voelter W, Welters P;
 XX

DR WPI; 1999-44535/38.
 XX

DR N-PSDB; AAZ09118.
 XX

PT Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants

PS Disclosure; Fig 16B; 78pp; German.
 XX

CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)

CC of the mistletoe lectin binds to and inactivates the 268 subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and

CC lymphokine-producing macrophages, so stimulate immunity. (I) and its

CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (e.g., tumor-associated, bacterial or viral). The method allows production of
 CC mistletoe associated with individual chains, in many different isoforms
 CC and on a large scale. It also allows the production of recombinant products
 CC free from toxins present in natural mistletoe. Recombinant products are
 CC represents a fragment of a variant mistletoe lectin B3 protein.

XX Sequence 265 AA;

Query Match 93.9%; Score 133.5; DB 20; Length 265;

Best Local Similarity 95.4%; Pred. No. 1.5e-121; Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DDTYCSASEPTVAVRIVKRGKCTVTRDDPHQVQIQLMESKSNNDPNQMTTKRGGTIR 60
 DB 1 DDTYCSASEPTVAVRIVKRGKCTVTRDDPHQVQIQLMESKSNNDPNQMTTKRGGTIR 60
 QY 61 NSGCLTGYGVGYVMIFPDNTAVRATVQWNGTINPNSNVLAASSGKGTIT 120
 DB 61 NSGCLTGYGVGYVMIFPDNTAVRATVQWNGTINPNSNVLAASSGKGTIT 120
 QY 121 VQTLDTYLLQGMALANDTAREVTVVGFEDLCMESNGSVWETCVSSQOMQ-EMALYGD 179
 DB 121 VQTLDTYLLQGMALANDTAREVTVVGFEDLCMESNGSVWETCVSSQOMQ-EMALYGD 180
 QY 121 VQTLDTYLLQGMALANDTAREVTVVGFEDLCMESNGSVWETCVSSQOMQ-EMALYGD 180
 DB 121 VQTLDTYLLQGMALANDTAREVTVVGFEDLCMESNGSVWETCVSSQOMQ-EMALYGD 180
 QY 180 GSIRKQNOQCLTGSDSVTVINIVSCASGSGQWVFNTEGATILNKGLANDVQAN 239
 DB 181 GSIRKQNOQCLTGSDSVTVINIVSCASGSGQWVFNTEGATILNKGLANDVQAN 240
 QY 240 NPKLRRIIIVPATGKQNMALPV 262
 DB 241 NPKLRRIIIVPATGKQNMALPV 263

RESURF 15

AAW64667
 18064667 standard; Protein: 267 AA.

XX
 AC AAW64667;

DT 23-OCT-1998 (first entry)

XX Mistletoe rMB protein mutant.

DE Lectin B-chain; mistletoe; rMB; fusion protein; effector; cytotoxic;

XX intracellular; processing module; protease recognition; targeting module;

KM autoimmulation; treatment; disorder; cell proliferation; activation;

KM autoimmune disease; allergy; tumor; ricin; translocation; mutant.

XX Vascum album.

OS Synthetic.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

PT Misc-difference 235
 FT /label= D23A
 FT /note= "wild-type Asp is replaced by Ala"
 FT Misc-difference 249
 FT /label= Y249A
 FT /note= "wild-type Tyr is replaced by Ala"
 FT
 XX MO9629540-A2.
 XX
 XX 09-JUL-1998.
 XX
 XX 02-JAN-1998; 98RC-SP00009.
 XX
 XX 02-JAN-1997; 97EP-0100012.
 XX
 XX (BRAI-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.
 XX Beck U, Schmidt A, Zinke H;
 XX WPI; 1998-389122/33.
 XX Nucleic acid encoding fusion protein containing mistletoe lectin A
 XX chain - useful for treatment of proliferative and autoimmune
 XX diseases, allergies and tumors
 XX Claim 14; Page -; 115pp; German.

XX This sequence represents a mutant form of the mistletoe lectin B-chain,
 CC rMB. This protein is used in the construction of a fusion protein which
 CC comprises an effector module that is cytotoxic intracellularly, a
 CC processing module covalently bonded to the effector module and
 CC containing a protease recognition sequence, and a targeting module
 CC containing a signal sequence, which is used to bind specifically to
 CC the surface of a cell so as to enable the fusion protein to enter the
 CC cell. Such a fusion protein can be used for treating disorders
 CC involving proliferation and/or elevated activation of cells, especially
 CC autoimmune disease, allergy and tumors. The proteins can be
 CC administered e.g. by injection or topically but especially by intravenous
 CC injection, at 1 ng to 500 mg/kg/day, or for ex vivo use at 1 pg to 500
 CC ng/ml. Fusion proteins can develop toxic activity in a wide range of
 CC target cells. The processing module prevents extracellular dissociation,
 CC and fusion proteins based on mistletoe lectin A-chain are far more
 CC active than those based on ricin and do have the associated problems of
 CC non-specific toxicity. The protein may be expressed in a
 CC non-specific host cell, e.g. in the blood sugar receptors in the liver,
 CC and which has a long half-life in the blood stream. The lectin A-chain
 CC B-chain is used. It actively assists in translocation of the M₁-chain
 CC from the endoplasmic reticulum to the cytoplasm.
 CC NOTE: This sequence does not appear in the specification but has been
 CC constructed from the wild-type rMB represented in AAW64667.

XX Sequence 267 AA;

Query Match 93.8%; Score 133.7; DB 19; Length 267;

Best Local Similarity 95.8%; Pred. No. 2.1e-121; Matches 252; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 DDTYCSASEPTVAVRIVKRGKCTVTRDDPHQVQIQLMESKSNNDPNQMTTKRGGTIR 60
 DB 1 DDTYCSASEPTVAVRIVKRGKCTVTRDDPHQVQIQLMESKSNNDPNQMTTKRGGTIR 60
 QY 61 NSGCLTGYGVGYVMIFPDNTAVRATVQWNGTINPNSNVLAASSGKGTIT 120
 DB 61 NSGCLTGYGVGYVMIFPDNTAVRATVQWNGTINPNSNVLAASSGKGTIT 120
 QY 121 VQTLDTYLLQGMALANDTAREVTVVGFEDLCMESNGSVWETCVSSQOMQ-EMALYGD 180
 DB 121 VQTLDTYLLQGMALANDTAREVTVVGFEDLCMESNGSVWETCVSSQOMQ-EMALYGD 180
 QY 121 VQTLDTYLLQGMALANDTAREVTVVGFEDLCMESNGSVWETCVSSQOMQ-EMALYGD 180
 DB 121 VQTLDTYLLQGMALANDTAREVTVVGFEDLCMESNGSVWETCVSSQOMQ-EMALYGD 180
 QY 181 GSIRKQNOQCLTGSDSVTVINIVSCASGSGQWVFNTEGATILNKGLANDVQAN 240
 DB 181 GSIRKQNOQCLTGSDSVTVINIVSCASGSGQWVFNTEGATILNKGLANDVQAN 240

Thu Dec 11 17:00:23 2003

us-09-601-667c-6.rag

Page 10

Qy 241 PKRRRIIYPATGKPNQWMLPVP 263
Db 241 PKRRRIIAPNGKPNQWMLPVP 263
Search completed: December 11, 2003, 16:57:49
Job time : 45 secs

Thu Dec 11 16:10:01 2003

US-09-601-667C-6.rapb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: December 11, 2003, 14:01:14 ; Search time 16.9484 Seconds
(without alignments)
2886.029 Million cell updates/sec

Title: US-09-601-667C-6
Perfect score: 1420
Sequence: 1 DVTCSASEPTVRIYGNM.....RITTPATGKNGMFLFP 263

Scoring table: BLOSUM62, Gapop 10.0, Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications PA:
1: /cgm2_6/prodata/1/pubpa/US07_PUBCOMB.pep.*
2: /cgm2_6/prodata/1/pubpa/US08_PUBCOMB.pep.*
3: /cgm2_6/prodata/1/pubpa/US06_NEW_PUB.pep.*
4: /cgm2_6/prodata/1/pubpa/US06_PUBCOMB.pep.*
5: /cgm2_6/prodata/1/pubpa/US07_NEW_PUB.pep.*
6: /cgm2_6/prodata/1/pubpa/US08_PUBCOMB.pep.*
7: /cgm2_6/prodata/1/pubpa/US08_NEW_PUB.pep.*
8: /cgm2_6/prodata/1/pubpa/US08_PUBCOMB.pep.*
9: /cgm2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
10: /cgm2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
11: /cgm2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
12: /cgm2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
13: /cgm2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
14: /cgm2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
15: /cgm2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
16: /cgm2_6/prodata/1/pubpa/US10_NEW_PUB.pep.*
17: /cgm2_6/prodata/1/pubpa/US60_NEW_PUB.pep.*
18: /cgm2_6/prodata/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1406	99.0	263	9	US-09-347-064-10
2	1406	99.0	267	9	US-09-347-064-4
3	913	64.3	576	12	US-10-083-356-1
4	198	13.9	144	15	US-10-137-077-17
5	198	13.9	144	15	US-10-074-527-5
6	164	10.3	458	15	US-10-156-761-14970
7	147.5	10.3	458	15	US-10-156-761-14970
8	146.5	10.3	458	15	US-10-156-761-14970
9	146.5	10.3	458	15	US-10-156-761-14970
10	138	9.7	536	15	US-10-156-761-14970
11	136.5	9.6	135	10	US-09-973-457-5
12	136.5	9.6	135	14	US-10-074-527-6
13	135	9.5	480	9	US-09-770-621-5
14	135	9.5	492	9	US-09-770-621-4
15	135	9.5	492	9	US-09-770-621-7

16	135	9.5	492	12	US-10-286-993-4
17	127	8.9	41	15	US-10-137-077-18
18	116	8.2	45	15	US-10-137-077-19
19	111.5	7.9	625	15	US-10-156-761-15008
20	109	7.7	41	15	US-10-137-077-20
21	107.5	7.6	612	15	US-10-001-851-25
22	102	7.2	464	15	US-09-385-748-9547
23	91.9	6.4	173	13	US-09-385-748-9547
24	91.9	6.4	173	13	US-09-385-748-9547
25	91	6.4	955	15	US-10-156-761-15004
26	90	6.3	509	14	US-10-072-152-6
27	87.5	6.2	201	15	US-10-128-714-3153
28	87.5	6.2	216	15	US-10-128-714-3153
29	87.5	6.2	2353	10	US-09-797-862-33
30	87	6.1	434	9	US-09-770-621-6
31	86.5	6.1	395	9	US-09-815-242-11833
32	85.5	6.0	355	12	US-10-203-708-44
33	85.5	6.0	1032	11	US-09-733-643-16
34	85.5	6.0	1032	12	US-10-120-801-64
35	84.5	6.0	358	15	US-10-128-714-3153
36	84.5	6.0	358	15	US-10-128-714-3153
37	84.5	6.0	247	11	US-09-880-748-1127
38	84.5	6.0	247	11	US-09-880-748-1127
39	84	5.9	770	9	US-09-815-242-11833
40	83	5.8	559	14	US-10-001-851-23
41	82.5	5.8	626	14	US-10-001-851-27
42	82.5	5.8	665	12	US-10-121-593-2
43	82.5	5.8	665	15	US-10-121-593-2
44	82	5.8	44	10	US-09-924-358-30
45	82	5.8	44	10	US-09-924-358-31

ALIGNMENTS

RESULT 1	US-09-347-064-10	Sequence 10, Appl1
1	US-09-347-064-10	Sequence 10, Appl1
2	US-09-347-064-10	Sequence 10, Appl1
3	US-09-347-064-10	Sequence 10, Appl1
4	US-09-347-064-10	Sequence 10, Appl1
5	US-09-347-064-10	Sequence 10, Appl1
6	US-09-347-064-10	Sequence 10, Appl1
7	US-09-347-064-10	Sequence 10, Appl1
8	US-09-347-064-10	Sequence 10, Appl1
9	US-09-347-064-10	Sequence 10, Appl1
10	US-09-347-064-10	Sequence 10, Appl1
11	US-09-347-064-10	Sequence 10, Appl1
12	US-09-347-064-10	Sequence 10, Appl1
13	US-09-347-064-10	Sequence 10, Appl1
14	US-09-347-064-10	Sequence 10, Appl1
15	US-09-347-064-10	Sequence 10, Appl1
16	US-09-347-064-10	Sequence 10, Appl1
17	US-09-347-064-10	Sequence 10, Appl1
18	US-09-347-064-10	Sequence 10, Appl1
19	US-09-347-064-10	Sequence 10, Appl1
20	US-09-347-064-10	Sequence 10, Appl1
21	US-09-347-064-10	Sequence 10, Appl1
22	US-09-347-064-10	Sequence 10, Appl1
23	US-09-347-064-10	Sequence 10, Appl1
24	US-09-347-064-10	Sequence 10, Appl1
25	US-09-347-064-10	Sequence 10, Appl1
26	US-09-347-064-10	Sequence 10, Appl1
27	US-09-347-064-10	Sequence 10, Appl1
28	US-09-347-064-10	Sequence 10, Appl1
29	US-09-347-064-10	Sequence 10, Appl1
30	US-09-347-064-10	Sequence 10, Appl1
31	US-09-347-064-10	Sequence 10, Appl1
32	US-09-347-064-10	Sequence 10, Appl1
33	US-09-347-064-10	Sequence 10, Appl1
34	US-09-347-064-10	Sequence 10, Appl1
35	US-09-347-064-10	Sequence 10, Appl1
36	US-09-347-064-10	Sequence 10, Appl1
37	US-09-347-064-10	Sequence 10, Appl1
38	US-09-347-064-10	Sequence 10, Appl1
39	US-09-347-064-10	Sequence 10, Appl1
40	US-09-347-064-10	Sequence 10, Appl1
41	US-09-347-064-10	Sequence 10, Appl1
42	US-09-347-064-10	Sequence 10, Appl1
43	US-09-347-064-10	Sequence 10, Appl1
44	US-09-347-064-10	Sequence 10, Appl1
45	US-09-347-064-10	Sequence 10, Appl1

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rapb

Page 2

QY 121 VOTLDYTLGGGMLAGNDTAPREVTIYGRDLCSNNGSVWETCVSSQONRMLYXDG 180
DB 121 VOTLDYTLGGGMLAGNDTAPREVTIYGRDLCSNNGSVWETCVSSQONRMLYXDG 180
QY 181 SIRPKONODCLTCGRDSVSVTINIVSCSAGSQGRWFTMEGALINIKKGLAMDVAKAN 240
DB 181 SIRPKONODCLTCGRDSVSVTINIVSCSAGSQGRWFTMEGALINIKKGLAMDVAKAN 240
QY 241 PKLRRIIIVPATGKPNQMWLPV 263
DB 241 PKLRRIIIVPATGKPNQMWLPV 263

RESULT 2
US-09-347-064-4
Sequence 4, Application US/09347064A
Patent No. US2003045208A1
GENERAL INFORMATION:
APPLICANT: BGR, Jurgens
INVENTOR: Schmidt, Arno
APPLICANT: BGR, Jurgens
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe viscum
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
EARLIER FILING DATE: 1999-07-02
PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 267
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-4

Query Match 99.98; Score 1406; DB 9; Length 267;
Best Local Similarity 98.98; Pred. No. 36-134;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDTCSASPTVIRVGRNKGWVDDDFDNGIOLMPSKNDPQMLTIKDDITRS 60
DB 1 DDTCSASPTVIRVGRNKGWVDDDFDNGIOLMPSKNDPQMLTIKDDITRS 60
QY 61 NSCLTYTGYAGYVMTFDQNTAVREAIWQWNGTIIINPSRLVLAASGIGKTTILT 120
DB 61 NSCLTYTGYAGYVMTFDQNTAVREAIWQWNGTIIINPSRLVLAASGIGKTTILT 120
QY 121 VOTLDYTLGGGMLAGNDTAPREVTIYGRDLCSNNGSVWETCVSSQONRMLYXDG 180
DB 121 VOTLDYTLGGGMLAGNDTAPREVTIYGRDLCSNNGSVWETCVSSQONRMLYXDG 180
QY 181 SIRPKONODCLTCGRDSVSVTINIVSCSAGSQGRWFTMEGALINIKKGLAMDVAKAN 240
DB 181 SIRPKONODCLTCGRDSVSVTINIVSCSAGSQGRWFTMEGALINIKKGLAMDVAKAN 240
QY 241 PKLRRIIIVPATGKPNQMWLPV 263
DB 241 PKLRRIIIVPATGKPNQMWLPV 263

RESULT 3
US-10-083-336A-1
Sequence 1, Application US/10083336A
Publication No. US2003018165A1
GENERAL INFORMATION:
APPLICANT: Olsson, Mark A
INVENTOR: Millard, Charles B
APPLICANT: Byrne, Michael P
INVENTOR: Wamnenmacher, Robert W

QY 5 CSASEPTVIRVGRNKGWVDDDFDNGIOLMPSKNDPQMLTIKDDITRS 64
DB 5 CSASEPTVIRVGRNKGWVDDDFDNGIOLMPSKNDPQMLTIKDDITRS 64
QY 318 CHDEPTVIRVGRNKGWVDDDFDNGIOLMPSKNDPQMLTIKDDITRS 377
DB 318 CHDEPTVIRVGRNKGWVDDDFDNGIOLMPSKNDPQMLTIKDDITRS 377
QY 65 LTTGYTGYAGYVMTFDQNTAVREAIWQWNGTIIINPSRLVLAASGIGKTTILT 124
DB 65 LTTGYTGYAGYVMTFDQNTAVREAIWQWNGTIIINPSRLVLAASGIGKTTILT 124
QY 125 DDTCSASPTVIRVGRNKGWVDDDFDNGIOLMPSKNDPQMLTIKDDITRS 184
DB 125 DDTCSASPTVIRVGRNKGWVDDDFDNGIOLMPSKNDPQMLTIKDDITRS 184
QY 185 KONDODCLTCGRDSVSVTINIVSCSAGSQGRWFTMEGALINIKKGLAMDVAKAN 244
DB 185 KONDODCLTCGRDSVSVTINIVSCSAGSQGRWFTMEGALINIKKGLAMDVAKAN 244
QY 498 QONRNDCLTSPDSIKRETVKIIISCPASSQGRWFTMEGALINIKKGLAMDVAKAN 557
DB 498 QONRNDCLTSPDSIKRETVKIIISCPASSQGRWFTMEGALINIKKGLAMDVAKAN 557
QY 245 RIIIVPATGKPNQMWLPV 262
DB 245 RIIIVPATGKPNQMWLPV 262

Query Match 64.3%; Score 913; DB 12; Length 576;
Best Local Similarity 63.6%; Pred. No. 9-1e-9;
Matches 164; Conservative 32; Mismatches 62; Indels 0; Gaps 0;
US-10-083-336A-1

RESULT 4
US-10-137-077-17
Sequence 17, Application US/10137077
Publication No. US2003082109A1
GENERAL INFORMATION:
APPLICANT: Goldstein, Irwin J.
INVENTOR: Krieger, Robert P.
APPLICANT: Krieger, Robert P.
TITLE OF INVENTION: Characterization, Cloning and Use of a Mushroom
FILE REFERENCE: US-0772-0772-0772
CURRENT APPLICATION NUMBER: US/10/137,077
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/288,596
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 60/354,322
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent In Ver. 3.1
SEQ ID NO 17
LENGTH: 44
TYPE: PRT
ORGANISM: Ricinus communis
US-10-137-077-17

Query Match 13.98; Score 198; DB 15; Length 44;
Best Local Similarity 79.58; Pred. No. 7.9e-13;
Matches 35; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 12 VAVGNNGWCVDRDDDFDNGIOLMPSKNDPQMLTIKDDITRS 55
DB 12 VAVGNNGWCVDRDDDFDNGIOLMPSKNDPQMLTIKDDITRS 55
QY 1 VAVGNNGWCVDRDDDFDNGIOLMPSKNDPQMLTIKDDITRS 44
DB 1 VAVGNNGWCVDRDDDFDNGIOLMPSKNDPQMLTIKDDITRS 44

RESULT 5
US-C-0-074-527-5
Sequence 5, Application US/10074527

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rapp

Page 3

```

1  Publication No. US20020142456A1
2  INFORMATION:
3  APPLICANT: Oladit, Peter J.
4  APPLICANT: Olayinka, Rachel E.
5  APPLICANT: Oladit, Peter J.
6  APPLICANT: Millennium Pharmaceuticals Inc.
7  TITLE OF INVENTION: 32945 "A Human Glycosyltransferase and
8  FILE REFERENCE: ME12001-018P/PROPI (M)
9  CURRENT APPLICATION NUMBER: US/10/074,527
10  PRIOR APPLICATION DATE: 2002-07-12
11  PRIOR APPLICATION NUMBER: 60/2659202
12  NUMBER OF SEQ ID NOS: 2
13  NUMBER OF SEQ ID NOS: 02-15
14  SOFTWARE: ParatSeq for Windows Version 4.0
15  SEQ ID NO 5
16  LENGTH: 145
17  TYPE: PRT
18  ORGANISM: Artificial Sequence
19  FEATURE:
20  OTHER INFORMATION: consensus
21  US-10-074-527-5

```

Query Match 13.0%; Score 184; DB 14; length 145;
 Best Local Similarity 23.4%; P_{red.} 10; le-100;
 Matches 50; Conservative 27; Mismatches 53; Indels 40; Gaps 7;

QY 11 TTRIVGNDGCTCYRDDFDGNGOILMPSKSNDFNOLMTI--KDGRTIR--NSSC 64
 Db 7 TLIVNGISGRCDITNNSSEBSSNOVQMGNSCHNKGKQKNSLTHDESDGILSYVNRDK 66

QY 65 LRTTGVAAVYVPEPCATVRAVITQIMGNSGIVINPRNSVLAASGAKGTTLVQTL 124
 Db 67 LTVANSPSESEVLYQCSGATSDNOKMELNDGLGN--KILNLTNVYTG--VL 116

QY 125 DYTLAGGMLAGNDLAFREVTITVFYFGLDMESGSGSVWETCTVSSQOQNGN 174
 Db 117 D-----KASQSDT-----QNGKTLILYTC-SGGNRQOQ 142

```
US-10-156-761-14970 RESULT=6
US-10-156-761-14970
Sequence 14970, Application US/10156761
Publication No. US20030119018A1
INVENTOR: OZONUMA, SHIRO
APPLICANT: OZONUMA, SHIRO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBU, TADAYOSHI
APPLICANT: SAKAKI, YOSHIOYUKI
APPLICANT: HATENO, MASAHISA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCES: 243-262
CURRENT APPLICATION NUMBER: US/10/156_761
PRIOR FILING DATE: 2002-05-29
PRIOR FILING DATE: 2003-01-20
PRIOR FILING DATE: 2003-05-21
PRIOR FILING DATE: 2003-05-21
PRIOR FILING DATE: 2003-05-21
PRIOR FILING DATE: 2003-05-21
PRIOR FILING DATE: 2003-05-21
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14970
LENGTH: 420
TYPER: EXT
ORGANISM: Streptomyces avermitilis
US-10-156-761-14970
```

```

Query Match      11.9%  Score 169;  DB 15;  Length 420;
Best Local Similarity 31.9%  Pred. No. 1,45-08;
Matches 43;  Conservative 19;  Mismatches 67;  Indels 10;  Gaps 5
QY      1 DD--VCSASAPFVTRVGRKMGVQDDDFHGDGNDGIDWPSKSNRNPQWMTTKECTIT 58
      || || | | | | | | | | | | | | | | | | | | | | | | | | | |

```

D_b 284 DAKTTCGSSGSGFTGAGKGVKDVAGSSSANAAPOLY -DGNATGAATTVASDGL 344
Q_y 59 KNSNSC -TITGYTAGVYMAIFDONTAAREKTTQMNGTIIIPRN -LVIASSGI 114
D_b 342 FALCKLIDPTNGSTGATGALDDGGSANOK -WYVPAEDTINPQNKCLDPTVGNRA 399
Q_y 115 KGTITVOTLIDVLTGGGSMAG 135
D_b 400 NGTRIDQWSCGSAANOKXKFG 420

```

RESULT 7
US-10-156-761-9724
? Sequence 9724, Application US/10156761
? Publication No. US20030119018A1
? GENERAL INFORMATION:
? APPLICANT: OMURA, SATOSHI
? APPLICANT: IREDA, HARUO
? APPLICANT: ISHERKAWA, JUN
? APPLICANT: SHIBATA, YOSHIO
? APPLICANT: SAKAKI, YOSHIYUKI
? APPLICANT: HATTORI, MASAHIRA
? TITLE OF INVENTION: NOVEL POLYMERISOTIDES
? FILE REFERENCE: 249-262
? CURRENT APPLICATION NUMBER: US/10/156,761
? CURRENT FILING DATE: 2002-05-29
? PRIOR APPLICATION NUMBER: JP 2001-204089
? PRIOR FILING DATE: 2001-05-10
? PRIOR REFERENCE: 2001-08-02
? PRIOR FILING DATE: 2001-272697
? NUMBER OF SEQ ID NOS: 15109
? SEQ ID NO 9724
? LENGTH: 658
? TYPE: PRT
? ORGANISM: Streptomyces avermitilis
US-10-156-761-9724

```

	Query Match	10.4%	Score 147.5	DB 15	Length 658
	Best Local Similarity	32.2%	Pred. No. 3.9e-06		
	Matches	33	Conservative 13	Mismatches 55	Indels 9
					Gaps 5
QY	17	KNKCACVADVEDDFHDSNDGLQVLKSCSNDDPQJMT-IRDSITIRNSGCLITTY-GYTNG	73		
Db	559	GGKGCADITNNITNIGDGLM-DGCGSGSGSTITSRKEVLVYKGCGLADNVLGTNG	596		
QY	74	VYVMEPCNCTVSEKATVQWNGFTINPNSNVLAA-SSGKKTITVQGLDLYTGG	121		
Db	597	TYVIMDCNGQANCK-WINSDGFTINVAGCLDAYNATFANSTSLVNSCGTDNCK	654		
QY	132	W 132			
Db	655	W 655			

RESULT 8
 US-09-770-621-8
 ? Sequence 8, Application US/09770621
 ? Patent No. US20010024815a1
 ?
 ? GENERAL INFORMATION:
 ?
 ? APPLICANT: M nyl, Aza
 ?
 ? APPLICANT: Vermaaspr, Jaci
 ?
 ? APPLICANT: Fagerstrm, Richard
 ?
 ? APPLICANT: Lantto, Raija
 ?
 ? APPLICANT: Paloheimo, Marja
 ?
 ? APPLICANT: Suominen, Pirkko
 ?
 ? APPLICANT: Lantinen, Teija
 ?
 ? TITLE OF INVENTION: Production and Secretion of Proteins of
 ?
 ? NUMBER OF SEQUENCES: 35
 ?
 ? CORRESPONDENCE ADDRESS:
 ?
 ? ADDRESSES: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 ? STREET: 1100 New York Ave., N.W. Suite 600
 ? CITY: Washington

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rabp

Page 4

```
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ CURRENT APPLICATION DATA: PC-DOS/MS-DOS
/ APPLICATION NUMBER: US/09/770.621
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/590.563
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/332.412
/ FILING DATE: 31-OCT-1994
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/282.001
/ FILING DATE: 29-JUL-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 1050.0340003
/ TELEPHONE: 202-311-2600
/ FAX: 202-311-2550
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 491 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: No. US20010024815A1 Relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT: M64551
/ US-09-770-621-8

Query Match
Best Local Similarity 10.3%; Score 146.5; DB 9; Length 491;
Matches 49; Conservative 20; Mismatches 54; Indels 57; Gaps 8;

QY 7 ASEP-----TWRIYGNMGCVDVRDDPDHGNQIQIAMPKSNNDPNQIATIKED 55
DB 354 SSEPXXXXXXXXXADQGIKGVG-SRCLIDVPASTDGTOLQIMDCISGT--NQWAAATRA 410
QY 56 GTIRNSG-SCITTYGTAYVMTFPDONTAVREAITIQTWNGTIIINPSNLVLAASSGI 114
DB 411 GELRYGDKCLDPAAGTSGSKQIITSGWGNQR--WLNISDSSVVGSGCLCLDA---- 464
QY 115 KGTILVTQITLDYTLGGWLAGNDPAAREVITTYGFDLCWESNGSVWVEGTSSQONQW 174
DB 465 -----VGNQTA-----NQTLLQIQLYTC-SINSGNQH 488

RESULT 9
US-10-156-761-10246
/ Sequence 10246, Application US/10156761
/ Publication No. US20030119018A1
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: ISHIKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HAYTORI, MASAHIRA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCE: 249-262
```

```
/ CURRENT APPLICATION NUMBER: US/10/156.761
/ CURRENT FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: JP 2001-204089
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/ SEQ ID NO 10246
/ LENGTH: 647
/ ORIGIN: Ect. Streptomyces avermitilis
/ US-10-156-761-10246

Query Match
Best Local Similarity 10.3%; Score 146.5; DB 15; Length 647;
Matches 45; Conservative 21; Mismatches 59; Indels 45; Gaps 7;

QY 9 EPTVAIYGRNMCVDVRDDPDHGNQIQIAMPKSNNDPNQIATIKEDGIRANSQCL--T 66
DB 520 DQGSFVGLAGKCLDPAASNGATGAVLY--DGNSTAGKRTVADSDVQALDKCLDVT 577
QY 67 TGTGTATGYVMTFPDONTAVREAITIQTWNGTIIINPSNLVLAASSGIKTTLVTQITLDY 126
DB 578 SASTNDARKIQLYDCA-----GTAAQKRSYN-----ASTGVTNPAADKCLDV 620
QY 127 TLGGWLAGNDPAAREVITTYGFDLCWESNGSVWVEGTSSQONQWAL 176
DB 621 T-----GNSSA-----NGAPAQWISCTGA-AHQKWL 646

RESULT 10
US-10-156-761-8170
/ Sequence 8170, Application US/10156761
/ Publication No. US20030119018A1
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: ISHIKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HAYTORI, MASAHIRA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCE: 249-262
/ CURRENT APPLICATION NUMBER: US/10/156.761
/ CURRENT FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: JP 2001-204089
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/ SEQ ID NO 8170
/ LENGTH: 536
/ ORIGIN: Ect. Streptomyces avermitilis
/ US-10-156-761-8170

Query Match
Best Local Similarity 9.7%; Score 138; DB 15; Length 536;
Matches 40; Conservative 19; Mismatches 59; Indels 16; Gaps 6;

QY 14 IIV-ENKVCVDVRDDPDHGNQIQIAMPKSNNDPNQIATIKEDGIRANSQ--SCITTY-- 68
DB 409 LVNASNRCLDPAAGTSGSKQIITSGWGNQR--GQANQAVTIAAGELRVYGTQICLDAYN 465
QY 69 GTYATGYVMTFPDONTAVREAITIQTWNGTIIINPSNLV-----AASGKIKTTLVTQ 122
DB 466 GTTSGIKTQIITCGANQR--NSLNPQIVTGTGSCLDITGDDQSSANVGTALSLW 523
QY 123 TLVTYTLGGWLAG 135
DB 524 TONGANQONRIG 536
```

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rapb

Page 5

```

RESULT 11
US-09-973-457-5
Sequence 5, Application US/09973457
Patent No. US2002016476A1
GENERAL INFORMATION:
APPLICANT: Kappelier, Libermann, Rosana
TITLE OF INVENTION: AND TRANSFERASE
FILE REFERENCE: 10448-099001
CURRENT APPLICATION NUMBER: US/09/973,457
CURRENT FILING DATE: 2001-10-09
PRIORITY APPLICATION NUMBER: 60/238,849
PRIORITY FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 6
SOURCE: FASTSEQ for Windows Version 4.0
SEQ ID NOS: 1-6
LENGTH: 135
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence
US-09-973-457-5

```

	9.6%; Score 136.5; Db 10; Length 135; Best Local Similarity 30.5%; Pred. No. 6.1e-06; Matches 43; Conservative 18; Mismatches 59; Indels 21; Gaps 8;
Qy	14 IYERNNGCTVY--RDDDEFGNDIOLWPSKSNDEPVOCLMT---KEQGTIRSNSS--CITT 67
Db	7 IGSNGLVGLCDNDGSSKSDSDNVDLADCHGG--NQLMELTYNSDGIARNSDLCITY 64
Qy	68 YGRTVGYVGLVDFPQGNARR--EKTINQINGNGLIIPSPSNVLVAASGIGKFTLLVQTILD 125
Db	65 NG---TTLTYSDDGIDIKRKNQKQWGVKMTQIRNRK-ASKSKGSDG-----LCIDPXD 113
Qy	136 YTLGGGGLGANDPDPPEVETVY 146
Db	114 GAKQVQLWTGNASDPADEQETIF 134

```

RESULT 12
US-10-074-527-6
/ Sequence 6, Application US/1,0074,527
/ Publication No. US5002014,426M1
/ INFORMATION:
/ APPLICANT: Pfizer J.
/ APPLICANT: Meyers, Rachel E.
/ APPLICANT: Galvin, Katherine A.
/ TITLE OF INVENTION: 33945, A Human Glycosyltransferase and
/ TITLE OF INVENTION: Uses Therefor
/ REFERENCE: WPI/2001-019P001(W)
/ CURRENT FILING DATE: NUMBER: US/10,074,527
/ PRIOR FILING DATE: 2001-02-15
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: FastSQ For Windows Version 4.0
/ SEQ ID NO 6
/ TYPE: 135
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: consensus
/ US-10-074-527-6

```

```
Query Match      9.6%; Score 136.5; DB 14; Length 135;  
Best Local Similarity 30.5%; Pred. Mo. 6-le-06;  
Matches 43; Conservative 18; Mismatches 59; Indels 21; Gaps 8;  
  
14 IVGNAGNCVCDV--RDDPEHNGQOTLWPKSKNDPNDPLGAT---KRDGTISNKS-CITF 67  
| | | | | : | | | | | | | | | | | | | | |
```

[illegible]

RESULT 13
 US-09-770-621-5
 Sequence 5, Application US/09770621
 Patent No. US20010024815A1
 GENERAL INFORMATION:
 APPLICANT: Mnevyl, Arja
 APPLICANT: Shmashper, Jari
 APPLICANT: Baskin, Richard
 APPLICANT: Lerner, Rajko
 APPLICANT: Palohelmo, Marja
 APPLICANT: Suominen, Pirkko
 APPLICANT: Lantinen, Tatja
 TITLE OF INVENTION: Production and Secretion of Proteins of
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESSES:
 ADDRESSER: STERNER, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 STREET: 1100 New York Ave., N.W. Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/770/621

CLASSIFICATION: DATA
PRIOR APPLICATION NUMBER: 06/590,563
FILING DATE: 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: DATA
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.034003
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STANDARD: No. US20010024815A1 Relevant
MOLECULE TYPE: linear
POSITION IN GENE: 1
CHROMOSOME/SEGMENT: AM50
15-09-770-621-5

Query Match 9.5%; Score 135; DB 9; Length 480;
Best Local Similarity 33.0%; Pred. No. 4.8e-05;

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rapb

Page 6

Matches 37; Conservative 17; Mismatches 52; Indels 6; Gaps 4;
QY 12 VRIYGRNMCVYVDDDDPHDNGIQIOWPSKSNNDPQOLMTIKRDTIRSNKS-CLTTYGY 70
DB 370 INGVASN-RCIDVFNKNTADGTQVLYDCHSGS--NQMTYTSGEFRIRFNKCLDAGS 426
QY 71 TQGVYVMEPCNTAVREATTWQGTWGTITINRSNIVLAASGIXKTLTVQ 122
DB 427 SNGAVQIYSCWGANOK--WEIRADGITVYGSGCLDAVGGGTGNGTRIQ 476

RESULT 14
US-09-770-621-4
Sequence 4, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vehmaerper, Jari
APPLICANT: Pajestier m, Richard
APPLICANT: Lantto, Ralja
APPLICANT: Pajestier m, Richard
APPLICANT: Suominen, Pirkko
APPLICANT: Lantto, Ralja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770.621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590.563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332.412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282.001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35.086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-770-621-4

Query Match 9.5%; Score 135; DB 9; Length 492;
Best Local Similarity 33.0%; Pred. No. 4.9e-05;
Matches 37; Conservative 17; Mismatches 52; Indels 6; Gaps 4;
QY 12 VRIYGRNMCVYVDDDDPHDNGIQIOWPSKSNNDPQOLMTIKRDTIRSNKS-CLTTYGY 70

DB 370 INGVASN-RCIDVFNKNTADGTQVLYDCHSGS--NQMTYTSGEFRIRFNKCLDAGS 426
QY 71 TQGVYVMEPCNTAVREATTWQGTWGTITINRSNIVLAASGIXKTLTVQ 122
DB 427 SNGAVQIYSCWGANOK--WEIRADGITVYGSGCLDAVGGGTGNGTRIQ 476

RESULT 15
US-09-770-621-7
Sequence 7, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vehmaerper, Jari
APPLICANT: Pajestier m, Richard
APPLICANT: Lantto, Ralja
APPLICANT: Pajestier m, Richard
APPLICANT: Suominen, Pirkko
APPLICANT: Lantto, Ralja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770.621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590.563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332.412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282.001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35.086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
STRANDNESS: NO. US20010024815A1 Relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-09-770-621-7

Query Match 9.5%; Score 135; DB 9; Length 492;
Best Local Similarity 33.0%; Pred. No. 4.9e-05;
Matches 37; Conservative 17; Mismatches 52; Indels 6; Gaps 4;
QY 12 VRIYGRNMCVYVDDDDPHDNGIQIOWPSKSNNDPQOLMTIKRDTIRSNKS-CLTTYGY 70

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rapb

Page 7

Db 370 IRGVASH-RCIDVPNGNTADDTVOYLDCHSSS--NQOMTYTS83EPRIFENKCLDAQSS 426
QY 71 TAGVTWMTFCNTAVREKTIWQIMWENTTINPESNVLAASSGKGTTLTVO 122
Db 427 SNAVVOITSCWGANOK--WELRADSTIWOVS9GCLDAVGGTGKGTRO 476
Search completed: December 11, 2003, 14:48:48
Job time : 17.9484 secs


```
RESULT 2
US-08-776-059-33
Sequence 33, Application US/087760598
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LEWTEZEN, Hans
INVENTOR: LEWTEZEN, Hans
APPLICANT: BALT, Jürgen
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1999-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 564
TYPE: PRT
ORGANISM: Viscum album

Query Match
Best Local Similarity 98.9%; Score 1406; DB 3; Length 264;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDTYCSAEPPTAVIGNKNVCVDRDDFDGNOIOLMFSKSNNDPNQWTIRKDTIRG 60
DB 2 DDTCSASPTAVIGNKNVCVDRDDFDGNOIOLMFSKSNNDPNQWTIRKDTIRG 61
QY 61 NSCLTYGTAGVYWMIFDONTAVREATIMQWNGIINPNSNVLAASSGIGKTLT 120
DB 62 NSCLTYGTAGVYWMIFDONTAVREATIMQWNGIINPNSNVLAASSGIGKTLT 121
QY 121 VQTLIDYTLGGMLAGNTAPREVITVGFRLCMESNGSWVETCVSSQONRMALYDGG 180
DB 122 VQTLIDYTLGGMLAGNTAPREVITVGFRLCMESNGSWVETCVSSQONRMALYDGG 181
QY 181 SIREKQNDQCTGCRDSVTVINIVSCNAGSSGQWTFNKGALINRGNLANMDVAQAN 240
DB 182 SIREKQNDQCTGCRDSVTVINIVSCNAGSSGQWTFNKGALINRGNLANMDVAQAN 241
QY 241 PKLRRIITPATCKRQNMWLPVP 263
DB 242 PKLRRIITPATCKRQNMWLPVP 264

RESULT 3
US-08-776-059-35
Sequence 35, Application US/087760598
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LEWTEZEN, Hans
INVENTOR: LEWTEZEN, Hans
APPLICANT: BALT, Jürgen
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1999-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 564
TYPE: PRT
ORGANISM: Viscum album

Query Match
Best Local Similarity 98.9%; Score 1406; DB 3; Length 264;
Matches 260; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDTYCSAEPPTAVIGNKNVCVDRDDFDGNOIOLMFSKSNNDPNQWTIRKDTIRG 60
DB 2 DDTCSASPTAVIGNKNVCVDRDDFDGNOIOLMFSKSNNDPNQWTIRKDTIRG 61
QY 61 NSCLTYGTAGVYWMIFDONTAVREATIMQWNGIINPNSNVLAASSGIGKTLT 120
DB 62 NSCLTYGTAGVYWMIFDONTAVREATIMQWNGIINPNSNVLAASSGIGKTLT 121
QY 121 VQTLIDYTLGGMLAGNTAPREVITVGFRLCMESNGSWVETCVSSQONRMALYDGG 180
DB 122 VQTLIDYTLGGMLAGNTAPREVITVGFRLCMESNGSWVETCVSSQONRMALYDGG 181
QY 181 SIREKQNDQCTGCRDSVTVINIVSCNAGSSGQWTFNKGALINRGNLANMDVAQAN 240
DB 182 SIREKQNDQCTGCRDSVTVINIVSCNAGSSGQWTFNKGALINRGNLANMDVAQAN 241
QY 241 PKLRRIITPATCKRQNMWLPVP 263
DB 242 PKLRRIITPATCKRQNMWLPVP 264

RESULT 4
US-08-776-761A-77
Sequence 77, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: TERENCE A
INVENTOR: HEY TIMOTHY D
APPLICANT: MORGAN ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
NUMBER OF INVENTIONS: 1
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: ANDREA T. BORUCKI
STREET: 9330 ZIONVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: C12N 1/33
INVENTOR: ANDREA T. BORUCKI
NAME: BORUCKI ANDREA T
REGISTRATION NUMBER: 382728
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
STRANDNESS: single
TOPLOGY: linear
MOLECULE TYPE: protein

US-08-378-761A-77

Query Match
Best Local Similarity 56.1%; Score 797; DB 1; Length 540;
Matches 146; Conservative 38; Mismatches 74; Indels 0; Gaps 0;
```

Thu Dec 11 16:10:01 2003

us-09-601-67c-6.rat

Page 3

QY 5 CSASEPTVAVGKNCVVDVDDPFHDNOIQIAMPKSNNDPNQIWTIKDGTIRNSGSC 64
DB 282 CMDEPVIIVGKNCVVDVDDPFHDNOIQIAMPKSNNDPNQIWTIKDGTIRNSGSC 341
QY 65 LITVGTAGVYVMEPCNTAVREATTIWOIKNGSTIINPSKVLTAASGIGKTLTVOYL 124
DB 342 LITKSSRQGVYVINSSTVAGTATKQIMNDRTIINPSGLVLAASGIGKTLTVOYL 401
QY 125 DYLGGQMLAGNDTAPREVITYGPRDLCKESNGSVWETCVSSQOQKQALYDGSIRP 184
DB 402 IYAVSGMLPTNNTPCFVTTIVGLYKQCLQANSKGWLEDCISEKAEQOMALYADGSIRP 461
QY 185 KQNDQCLTCGRDSVSTVINIVSCASSGSGRWVFTNEGAIINIKGLMDVQAQNPRLR 244
DB 462 QQNRDNCITTDANIKQIVYKLSGCPASSGQRMWFPNDGTITLINTGLVLDVRSDESLK 521
QY 245 RIIIVPATGRKQKQMLFV 262
QY 522 QIIIVPFRGNMQIMLPL 539

RESULT 5

US-08-485-286-77
Sequence 77, Application US/08485286
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
INVENTOR: WALSH, TERENCE A
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 08/378761
FILING DATE: 26-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 382728
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPED: amino acids
SYNTHESIS: sample
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-77

Query Match 56.1%; Score 797; DB 1; Length 540;
Best Local Similarity 56.6%; Pred. No. 8.5e-75;
Matches 146; Conservative 38; Mismatches 74; Indels 0; Gaps 0;

QY 5 CSASEPTVAVGKNCVVDVDDPFHDNOIQIAMPKSNNDPNQIWTIKDGTIRNSGSC 64
DB 282 CMDEPVIIVGKNCVVDVDDPFHDNOIQIAMPKSNNDPNQIWTIKDGTIRNSGSC 341
QY 65 LITVGTAGVYVMEPCNTAVREATTIWOIKNGSTIINPSKVLTAASGIGKTLTVOYL 124
DB 342 LITKSSRQGVYVINSSTVAGTATKQIMNDRTIINPSGLVLAASGIGKTLTVOYL 401
QY 125 DYLGGQMLAGNDTAPREVITYGPRDLCKESNGSVWETCVSSQOQKQALYDGSIRP 184
DB 402 IYAVSGMLPTNNTPCFVTTIVGLYKQCLQANSKGWLEDCISEKAEQOMALYADGSIRP 461
QY 185 KQNDQCLTCGRDSVSTVINIVSCASSGSGRWVFTNEGAIINIKGLMDVQAQNPRLR 244
DB 462 QQNRDNCITTDANIKQIVYKLSGCPASSGQRMWFPNDGTITLINTGLVLDVRSDESLK 521
QY 245 RIIIVPATGRKQKQMLFV 262
QY 522 QIIIVPFRGNMQIMLPL 539

RESULT 6

US-09-512-342-14
Sequence 14, Application US/09512342
Patent No. 638068
GENERAL INFORMATION:
APPLICANT: MASUD, SHINOBU
INVENTOR: MASUD, SHINOBU
TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
CURRENT APPLICATION NUMBER: US/09/512,342
FILING DATE: 08/15/2000
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 14
LENGTH: 293
TYPE: PRT
ORGANISM: Cucumis sativus
US-09-512-342-14

Query Match 13.7%; Score 195; DB 4; Length 293;
Best Local Similarity 28.3%; Pred. No. 3e-12;
Matches 63; Conservative 29; Mismatches 93; Indels 38; Gaps 9;

QY 14 IYGNMNCVVDVDDPFHDNOIQIAMPKSNNDPNQIWTIKDGTIRNSGSC 59
DB 41 LITVGTAGVYVMEPCNTAVREATTIWOIKNGSTIINPSKVLTAASGIGKTLTVOYL 89
QY 60 SNNSCITL--VGTAGVYVMEPCNTAVREATTIWOIKNGSTIINPSKVLTAASGIGK 116
DB 90 NKKCTLAERFVIVIN--FAVSSCKRSPDKKXTQANDGIIALVDSRWVLGDLV-- 145
QY 117 TITVGTAGVYVMEPCNTAVREATTIWOIKNGSTIINPSKVLTAASGIGKTLTVOYL 174
DB 146 --VTLGSGMLPTNNTPCFVTTIVGLYKQCLQANSKGWLEDCISEKAEQOMALYADGSIRP 203
QY 175 ALYDGSIRPQKQKQALYDGSIRP 217
DB 204 ALYDGSIRPQKQKQALYDGSIRP 244

RESULT 7

US-09-459-106-15
Sequence 15, Application US/09159106
Patent No. 672502
GENERAL INFORMATION:
APPLICANT: Ferrer, Pau
INVENTOR: Ferrer, Pau
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
CURRENT APPLICATION NUMBER: US/09/459,106
FILING DATE: 08/15/2000
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 15
LENGTH: 293
TYPE: PRT
ORGANISM: Cucumis sativus
US-09-459-106-15

Query Match 56.1%; Score 797; DB 1; Length 540;
Best Local Similarity 56.6%; Pred. No. 8.5e-75;
Matches 146; Conservative 38; Mismatches 74; Indels 0; Gaps 0;

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.ra1

```
FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159.106
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1996-12-04
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; EARLIER FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-15
```

```
Query Match
Seq. Local Similarity 10.7%; Score 152; DB 3; Length 132;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 5;
```

```
Db
18 NMCVDVPMADPFDGNDGQIOWPMSKNDPQWLTIRKGTIRNSGCLTY--GYAGY 75
14 NMCVDVPMADPFDGNDGQIOWPMSKNDPQWLTIRKGTIRNSGCLTY--GYAGY 71
76 VMFPCNTAVREATIQIY---GNGTIIPRSNLVLAASG--KATLTVOGTLDTL 128
72 VQWTCN-----GTGAKWADGSKALRNPQSLCLDTGAPLRDQGRLOTWTCNGT 126
QY 129 GCGW 132
DB 127 AQOW 130
```

RESULT 6

```
US-09-159-106-11
; Sequence 11, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: Petter, Pau
; APPLICANT: Hakkar, Ivan
; APPLICANT: Hegerard, Lisbeth
; TITLE OF INVENTION: Active site of glucanase
; TITLE OF INVENTION: Active site of glucanase
; FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159.106
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1996-12-04
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; EARLIER FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11
```

```
Query Match
Seq. Local Similarity 10.7%; Score 152; DB 3; Length 435;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 5;
Db
317 NMCVDVPMADPFDGNDGQIOWPMSKNDPQWLTIRKGTIRNSGCLTY--GYAGY 75
76 VMFPCNTAVREATIQIY---GNGTIIPRSNLVLAASG--KATLTVOGTLDTL 128
375 VQWTCN-----GTGAKWADGSKALRNPQSLCLDTGAPLRDQGRLOTWTCNGT 429
```

```
QY 129 GCGW 132
DB 430 AQOW 433
```

RESULT 9

```
US-08-468-812-8
; Sequence 8, Application US/08468812
; Patent No. 6552838
; GENERAL INFORMATION:
; APPLICANT: Weinmayer, Jari
; APPLICANT: M etyl, Aija
; APPLICANT: Fagerstr m, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Maria
; APPLICANT: Suominen, Pirkko
; APPLICANT: Laitinen, Tarja
; APPLICANT: Kristo, Paula
; TITLE OF INVENTION: Actinomadura xylinase Sequences and Methods
; NUMBER OF SEQ ID NOS: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERN PRESSURE, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION NUMBER: 1.0, Version #1.30
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332,412
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/282,001
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugarsky, Larry B.
; REGISTRATION NUMBER: 35,086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2640
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 431 amino acids
; TYPE: amino acids
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: M64551
US-08-468-812-8
```

```
Query Match
Seq. Local Similarity 10.3%; Score 146.5; DB 2; Length 491;
Matches 43; Conservative 27; Mismatches 54; Indels 57; Gaps 8;
Db
354 SEEPXXXXXXADGQIKXG--SQRCLVDPASTSGTCLQWCHSGT--NQMAATDA 430
7 ASRP-----TAYIGNCKVCVDEDDPFDGNDGQIOWPMSKNDPQWLTIRKGTIRNSGCLTY--GYAGY 75
56 GTIRNSG--CLTYGYAGYVVMFPCNTAVREATIQIYINPRSNLVLAASG 114
```

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rat

Page 5

Db 411 GELIVYGDKCLDAAGTNSGKRVQVYSCWQGNOK--KRLNSDGSVVGVSGLCLDA-----464
Qy 115 KCTITVQTLDITLGGGMLAGNDTPREVTITIGFRDLCWESNGSVWETCVSSQGNRM 174
Db 465 -----VGNGLT-----NGLIQLTLC-SKNSGNRM 488

RESULT 10
US-08-590-563-8
Sequence 8, Application US/08590563
Patent No. 6300114
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Permaaper, Jari
APPLICANT: Lester M, Richard
APPLICANT: Lehto Raimo
APPLICANT: Palohelmo Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Laitinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIORITY INFORMATION: EAR: US 08/468,812
APPLICATION NUMBER: 06-JUN-1995
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugelsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
NOTICE TYPE: linear
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-08-590-563-8

Query Match 10.3%; Score 146.5; DB 4; Length 491;
Best Local Similarity 27.2%; Pred. No. 7.5e-07;
Matches 49; Conservative 20; Mismatches 54; Indels 57; Gaps 8;
Qy 7 ASEP-----TWIVGNQCVVDREDDFHQGNQLQMSKSNNDPMTAKHD 55

Db 354 SEEPXXXXXXADGGQKVG--SGRLDVPDASTDSTQLOLMDCHSGT--NOQMAATDA 410
Qy 56 GTIRNG-SCITVGYTAGVYVIFDCTVAREBATIMQIMRGITINFRNLVLAASGI 114
Db 411 GELIVYGDKCLDAAGTNSGKRVQVYSCWQGNOK--KRLNSDGSVVGVSGLCLDA-----464
Qy 115 KCTITVQTLDITLGGGMLAGNDTPREVTITIGFRDLCWESNGSVWETCVSSQGNRM 174
Db 465 -----VGNGLT-----NGLIQLTLC-SKNSGNRM 488

RESULT 11
US-09-770-621-8
Sequence 8, Application US/09770621
Patent No. 6506593
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Permaaper, Jari
APPLICANT: Lester M, Richard
APPLICANT: Lehto Raimo
APPLICANT: Palohelmo Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Laitinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIORITY INFORMATION: EAR: US 08/550,563
APPLICATION NUMBER: 08/550,563
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugelsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
NOTICE TYPE: linear
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M65551
US-09-770-621-8

Query Match 10.3%; Score 146.5; DB 4; Length 491;
Best Local Similarity 27.2%; Pred. No. 7.5e-07;
Matches 49; Conservative 20; Mismatches 54; Indels 57; Gaps 8;
Qy 10.3%; Score 146.5; DB 4; Length 491;

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rai

Page 6

Best Local Similarity 27.2%; Pred. No. 7.5e-07;
Matches 49; Conservative 20; Mismatches 54; Indels 57; Gaps 8;

QY 7 ASBP-----TWAVRNAGCVDVDDPHDQNOIQWPSKSNDDPQWLTIKD 55
DB 354 SDEPRXXXXXADGGQIKGV-SGRCLDVPDASTSDTOLQMDCHSGT--NQOMATDA 410
QY 56 GTIRANG-SCLTITVGTAGVYVWIPDCTVREAITWQNGCTINPSNVLAASSGI 114
DB 411 GELAVYGPDKLDAAGTSNKSVOYISCVGQDNOK--WRLNSDGSVGVQSGLCIDA--- 464
QY 115 KQTLVTVQTLIDYTLGGQWMAAGNDTAPREVTIGFRDLCSNNGSVWETCVSSQONRW 174
DB 465 -----VANGTA-----NGTLIDLYTC-SNNGSNRW 488

RESULT 12

US-08-392-828C-39
; Sequence 39, Application US/08392828C
; Patent No. 5795962

GENERAL INFORMATION:

APPLICANT: IWANAGA, SADAKI

APPLICANT: MUTO, TATSUSHI

APPLICANT: SEKI, NORIHI

APPLICANT: ODA, TOSHIO

TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS: ADMINISTRATOR, TESTA, HIRWITZ &

ADDRESSER: THIRBULT LLP

STREET: 125 HIGH STREET

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/392,828C

FILING DATE: 28-FEB-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, PAULA A

REGISTRATION NUMBER: 32,503

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: FUN-033

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7000

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS: 39:

LENGTH: 127 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURES:

NAME/KEY: Peptide

LOCATION: 1..127

OTHER INFORMATION: /note= "XIN A SEQUENCE (FIGURE 4)"

Query Match 10.3%; Score 146; DB 1; Length 127;

Best Local Similarity 28.0%; Pred. No. 1.2e-07;

Matches 46; Conservative 19; Mismatches 53; Indels 46; Gaps 7;

QY 12 VAVRNAGCVDVDDPHDQNOIQWPSKSNDDPQWLTIKDGTIRANG-SCLTITVGT 70
DB 6 IKGV-SGRCLDVPDASTSDTOLQMDCHSGT--NQOMATDAAGELVYDCKLDAAGT 62

QY 71 TAGVYVWIPDCTVREAITWQNGCTINPSNVLAASSGIKQTLVTVQTLIDYTLGG 130
DB 63 SNKQVOYISCVGQDNOK--WRLNSDGSVGVQSGLCIDA----- 100

QY 131 GMLAGNDTAPREVTIGFRDLCSNNGSVWETCVSSQONRW 174
DB 101 ---VANGTA-----NGTLIDLYTC-SNNGSNRW 124

RESULT 13

US-09-330-945-39
; Sequence 39, Application US/09330945
; Patent No. 6077946

GENERAL INFORMATION:

APPLICANT: IWANAGA, SADAKI

APPLICANT: MUTO, TATSUSHI

APPLICANT: SEKI, NORIHI

APPLICANT: ODA, TOSHIO

TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS: ADMINISTRATOR, TESTA, HIRWITZ &

ADDRESSER: THIRBULT LLP

STREET: 125 HIGH STREET

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/330,945

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/119,995

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: PITCHER, EDWARD R

REGISTRATION NUMBER: 27,829

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: FUN-032DV

TELEPHONE: (617) 248-7000

TELEFAX: (617) 248-7000

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS: 39:

LENGTH: 127 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURES:

NAME/KEY: Peptide

LOCATION: 1..127

OTHER INFORMATION: /note= "XIN A SEQUENCE (FIGURE 4)"

Query Match 10.3%; Score 146; DB 3; Length 127;

Best Local Similarity 28.0%; Pred. No. 1.2e-07;

Matches 46; Conservative 19; Mismatches 53; Indels 46; Gaps 7;

QY 12 VAVRNAGCVDVDDPHDQNOIQWPSKSNDDPQWLTIKDGTIRANG-SCLTITVGT 70
DB 6 IKGV-SGRCLDVPDASTSDTOLQMDCHSGT--NQOMATDAAGELVYDCKLDAAGT 62
QY 71 TAGVYVWIPDCTVREAITWQNGCTINPSNVLAASSGIKQTLVTVQTLIDYTLGG 130
DB 63 SNKQVOYISCVGQDNOK--WRLNSDGSVGVQSGLCIDA----- 100

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rat

Page 7

QY 131 GMLAGNTAPREVTYFRLCMESNGSVWETCVSSQONRW 174
DB 101 --VENGTJ-----NOTLIDLYTC-SNGSNQW 124

RESULT 14
US-08-468-812-5
Sequence 5, Application US/08468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vehmaaper, Jari
APPLICANT: M nyl, Aija
APPLICANT: Pajestr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Pajohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lantinen, Taina
APPLICANT: Kietto, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050, 0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
FAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-08-468-812-5

Query Match 9.5%; Score 135; DB 2; Length 480;
Best Local Similarity 33.0%; Pred. No. 1,2e-05;
Matches 37; Conservative 17; Mismatches 52; Indels 6; Gaps 4;

QY 12 VRIYGNMVCVDDDFHGNQIOLMPSKSNDFPOLITIRDDGITSNGS-CLITGY 70
DB 370 IRGVASN-RCIDIVNGNTADGTVOLYDCHSGS--NQMWTYSGGEFRIFGNKCDIAGGS 426
QY 71 TAGVYMTFCNTAVRATQIWNQGTIIINPSNVLVAASGIKOTLTWQ 122

DB 427 SNGAVQVYSQMGANOK--WELRADTIVYQSLCLAVAGGTGNGTRLQ 476

RESULT 15
US-08-590-563-5
Sequence 5, Application US/08590563
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vehmaaper, Jari
APPLICANT: M nyl, Aija
APPLICANT: Pajestr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Pajohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lantinen, Taina
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050, 0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
FAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-08-590-563-5

Query Match 9.5%; Score 135; DB 4; Length 480;
Best Local Similarity 33.0%; Pred. No. 1,2e-05;
Matches 37; Conservative 17; Mismatches 52; Indels 6; Gaps 4;

QY 12 VRIYGNMVCVDDDFHGNQIOLMPSKSNDFPOLITIRDDGITSNGS-CLITGY 70
DB 370 IRGVASN-RCIDIVNGNTADGTVOLYDCHSGS--NQMWTYSGGEFRIFGNKCDIAGGS 426
QY 71 TAGVYMTFCNTAVRATQIWNQGTIIINPSNVLVAASGIKOTLTWQ 122

Thu Dec 11 16:10:01 2003

us-09-601-667c-6.rai

Db 427 SNGAVQIYSCMGANOK-WELRADGTVGVSGICIDAVGGGTNGTRIQ 476
Search completed: December 11, 2003, 14:11:32
Job time : 9.10564 secs

Thu Dec 11 16:10:04 2003

us-09-601-667c-7.rpr

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 8.20622 Seconds

(without alignments)
3093.817 Million cell updates/sec

Title: US-09-601-667C-7

RefSeq score: 1418

Sequence: 1 DVTCSASEPTIRIVGRNGM.....RLIIIVATKGNQMWLPVF 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: PIR 76:*
2: Tr1:*
3: Tr2:*
4: Tr3:*
5: Tr4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1418	100.0	264	2 PD0019	mistletoe lectin I
2	1407.5	99.3	265	2 JMW090	lectin I B chain -
3	907.5	64.0	576	1 RLCD	ricin D precursor
4	877	61.8	263	2 S06330	ricin B - castor b
5	783.5	55.3	564	1 RLCSAG	agglutinin precursor
6	781	55.1	528	1 TLISA	abrin-a precursor
7	772	54.4	527	2 S32430	abrin-b precursor
8	766	54.0	528	2 S19432	abrin-c precursor
9	766	54.0	528	2 S62627	abrin-d precursor
10	543	38.3	570	2 J05589	chitinase (EC 3.2.1.15)
11	137.5	9.7	377	2 J05589	endo-1,4-beta-xyl
12	125.5	8.9	477	1 J05589	xylanase A - strep
13	122.5	8.6	383	2 T34603	arabinofuranosid
14	115.5	8.1	475	2 T35697	glucan endo-1,3-be
15	114	8.0	548	2 A35094	probable hydrolyti
16	111	7.8	464	2 T35943	protease RPI - R
17	110	7.8	525	2 A45053	actinohivin precu
18	107	7.5	525	2 J05589	actinohivin precu
19	102	7.2	525	2 J05589	actinohivin precu
20	102	7.2	525	2 J05589	actinohivin precu
21	100.5	7.1	545	2 T28663	probable polyepid
22	99.5	7.0	1067	2 T28663	probable polyepid
23	98.5	6.9	451	2 H31492	probable lipoprote
24	95	6.7	295	2 H31492	probable short-cha
25	94	6.6	386	2 ARI196	hypothetical prote
26	94	6.6	1723	2 H86557	hypothetical prote
27	94	6.6	1723	2 E72067	polymorphic membra
28	94	6.6	1723	2 C81601	polymorphic membra
29	93.5	6.6	3624	2 AD0835	large repetitive p

30	93	6.6	875	2 I40862	iota toxin compo
31	92	6.5	895	1 I4XLC6	Ep-cadherin precu
32	91.5	6.5	471	2 A1478	cytolysin vsh pre
33	90.5	6.4	1008	2 T32986	hypothetical prote
34	89.5	6.3	624	2 T42447	polypeptide N-acet
35	89.5	6.3	962	2 S58107	hypothetical WD-40
36	89.5	6.3	962	2 S58107	hypothetical prote
37	89.5	6.3	962	2 S58107	hypothetical prote
38	89.5	6.3	962	2 S58107	hypothetical prote
39	89.5	6.3	962	2 S58107	hypothetical prote
40	88.5	6.2	1528	2 D85912	hypothetical prote
41	88.5	6.2	1571	2 C91068	hypothetical prote
42	88.5	6.2	1571	2 C91068	hypothetical prote
43	88	6.2	623	2 T42245	hemolysin A precu
44	88	6.2	870	2 S27514	probable polypepti
45	88	6.2	908	2 A82254	mosquitoficial toxi

ALIGNMENTS

RESULT 1	
PD0019	mistletoe lectin I B chain - Viscum album (fragment)
C/Date: 03-Jul-1998	#sequence_revision 10-Jul-1998 #extl_change 07-May-1999
C/Species: Viscum album	
C/Accession: PD0019	
R/Biochem: R. Krauspenhaar, R. Mikhalov, A. Stoeva, S. Betzel, C. Voelter, Biochem. Biophys. Res. Commun. 247, 367-372, 1998	
A/Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum	
A/Reference number: PD0019; PMID:98108123; PMID:9641233	
A/Accession: PD0019	
2 PD0019	protein
2 Residues: 1-264	residues
C/Superfamily: ricin; rRNA N-glycosidase homology	
Query Match	100.0%; Score 1418; DB 2; Length 264;
Best Local Similarity	100.0%; Pred.No. 9.5e-112;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 DVTCSASEPTIRIVGRNGMVDVDDPHDNGIQLPKSKNDPQWLTKEDGTIRS 60
DB	1 DVTCSASEPTIRIVGRNGMVDVDDPHDNGIQLPKSKNDPQWLTKEDGTIRS 60
QY	61 NSGCTLYGTCGYVTFMFOGTARARNTQIMDNTINPSNVLAAAGCKRTTT 120
DB	61 NSGCTLYGTCGYVTFMFOGTARARNTQIMDNTINPSNVLAAAGCKRTTT 120
QY	121 VQGLDYTLAQGLMGNDAPPEPTLYTGFRLDMSNGSVMWETCDSSQNGKMLYVD 180
DB	121 VQGLDYTLAQGLMGNDAPPEPTLYTGFRLDMSNGSVMWETCDSSQNGKMLYVD 180
QY	181 GSIRKQNDQCLTSGRDSVATVIVSGSGASQSPWTFMEGAILNLKGLANDVAQA 240
DB	181 GSIRKQNDQCLTSGRDSVATVIVSGSGASQSPWTFMEGAILNLKGLANDVAQA 240
QY	241 NPTLRRIIVPATKGNQMWLPVF 264
DB	241 NPTLRRIIVPATKGNQMWLPVF 264
RESULT 2	
JMW090	lectin I B chain - European mistletoe
A/Accession names: Mw-I	(European mistletoe)
C/Date: 03-Jul-1998	#sequence_revision 10-Jul-1998 #extl_change 19-May-2000
C/Species: Viscum album	
C/Accession: JMW090	
R/Soler: M.H., Stoeva, S., Voelter, M. Biochem. Biophys. Res. Commun. 246, 596-601, 1998	
A/Title: Complete amino acid sequence of the B chain of mistletoe lectin I.	
A/Reference number: JMW090; PMID:98289575; PMID:9618256	
A/Accession: JMW090	

Thu Dec 11 16:10:04 2003

us-09-601-667c-7.rpr

Page 2

A:Molecule type: protein
A:Residues: 1-265 (80%)
C:Superfamily: Ricin; RNA N-glycosidase homology
C:Keywords: glycoprotein
F:61.96.135/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 99.3%; Score 1407.5; DB 2; Length 265;
Best Local Similarity 99.6%; Pred. No. 7.3e-111;
Matches 264; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 DDTGCSAEPTRVHGRNQRVNDPDDHNGNQIQMPSKSNDDPQNTTKRGGTTR 60
DB 1 DDTGCSAEPTRVHGRNQRVNDPDDHNGNQIQMPSKSNDDPQNTTKRGGTTR 60
QY 61 NSGCLTYGTVAGVYVNFPCNTAVRATIQIWDKGTINPRSLVLAASGIGKTTTL 120
DB 61 NSGCLTYGTVAGVYVNFPCNTAVRATIQIWDKGTINPRSLVLAASGIGKTTTL 120
QY 121 VQTDYTLQCGMLAGNDTAPREVITYGFDLCNENSGGQVWYETGDSQKQKALYGD 180
DB 121 VQTDYTLQCGMLAGNDTAPREVITYGFDLCNENSGGQVWYETGDSQKQKALYGD 180
QY 181 GSIRKXNDQCLSGRDSVYIVVSSGASGQKRVYTHGALINSGIANDVAGQ 240
DB 181 GSIRKXNDQCLSGRDSVYIVVSSGASGQKRVYTHGALINSGIANDVAGQ 240
QY 241 NPELRITITPATKRNQMLPVP 264
DB 241 NPELRITITPATKRNQMLPVP 265

RESULT 3
R1CSD
A:Title: Ricin D precursor - caenor bean
A:Accession: X52908; NID:921084; PIDN:CAA6939.1; PID:921083
C:Species: Ricinus communis (Castor bean)
C:Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
C:Accession: A24041; S20513; A24614; A03372; A24010; A03376; S10903
R:Halling, K.C.; Halling, A.C.; Murray, E.S.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A:Reference number: A24041; PMID:86067214; PMID:2593712
A:Accession: A24041
A:Molecule type: DNA
A:Residues: 1-576 (80%)
A:Cross-references: EMBL:X52908; NID:921084; PIDN:CAA6939.1; PID:921083
R:Land, F.I.; Roberts, L.M.; Lord, J.M.
Eur. J. Biochem. 148, 265-270, 1985
A:Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A:Accession: A24614; PMID:85179479; PMID:3638723
A:Accession: A24614
A:Molecule type: mRNA
A:Residues: 12-75, 'D', '77-550, 'R', '552-576 (LMM)
A:Cross-references: GB:X02388; NID:921077; PIDN:CAA6230.1; PID:921078
R:Yoshitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
A:Title: Isolation and sequences of peptic peptides, and the complete sequence of ile of
A:Accession: A03372
A:Molecule type: protein
A:Residues: 1-109, 'S', '111-269, 'D', '272-283, 'U', '285-288, 290-302 (XOS)
A:Note: This paper cites the others in the series providing experimental details for the
R:Aoki, T.; Puntius, G.
FEBS Lett. 191, 121-124, 1985
A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A:Reference number: A24010
A:Accession: A24010
A:Molecule type: protein
A:Residues: 315-383, 'PS', '386-576 (RA)
R:Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A:Title: Primary structure of Ala chain of ricin D.
A:Reference number: A03374
A:Accession: A03374
A:Molecule type: protein
A:Residues: 215-335, 'R', '337-342, 'NH', '345-362, 364-383, 'PS', '386-399, 'T', '401, 'D', '403, '
A:Note: This paper cites the others in the series providing experimental details for the de
R:Ready, M.P.; Kim, Y.; Roberts, J.D.
Protein 10, 270-278, 1991
A:Title: Site-directed mutagenesis of ricin A-chain and implications for the mechan
A:Reference number: A48237; PMID:9135006; PMID:1881883
A:Accession: A48237
A:Contents: annotation; active site
R:Rutember, B.; Roberts, J.D.
Protein 10, 260-269, 1991
A:Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A:Reference number: A48238; PMID:9135005; PMID:1881882
A:Accession: A48238
A:Contents: annotation; X-ray crystallography, 2.5 angstroms
R:Krauss, R.S.; Collins, E.O.; Roberts, J.D.
Protein 10, 251-258, 1991
A:Title: Structure of ricin A-chain at 2.5 angstroms.
A:Reference number: A48239; PMID:9135004; PMID:1881881
A:Accession: A48239
A:Contents: annotation; X-ray crystallography, 2.5 angstroms
C:Comment: The functional molecule is a disulfide-linked dimer of A and B chains, w
nto the cell of the A chain; B chains are also responsible for cell agglutination (C:Comment: This protein is cytotoxic and very poisonous to animals.
C:Superfamily: ricin; rRNA N-glycosidase homology
F:1.25/Domain: signal sequence #status predicted <S10> <ACH>
F:1.46-2/3/Domain: rRNA N-glycosidase homology #status predicted <ACH>
F:311-372/product: ricin D chain B #status experimental <CH>
F:445,409,449/Binding site: carbohydrate (asn) (covalent) #status experimental
F:115,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:212/Active site: Gly #status predicted
F:294-318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental
F:335-348,360/Binding site: N-acetylgalactosamine (asp, Glu, Asn) #status experimental
F:384,386/Binding site: N-acetylglucosamine (asp, Asn) #status experimental

Query Match 64.0%; Score 907.5; DB 1; Length 576;
Best Local Similarity 63.8%; Pred. No. 2e-60;
Matches 166; Conservative 33; Mismatches 60; Indels 1; Gaps 1;

QY 5 CAAEPTVRIYVGNQNVGRDPPDQNOIQMPSKSNDDPQNTTKRGGTTRSGSC 64
DB 318 CAAEPTVRIYVGNQNVGRDPPDQNOIQMPSKSNDDPQNTTKRGGTTRSGSC 377
QY 65 LITTYGYAGVYVNFPCNTAVRATIQIWDKGTINPRSLVLAASGIGKTTTLVQTL 124
DB 378 LITTYGYAGVYVNFPCNTAVRATIQIWDKGTINPRSLVLAASGIGKTTTLVQTL 437
QY 125 DDTGCSAEPTRVHGRNQRVNDPDDHNGNQIQMPSKSNDDPQNTTKRGGTTR 184
DB 438 IYAVSQGWLPPNNTQPVFTVITGYGLCLQNGQGVIEDC-SEERADQWLYADSGIR 496
QY 185 PQKQHQCLTSGDSVFTVITVYSCGASGQKRVYTHGALINSGIANDVAGQ 244
DB 497 PQKQHQCLTSGDSVFTVITVYSCGASGQKRVYTHGALINSGIANDVAGQ 556
QY 245 RIIITPATKRNQMLPVP 264
DB 557 RIIITPATKRNQMLPVP 576

RESULT 4

506330
Riclin E - castor bean (fragment)
N/Contains: chain B; rRNA N-glycosidase (EC 3.2.2.22) (chain A)
C/Species: Ricinus communis (castor bean)
C/Accession: S06330 J05381
C/Date: 31-Dec-1993 #sequence_revision 31-Mar-1990 #text_change 20-Aug-1999
R/Author: B.P. Murray, B.E. Halling, A.C. Halling, K.C. Tilakaratne, N. Long, G.L. Plant Mol. Biol. 9, 287-295, 1987
A/Title: Characterization of a cDNA encoding ricin E, a hybrid ricin-Ricinus communis agglutinin
A/Reference number: S06330
A/Accession: S06330
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-263 <LAD>
A/Cross-references: EMBL:M17631; NID:G169714; PIDD:AAA3506.1; PTD:G169715
R/Mark: T.; Funatsu, G.
A/Title: The complete amino acid sequence of the B-chain of ricin E isolated from small-plant Ricinus communis
A/Reference number: J05381; NID:G101186; PMID:3601493
A/Accession: J05381
A/Molecule type: protein
A/Residues: 1-69; PS: 72-209; A: 211-241, 243-250; V: 252-263 <RH>
A/Experimental source: seed
C/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase
F:1-753/Product: ricin B #status experimental <ECH>
F:17-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40-residue repeats
F:20-32, 63-80, 151-164, 190-207/Distal/Id bonds: #status predicted
F:95, 105/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 61.8%; Score 877; DB 2; Length 263;
Best Local Similarity 61.7%; Pred. No. 2, 7e-66;
Matches 161; Conservative 37; Mismatches 61; Indels 2; Gaps 2;
QY 5 CSASEPTVAIVGNKRNKRVADDDPHDQNOIQLPKSKNDPNQMTIKRDTIRNSGC 64
DB 4 CMDEPPIVAVGNKGLCVDRGGRFHGMALQMPCKSNIDANOQTLKRNITISNGKC 63
QY 65 LTTGTGAGVYVIMPCDNTAVRENTIWIQNDGIIINPSNVLVAASSGIGKTLITVQTL 124
DB 64 LTTGTSPGVYVIMPCDNTAVRENTIWIQNDGIIINPSNVLVAATSGITLITVQTN 123
QY 125 DYTGGGMLAGNDTPAREVTIYGRDLCMEENGSGVYVETCDSSQNGKRALYDGSIR 184
DB 124 IVAVSGMLPTNNTQPFVITVGLVGLKGLQANSGVMEHC-TEBAHQMALYDGSIR 182
QY 185 PRONQDCLTSGRDSVSTVINTVSCGASGSGRWVTEGAILNLKNGLAMDPVAQANP-K 243
DB 183 PQQRNDCLTIDANKITVAVKLSGCVSSQGNRMKNDITLNLVGLVLDVRSDDPS 242
QY 244 LKRIITVATKRNQMTLPVF 264
DB 243 LKQIVAFPHANQMTLPVF 263
RESULT 5
R/CSAG
N/Contains: rRNA N-glycosidase (EC 3.2.2.22)
C/Species: Ricinus communis (castor bean)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
R/Author: B.P. Murray, B.E. Halling, A.C. Halling, K.C. Tilakaratne, N. Long, G.L. Plant Mol. Biol. 9, 287-295, 1987
A/Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
A/Reference number: A24261; NID:86059449; PMID:2993130
A/Accession: A24261
A/Molecule type: mRNA
A/Residues: 1-564 <ROB>
A/Cross-references: GB:M12089; NID:G169700; PIDD:AAA3869.1; PTD:G169701
R/Mark: T.; Yoshioaka, Y.; Funatsu, G.
A/Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin

A/Reference number: A24210
A/Accession: A24210
A/Molecule type: protein
A/Residues: 303-325; P: 327-330; T: 332-361; D: 363-373; G: 375-403; T: 405-551; V: 553-564
C/Comment: This protein has strong agglutinating activity and weak cytotoxicity com
C/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; rRNA
F:1-325/Product: ricin B #status predicted <SIC>
F:125-200/Product: ricin B #status predicted <SIC>
F:325-281/Domains: rRNA N-glycosidase homology; rRNA N-glycosidase homology
F:303-564/Product: agglutinin chain B #status experimental <ROB>
F:319-361, 363-402, 405-443, 450-489, 528-531, 564/Region: 40-residue repeats
F:104, 147, 231, 232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:200, 203/Active site: Glu, Arg #status predicted
F:262, 306, 322-341, 365-382, 453-466, 492-509/Distal/Id bonds: #status predicted
F:324, 337, 348/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status predicted
F:357, 437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:556, 557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
Query Match 55.3%; Score 793.5; DB 1; Length 564;
Best Local Similarity 55.2%; Pred. No. 5e-58;
Matches 146; Conservative 41; Mismatches 72; Indels 1; Gaps 1;
QY 5 CSASEPTVAIVGNKRNKRVADDDPHDQNOIQLPKSKNDPNQMTIKRDTIRNSGC 64
DB 306 CMDEPPIVAVGNKGLCVDRGGRFHGMALQMPCKSNIDANOQTLKRNITISNGKC 365
QY 65 LTTGTGAGVYVIMPCDNTAVRENTIWIQNDGIIINPSNVLVAASSGIGKTLITVQTL 124
DB 366 LTTKSSRQGVYVIMPCDNTAVRENTIWIQNDGIIINPSNVLVAATSGITLITVQTN 425
QY 125 DYTGGGMLAGNDTPAREVTIYGRDLCMEENGSGVYVETCDSSQNGKRALYDGSIR 184
DB 124 IVAVSGMLPTNNTQPFVITVGLVGLKGLQANSGVMEHC-TEBAHQMALYDGSIR 184
QY 185 PRONQDCLTSGRDSVSTVINTVSCGASGSGRWVTEGAILNLKNGLAMDPVAQANP-K 243
DB 183 PQQRNDCLTIDANKITVAVKLSGCVSSQGNRMKNDITLNLVGLVLDVRSDDPS 242
QY 244 LKRIITVATKRNQMTLPVF 264
DB 243 LKQIVAFPHANQMTLPVF 263
RESULT 6
R/CSAG
N/Contains: rRNA N-glycosidase (EC 3.2.2.22)
C/Species: Abrus precatorius (indian jatropha)
C/Date: 31-Dec-1993 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
A/Title: The complete amino acid sequence of the A-chain of abrin-A, a toxic protein
A/Reference number: S32429; NID:86059449; PMID:2993130
A/Accession: S32429
A/Molecule type: mRNA
A/Residues: 1-564 <ROB>
A/Cross-references: GB:M12089; NID:G169700; PIDD:AAA3869.1; PTD:G169701
R/Mark: T.; Yoshioaka, Y.; Funatsu, G.
A/Title: The complete amino acid sequence of the A-chain of abrin-A, a toxic protein

[illegible]

Oy	124	LDYTLGGMLAGNDTAPREVTLYTFEDLOMESNGSWEVETCSGASQGNWAKALYEDGSI	183
Db	359	NEILMRGMRHNNISPEPTVSIIEGSLSDLNQASQSNWVDDCSHGED-CMALLYDSSI	447
Oy	144	RPKQVQDCLTSGSDSVETVYNVNSCSGASQGNWAFNFGALLNKLMDLVQANPF	243
Db	448	RSVQNTNCLTSSKHQSGSTILLMCSGNSQMSQGRWFDNGSISTYLDHVMVDKSDPS	507
Oy	244	LRRLITPAIKCPNQWALPWF	264
Db	508	KQILLMPLTSPNQWALPWF	528
RESULT 7			
CS24130		Abirin-b precursor - Indian licorice (fragment)	
Nl		Contains: RNA-N-glycosylase (EC 3.2.2.22)	
C/Species:		Abirus precatorius (Indian licorice)	
C/Date:		30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999	
C/Accession:		G324130, U01399	
C/Function:		C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.	
A/Title:		Biological structure of three distinct isobirins determined by cDNA sequencing	
A/Reference:		1993FEBS 523433, PMID:8421315	
A/Accession:		G324130	
A/Molecule type:		mRNA	
A/Residues:		1-527 <HUN>	
A/Cross-references:		GB:M69345; NID:1462296; PION:AAA12625.1; PID:g166297	
R/Kimura, M.; Sumiizawa, T.; Funatsu, G.			
B/Source:		Biotechnol. Biochem. 57, 166-169, 1993	
A/Title:		The complete amino acid sequences of the B-chains of Abirin-b and Abirin-b	
A/Reference number:		U01398; PMID:7763422	
A/Accession:		U01399	
A/Accession:		U01399	
A/Residues:		260-287, P.D. 283-290, 'N', 292-349, 'EQ', 352-377, 'N', 379-425, 'W', 427, 'D', 42	
C/Superfamily:		ricin: RNA-N-glycosylase homology	
C/Keywords:		classified bond; duplication; asparatus predicted <ACH>	
F/1-250/Product:		abirin-b chain A #status predicted <ACH>	
F/7-245/Domain:		RNA-N-glycosylase homology <RNG>	
F/260-527/Product:		abirin-b chain B #status experimental <BCH>	
F/282-324,335-365,368-406,413-440,442-491,494-527/Region:		40-residue repeats	
F/1/Modified site:		pyrrolidone carbonyl-lytic acid (Gln, Gly, Asn) #status predicted	
F/4/113,199,1995/Binding site:		substrate (Tyr, Glu, Asn) #status predicted	
F/163,166,166/Binding site:		carbamoylate (Asn) (covalent) #status predicted	
F/246-268,285-304,328-345,416-439,455-452/Diulfide bonds:		#status predicted	
F/287,311/Binding site:		N-acetylglucosamine (Asp, Asn) #status predicted	
F/499,520/Binding site:		N-acetylglucosamine (Asp, Asn) #status predicted	
Query Match		54.4%: Score 771; DB 2; Length 527;	
Best Local Similarity		55.2%: Pred. No. 5, 2e-57;	
Matches		144: Conservative 43; Mismatches 72; Indels 2; Gaps 2;	
Oy	5	CSAS-EPFVIRVGRNKKVVDVDDPHQDQILQPSKSNNDPMQMTIKKQDTRFNSG	63
Db	268	CSATVETVIRGNNKQCNVDVDDPHQDQILQPSKSNNDPMQMTIKKQDTRFNSG	327
Oy	64	CLTGGTGGVYVYVPEQDAAPEATITQKNDGNTINPMSVLAASGKIDTITVQY	123
Db	328	CLTGGTGGVYVYVPEQDAAPEATITQKNDGNTINPMSVLAASGKIDTITVQY	387
Oy	124	LDYTLGGMLAGNDTAPREVTLYTFEDLOMESNGSWEVETCSGASQGNWAKALYEDGSI	183
Oy	144	RPKQVQDCLTSGSDSVETVYNVNSCSGASQGNWAFNFGALLNKLMDLVQANPF	243
Db	388	NEILMRGMRHNNISPEPTVSIIEGSLSDLNQASQSNWVDDCSHGED-CMALLYDSSI	446
Oy	244	LRRLITPAIKCPNQWALPWF	264
Db	447	RSVQNTNCLTSSKHQSGSTILLMCSGNSQMSQGRWFDNGSISTYLDHVMVDKSDPS	506
Oy	244	LRRLITPAIKCPNQWALPWF	264

RESULT 8

abrin-c precursor - Indian licorice (fragment)
C:Accession: S16022
C:Species: abrin N-glycosidase homology
C:Date: 19-Mar-1997 #revision 19-Mar-1997 #text_change 20-Aug-1999
R:Wood, K.A.; Lord, J.M.; Nawroozak, E.J.; Platak, M.
Eur. J. Biochem. 198, 723-732, 1991
A:Title: Preprobrin: genomic cloning, characterization and the expression of the A-chain
A:Reference number: S16022; PMID:9166957; PMID:2050149
A:Accession: S16022

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-562 <MOD>

C:Comment: The A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.

C:Superfamily: ricin; RNA N-glycosidase homology

C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid

F:35-285/Product: abrin-c chain A #status predicted <RNG>

F:41-280/Domain: RNA N-glycosidase homology <RNG>

F:295-562/Product: abrin-c chain B #status predicted <RNG>

F:317-359/Product: abrin-c chain B #status predicted <RNG>

F:35/Modified site: pyroglyutamic acid (Gln) (in mature form) #status predicted

F:199-247/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted

F:234-287/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted

F:281-303/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:322-346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

RESULT 9

abrin-c precursor - Indian licorice (fragment)
C:Accession: S16022
C:Species: abrin N-glycosidase homology
C:Date: 19-Mar-1997 #revision 19-Mar-1997 #text_change 20-Aug-1999
R:Wood, K.A.; Lord, J.M.; Nawroozak, E.J.; Platak, M.
Eur. J. Biochem. 198, 723-732, 1991
A:Title: Preprobrin: genomic cloning, characterization and the expression of the A-chain
A:Reference number: S16022; PMID:9166957; PMID:2050149
A:Accession: S16022

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-562 <MOD>

C:Comment: The A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.

C:Superfamily: ricin; RNA N-glycosidase homology

C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid

F:35-285/Product: abrin-c chain A #status predicted <RNG>

F:41-280/Domain: RNA N-glycosidase homology <RNG>

F:295-562/Product: abrin-c chain B #status predicted <RNG>

F:317-359/Product: abrin-c chain B #status predicted <RNG>

F:35/Modified site: pyroglyutamic acid (Gln) (in mature form) #status predicted

F:199-247/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted

F:234-287/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted

F:281-303/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:322-346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

F:534-555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Thu Dec 11 16:10:04 2003

us-09-601-667c-7.rpr

DB 309 GPKCLDPAAGTNGSKVQIVSCWGDNDOK--NRINSDSVVGVQSLCDVAVNGTANGTL 366
QY 119 LTVQTLDTTLGGCM 132
DB 367 LQVTCGSGNSQNR 380

RESULT 14

135697
arabino furanoseidase - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Dec-1999
C/Accession: J35697
R/Murphy, L.; Hartig, D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, January 1998
A/Reference number: Z21548
A/Accession: J35697
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1475 <NDR>
A/Cross-references: EMBL:AL021411; PIRN:CAA15189.1; GSPDB:GM00070; SCOPEDB:SC7H1.02
A/Experimental source: strain AJ(2)
C/Genetics:
A/Genes: abfB; SCOPEDB:SC7H1.02

Query Match

Best Local Similarity 8.1%; Score 115.5; DB 2; Length 475;
Best Local Similarity 24.1%; Pred. No. 0.054; Indels 25; Gaps 10;

Matches 52; Conservative 35; Mismatches 104; Indels 25; Gaps 10;

DB 6 SASBPTRIVGRKNGKVDYDDPHDQIQOLPMSKSNDDPQLTKDGTIRSG-SC 64
QY 37 AAGSALRAGNSNRC-LDVAGSGDDGALLQVDCWGGT--NQWTSPTGRALVYGRKC 93
DB 65 LTVGYTA--GVYVMPDCAVREATVQIMDNGTINPSNLV-AAASG-IGKTLR 120
QY 94 LDVPGHATPGTRVQIMSCGAGNQC--NRVNSDGVVGVESGLCEAAGGTANGTAVQ 151
DB 121 VQTLDTTLGGCMLASNDTAPREVT---TGFEDLCMESNGSVWTECD-SSQNR 174
QY 152 LWCICGSGNQNRGTLGTPFDTCALPSTRMSSTGYVLAQPSKSWYALADPTTVHNGR 211
DB 175 MALVGDGS-----IRKNOQCTSGRDSVS 201
QY 212 HLIVGSTRSGSGSVSWPSPFTNMEWMAAGQANNN 247

RESULT 15

A39094
glucan endo-1,3-beta-glucosidase (EC 3.2.1.-) precursor - Oerskovia xanthineolytica

C/Species: Oerskovia xanthineolytica

C/Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 22-Oct-1999

C/Accession: A39094
C/Author: S.N. Oerskovian, P. Bastien, L. Siliaty, S.N.

T/Biol. Chem. 267:1058-1063, 1991

A/Title: Primary sequence of the glucanase gene from Oerskovia xanthineolytica. Express

A/Reference number: A39094; PMID:91093212; PMID:1985933

A/Accession: A39094

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-548 <SHE>

A/Cross-references: GB:M60826; GB:M8734; NID:5150444; PIRN:AAA25520.1; PIR:G150445

C/Keywords: glycosidase; hydrolase

Query Match 8.0%; Score 114; DB 2; Length 548;

Best Local Similarity 31.3%; Pred. No. 0.086; Indels 20; Gaps 7;

Matches 41; Conservative 18; Mismatches 52; Indels 20; Gaps 7;

DB 16 GRNGRY-----DVDDPHDQIQOLPMSKSNDDPQLTKDGTIRSGSC--TT 67
QY 422 GTGALRGSLCLVPMADPTDNOVCL--ATCGRAAQWTRGDTVRALGKCLDVAR 479
DB 68 YGTAGVYVMPDCAVREATVQIMDNGT--INPSNLVLAASG--KATTLV 121

DB 480 SGTAGTAVVYTCNGTNGKQRT---YDSATKLRNPQSKCLDAGGAPLRDQKVL 535
QY 122 QTLDTTLGGCM 132
DB 536 WTCNQTBNQR 546

Search completed: December 11, 2003, 13:55:43
Job time : 9.20622 secs

CC		cell.The B chain binds to cell receptors and facilitates the
CC		entry into the cell of the A chain; B chains are also responsible
CC		for cell agglutination (lectin activity). It binds to beta-D-
CC		galactopyranoside moieties.
CC	-1	GALACTIC ACCTIVITY. Endohydrolysis of the N-glycosidic bond at one
CC		specific adenosine on the 28S rRNA.
CC	-1	DNA BINDING. The B chain is composed of two domains each domain
CC	-1	consists of 3 homologous subdomains (alpha, beta gamma).
CC	-1	PMR: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE
CC	-1	MNR: A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
CC	-1	SIMILARITY: IN THE N-TERMINAL SECTOR; BELONGS TO THE RIBOSOME-
CC		INACTIVATING PROTEIN FAMILY. TYPE 2 RIT SUBFAMILY.
CC	-1	SIMILARITY: contains 2 ricin B-type lectin domains.
CC	-1	CAUTION: RES. 4 AND RES. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
CC	-1	WITH OTHER SEQUENCES FROM THIS SPECIES (RES. 1, RES.2 AND RES.3).
CC	-1	DATABASE: NAME:protein Spotlight;
CC		NORREUSE 31 of February 2003).
CC		WWW:"http://www.expasy.org/spotlight/articles/splic031.html".
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration -
CC		between the Swiss Institute of Bioinformatics and the EMBL consortium -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as their name is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC		or send an email to license@isb-sib.ch).
DR	EMBL:	X03179; CAA6939.1; -
DR	EMBL:	XS2908; CAA37095.1; -
DR	EMBL:	X02388; CAA26230.1; -
DR	EMBL:	A12892; CAA01058.1; -
DR	PIR:	A24041; RLCSB.
DR	PDB:	2A4I; 31-JUN-94.
DR	PDB:	1AFG; 31-JAN-94.
DR	PDB:	1IFG; 31-OCT-93.
DR	PDB:	1IFD; 14-JUN-93.
DR	PDB:	1IFU; 14-JUN-98.
DR	PDB:	1IRC; 31-OCT-93.
DR	PDB:	1OBT; 16-JUN-97.
DR	PDB:	1OBT; 16-JUN-97.
DR	PDB:	1BR5; 02-SEP-98.
DR	PDB:	1BR6; 02-SEP-98.
DR	PDB:	1IJ3; 16-JAN-02.
DR	PDB:	1IJ4; 16-JAN-02.
DR	PDB:	1J99; 16-MAY-92.
DR	GSD:	1XQBD; PDB972.
DR	InterPro:	IPR000773; Ricin_B_lectin.
DR	InterPro:	IPR001574; RIP.
DR	Pfam:	PF00652; Ricin_B_lectin, 6.
DR	Pfam:	PP00161; Rip, 1.
DR	PRINTS:	PR00396; SHIGABICIN.
DR	SMART:	SM00458; RICIN_2.
DR	PROSITE:	PS00231; SHIGA_RICIN_1.
DR	PROSITE:	PS00275; SHIGA_RICIN_1.
KM		Paul Delange, Hydrolaes; Ricoin synthetis inhibitor; Toxin; Repeat;
KM		Glutathione S-transferase; 3p-structures.
FT	SIGNAL	1..35
FT	CHAIN	36..302
FT	PEPTIDE	303..314 LINKER PEPTIDE.
FT	CHAIN	315..576 RICIN B CHAIN.
FT	DOMAIN	321..448 RICIN B-TYPE LECTIN 1.
FT	DOMAIN	451..575 RICIN B-TYPE LECTIN 2.
FT	REPEAT	331..373 1-ALPHA.
FT	REPEAT	377..414 1-BETA.
FT	REPEAT	417..452 2-GAMMA.
FT	REPEAT	455..480 2-BETA.
FT	REPEAT	501..540 2-GAMMA.
FT	REPEAT	543..570 2-GAMMA.
FT	ACT SITE	212..212
FT	DISULFID	294..318 INTERCHAIN.
FT	DISULFID	334..353

	Query Match	BLAST similarity	Score	60% ID	60% ID	DB 1	Length	576
	Matches	166	Conservative	33	Mismatches	60	Indels	1
FT	DISULFID	377	394					
FT	DISULFID	465	478					
FT	DISULFID	504	521					
FT	CARBOHYD	45	45					
FT	CARBOHYD	271	271					
FT	CARBOHYD	409	409					
FT	CARBOHYD	449	449					
FT	CONFLICT	76	76					
FT	CONFLICT	551	551					
FT	STRAND	43	47					
FT	TURN	49	50					
Query Match	64.0%	Score 607.5	DB 1	Length 576				
BLAST similarity	64.0%	Mismatches 70	Indels 1	Gaps 1				
Matches 166	Conservative 33	Mismatches 60	Indels 1	Gaps 1				
QY	5	CSASPEPVATYGRGMRHVDRODPEHNGNOQLMPSEKKNDDPVLQMTLRKDGITRNSGSC	64					
Db	318	CHDPPVATYGRNGLCVDVGRFHNGNAQLMPCKSTNDANQMTLRKDVITRNSKGC	377					
QY	65	LTFTYTAQYVW.PDQNTVEATITWIMNGTINPNSVLTAASSGIKOTLTLYOTL	124					
Db	378	LTFTYTAQYVW.PDQNTVEATITWIMNGTINPNSVLTAASSGIKOTLTLYOTL	124					
QY	125	DYTGAGGAGMGPATRYATYVPRDLCSENGSVYVWCCSGKQKQGNALYVGGSGIR	184					
Db	438	IYVSGQWPLNNTPQPTVITVGLVGLCLQNSQGVTEIDC-SSEKAEQNALYADGSR	496					
QY	185	PKRNDQCTGSRASVTVINIVSGASGASGRNVTMEGALINIKNGALMDVAKMPEL	244					
Db	497	FOQNDMDCLTSGNSIEVTVLISGPNASGQRFKNDGTLINLVGLVADYASDPL	556					
QY	245	RRLLTTPANGKRNQMLVPE	264					
Db	557	KQILIPEDKNDVWLP	576					
RESULT 3								
ID	AGGL_RICCO	STANDARD	PRT	564 AA.				
AC	P06750							
DT	01-JAN-1988 (Rel. 06, Created)							
DT	01-JUN-1988 (Rel. 06, Last sequence update)							
DT	28-FEB-2003 (Rel. 41, Last annotation update)							
DE	Agglutinin (EC 3.2.2.22), Agglutinin B chain. N-							
OS	Ricinus communis (Castor bean)							
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;							
OC	Spermatophyta; Magnoliopsida; eudicotyledons; Core eudicots; Rosidae;							
OC	eucotids I; Malpighiales; Euphorbiaceae; Ricinus.							
OX	NCBI_TaxID=3989;							
LN	[1]							
LN	SEQUENCE FROM N.A.							
RK	MEDLINE=8059449; PubMed=2999130;							
RK	Repetto L.N., Lamb F.I., Apple D.J.C., Lord J.M.;							
RK	Agglutinin: primary sequence of Ricinus communis agglutinin. Comparison with							
RT	ricin".							
RT	J. Biol. Chem. 260:15682-15686(1985).							
RN	[2]							
RN	SEQUENCE OF 303-564.							
RA	TRISUB-Seed.							
RA	Azaki, T., Yoshioka Y., Funatsu G.;							
RT	"The complete amino acid sequence of the B-chain of the Ricinus							
RT	communis agglutinin isolated from large-grain castor bean seeds".							
RJ	Biochim. Biophys. Acta 871:277-285(1986).							
RN	SEQUENCE OF 303-327.							
RK	MEDLINE=8018723; PubMed=676855;							
RK	Lin T.-S., Li S.-L.							
RT	"Purification and physicochemical properties of ricins and							
RT	agglutinins from Ricinus communis".							

```

NC Eur. J.Biochem. 105;453-459(1980).
CC -I- CATALYTIC ACTIVITY. Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
CC -I- SIMILARITY: IN THE N-TERMINAL SECTOR, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
CC -I- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC This Swiss-ProT entry is complete. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL institution CC the European Bioinformatics Institute. There are no restrictions on way CC use by non-profit institutions as long as its content is in no way CC modified and thus statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licenses@isb-sib.ch).
CC -----
DR EMBL, M43689, AAA33869.1, -,
DR EMBL, S40366, AAB22594.1, -,
DR HSP, P40379, RLCSA6.
DR GlycoSignalDB, PGCFB9.
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR000396; SHIGARICIN.
DR SMART: PS50231; RICIN_B_LLECTIN; 2.
DR PROSITE: PS00273; SHIGA_RICIN; 1.
DR Plant defense; Hydroxase; Protein synthesis inhibitor; Toxin; Repeat; K repeat; Lectin; Signal; CONCEPTUAL.
KT STORM.
FT CHAIN 25 280
FT PROPEP 231 302 AGGLUTININ A CHAIN.
FT CHAIN 303 564 AGGLUTININ B CHAIN.
FT DOMAIN 309 456 RICIN-B-TYPE LECTIN 1.
FT DOMAIN 439 563 RICIN-B-TYPE LECTIN 2.
FT REPEAT 319 361 1-ALPHA.
FT REPEAT 362 402 1-BETA.
FT REPEAT 405 437 1-GAMMA.
FT REPEAT 438 489 2-BETA.
FT REPEAT 489 558 2-GAMMA.
FT ACT SITE 200 200 BY SIMILARITY.
FT DISULFD 282 306 INTERCHAIN (BY SIMILARITY).
FT DISULFD 322 341 BY SIMILARITY.
FT DISULFD 365 382 BY SIMILARITY.
FT DISULFD 453 466 BY SIMILARITY.
FT DISULFD 492 509 BY SIMILARITY.
FT CARBOHD 34 34 N-LINKED (GlcNAc...) (POTENTIAL).
FT CARBOHD 259 259 N-LINKED (GlcNAc...) (POTENTIAL).
FT CARBOHD 437 437 N-LINKED (GlcNAc...).
FT CARBOHD 437 437 F -> T (IN REF. 2).
FT CONFLICT 331 331 F -> T (IN REF. 2).
FT CONFLICT 362 362 N -> D (IN REF. 2).
FT CONFLICT 374 374 R -> G (IN REF. 2).
FT CONFLICT 404 404 R -> T (IN REF. 2).
FT CONFLICT 552 552 R -> V (IN REF. 2).
SQ SEQUENCE 564 AA; 62851 MW; D455F2A7E6D09759 CRC64;

Query Match 55.3%; Score 783.5; DB 1; Length 564;
Ref: Local Similarity 55.2%; Frd. No. 15e-59;
Matches 141; Mismatches 72; Indels 1; Caps 1

QY CASPPVTVVRKGRVQRWDHDDPGHGNGIOITWPKSNRNDQATLKXDOGTETNSGC 64
Db CMNPFPFLRVIRVGKGVCDVTVEGEFFDNPIQLAPCKSTNMDQNLMLTRDSTIRSKXC 365
OY LTYYTGAVGYVMIFPCNTAFRAATLTWINDGGIIINPSNLVAASGIKKETLVQTLL 124
Db WTSSSSRQOVTVYSAAVAFAIRNQIDNRRIINFSQSVLAAISGNISTGLTLVTQN 425
OY DTTCGCLMAGNOTAREPVTTVGFDFDKCESNGSVWEVTDSDSGRNQGMALYRGDSIR 164

```

Db	426	IAVSGQMCPNNINQCPPTVITGLVGLGVCNAGSKVLEQC-TSEKAEQWALVYADASRIR	484
Qy	185	PQNQDDCTSGSDSVSTVNTVSCSASGSGQWPTBEALINLNGSLADYVQAMFKL	244
Db	485	POQRDQCLTIDNANIKGVVXKLSGSPASGQWFMFNDGTITLVLNGLVLEVRADPSL	544
Qy	245	RLIITPDATGSGQWQWMLP	264
Db	545	KQIVHPHAGNQLNQLLEFL	564
RESULT 4			
ID	ABRA_ABRFP	STANDARD	FR1, 528 AA.
CD	P11140; F28589;		
DT	01-JUN-1989 (Rel. 11, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	01-JUN-2002 (Rel. 10, Last annotation update)		
DE	ABRIN-2002 (Ref. 1), last mutation A to G at position 114 (NC 3 2 2 221) - Abria-A B chain (rRNA N-glycosidase)		
OC	Abus presaccharin (indian licorice) (crab's eye).		
OC	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Rosidae; eucotids 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.		
ON	NCBI_TaxID=3816;		
OX	[1]		
RF	SEQUENCE FROM N.A.		
RF	MEDLINE=9132786; PubMed=8421133;		
RF	PMID=8421133; PMID=8421133; PMID=8421133; PMID=8421133;		
RT	"Primary structure of three distinct isoforms determined by cDNA sequencing. Conservation and significance."		
RT	J. Mol. Biol. 229:263-267 (1993).		
RL	[2]		
RL	SEQUENCE OF 1-251.		
RC	TISSUE=Seed.		
RA	Funatsu G., Taguchi Y., Kameosono M., Yanaka M.;		
RA	"The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from the seed of Abrus precatorius (Andromeda).		
RA	Appl. Biol. Chem. 52:1095-1097 (1989).		
RL	[3]		
RF	SEQUENCE OF 1-251 FROM N.A.		
RC	TISSUE=Leaf.		
RA	Medline=91201329; PubMed=2016300;		
RA	Evans G., Mathiesen A., Sundan A.;		
RT	"Direct molecular cloning and expression of two distinct abrin A-chains."		
RT	J. Biol. Chem. 266:6848-6852 (1991).		
RL	[4]		
RF	SEQUENCE OF 262-528		
RA	MEDLINE=92317056; PubMed=1505674;		
RA	Chen Y.-L., Chow L.-P., Tseng A., Lin J.-Y.;		
RT	"The complete primary structure of abrin-a B chain."		
RT	FEBS Lett. 309:115-118 (1992).		
RF	[5]		
RF	X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).		
RA	MEDLINE=9533118; PubMed=7605980;		
RA	Talbot T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;		
RA	Crytallogr. Bioact. 250:35-47 (1995).		
CC	-1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA.		
CC	ABRIN-A IS MORE TOXIC THAN RABIN.		
CC	-1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.		
CC	-1- CATALYTIC ACTIVITY: endoglycosylase of the N-glycosidic bond at one specific asparagine on the 28S rRNA.		
CC	-1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).		
CC	-1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSE-INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.		

CC	-1 SIMILARITY: Contains 2 ricin B-type lectin domains.
CC	This SWISS-PROT entry is copyrighted. It is produced through a collaboration -
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its use by
CC	non-profit institutions as long as its content is in no way used for commercial
CC	purposes and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.isb-sib.ch/announcements)
CC	CC License: public domain.
DR	EMBL; M98344; AAA32624.1; ALT INIT.
DR	EMBL; X54879; -. NOT ANNOTATED_CDS.
DR	PIR; S32429; TZLSA.
DR	PDB; 1ABR; 07-FEB-95.
DR	InterPro; IPR000772; Ricin_B_lectin.
DR	InterPro; IPR001574; RLP.
DR	Fam; PF00652; Ricin_B_lectin; 6.
DR	Fam; PF00651; Ricin_A_lectin; 6.
DR	PRINTS; PR00366; RHICACIN.
DR	SMART; SMO0458; RCICIN; 2.
DR	PROSITE; PS50231; RCICIN_B_LECTIN; 2.
DR	PROSITE; PS00275; SHIGA_RICIN; 1.
KM	Plant defense; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;
XW	Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.
FT	CHAIN 1 251
FT	PEPTIDE 252 261
FT	LINKER PEPTIDE 262 268
FT	AHRIN A & CHAIN 269 528
FT	RICIN A-TYPE LECTIN 1. 529 597
FT	RICIN B-TYPE LECTIN 2. 598 625
FT	REPEAT 283 325
FT	REPEAT 326 366
FT	REPEAT 369 401
FT	REPEAT 404 449
FT	REPEAT 453 492
FT	REPEAT 495 528
FT	ACT_SITE 164 164
FT	DISULFID 267 269
FT	DISULFID 274 276
FT	DISULFID 326 328
FT	DISULFID 417 430
FT	DISULFID 456 473
FT	MOD_RES 1 1
FT	CARBONYD 361 361
FT	CARBONYD 401 401
FT	CONFLICT 202 202
FT	CONFLICT 298 298
FT	CONFLICT 427 427
FT	CONFLICT 457 457
FT	CONFLICT 483 483
FT	STRAND 5 5
FT	TURN 10 11
FT	HELIX 12 28
FT	STRAND 32 33
FT	TURN 34 34
FT	STRAND 36 38
FT	TURN 42 43
FT	HELIX 47 49
FT	STRAND 51 57
FT	TURN 61 62
FT	STRAND 70 72
FT	TURN 75 79
FT	STRAND 83 86
FT	TURN 88 89
FT	TURN 92 93
FT	HELIX 94 97
FT	TURN 100 101
FT	STRAND 103 106
FT	TURN 110 113
FT	HELIX 115 116
FT	TURN 124 126
FT	STRAND 129 129
FT	HELIX 131 142
FT	TURN 143 144

Query Match	ES 14, Score 781, DB 1, Length 529, Identity 94.8%, Fred. No. 3, 2e-570, Mismatches 145, Gaps 2
FT HELIX	148 167
FT STRAND	168 168
FT HELIX	169 180
FT TURN	181 182
FT STRAND	185 185
FT HELIX	189 196
FT TURN	197 197
FT STRAND	198 207
FT STRAND	212 223
FT TURN	222 223
FT STRAND	226 231
FT TURN	232 233
FT HELIX	235 239
FT STRAND	240 240
FT STRAND	243 243
FT STRAND	248 248
FT STRAND	268 268
FT STRAND	276 277
FT STRAND	277 284
FT HELIX	282 284
FT STRAND	286 289
FT HELIX	290 292
FT TURN	296 297
FT STRAND	299 303
FT HELIX	311 313
FT STRAND	315 317
FT TURN	319 320
FT STRAND	322 325
FT TURN	326 332
FT STRAND	332 337
FT TURN	337 338
FT STRAND	340 344
FT TURN	346 348
FT HELIX	351 353
FT STRAND	355 355
FT STRAND	357 358
FT TURN	360 361
FT STRAND	364 366
FT TURN	377 378
FT STRAND	377 381
FT TURN	380 383
FT STRAND	383 387
FT STRAND	385 395
FT HELIX	398 399
FT STRAND	406 408
FT STRAND	410 411
FT HELIX	413 415
FT STRAND	417 421
FT TURN	421 428
FT STRAND	424 428
FT TURN	432 433
FT HELIX	435 437
FT STRAND	439 441
FT TURN	443 444
FT STRAND	447 449
FT TURN	450 451
FT STRAND	452 459
FT TURN	464 465
FT STRAND	465 472
FT TURN	474 475
FT HELIX	478 480
FT STRAND	483 484
FT TURN	486 487
FT STRAND	490 492
FT TURN	496 496
FT STRAND	497 501


```

DR InterPro: IPR000772; Ricin B lectin.
DR Pfam: PF00331; Glyco_hydro_10; 1.
DR Pfam: PF00652; Ricin B lectin; 3.
DR PRINTS: PR00134; GHYDRLAS10.
DR SMART: SM00523; Glyco_10; 1.
DR SMART: SM00523; Ricin B lectin; 1.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE: PS00231; Ricin B lectin; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
KW 3D-structure.
FT SIGNAL 1 41
FT CHAIN 42 477 ENDO-1,4-BETA-XYLANASE A.
FT DOMAIN 361 477 RICHIN B-TYPE LECTIN.
FT ACT_SITE 169 189 PROTON DONOR.
FT ACT_SITE 277 277 NUCLEOPHILE.
SQ SEQUENCE 477 AA; 51162 MW; 514AF3E7BD68CC CRC64;

Query Match
Best local similarity 28.9%; Score 125.5; DB 1; Length 477;
Matches 40; Conservative 20; Mismatches 61; Indels 13; Gaps 6;

QY 7 ASPP-----TVAIGNNKRVYDDDDPHDQGIQIWPFSKSNDDNQLTIKRDGTIRSN 61
DB 346 SSEPPADGQIKVIG--SGRLDVPASTSTDTGLQIMCHSGT--NQQMAATDAGSLAVY 402
QY 62 G-SCLTGYTAYGVYVIFDCNTAVRNPITQIWDNGTIIINPSNLYIAA--SSGIGKTT 118
DB 403 GDKCLDAAGTSGSKVQIISGAGDNK--WALNSGVSAGVSGCLDANGANSTANFTL 460
QY 119 LVTQTLDTYTLGGW 132
DB 461 IQLYTCNSNSNGW 474

RESULT 9
ID ABBP_STRCO STANDARD; PRT; 475 AA.
AC 054161; 1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).
GN ABBP OR SC05932 OR SC7H.02.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteri; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID:1902;
OX (1)
RE SEQUENCE FROM N.A.
RX KINRINAS12 (10/10/98) W64-1200953.
RX BENTLEY3.D, Chatterjee K.E., Cerdas E., Farraga A.-M., Chellis G.L.,
RA Thomson N.P., James K.D., Harris D.E., Chail M.A., Kisser H.,
RA Harper D., Bateman A., Brown S., Chanda G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajadream M.A., Rutherford K., Rutter S., Taylor K.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorek A., Woodward J., Barrett B.G., Parkhill J.,
RA Hopwood D.A.;
RE Complete genome sequence of the model actinomycete Streptomyces
COelicolor A3(2) (12/002).
FT METADATA: 12/17/2003)
CC -1 CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-
CC arabinofuranoside residues in alpha-L-arabinosides.
CC -1 PATHWAY: Xylan degradation.
CC -1 SUBCELLULAR LOCATION: secreted.
CC -1 SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL_HYDROLASES.
CC -1 SIMILARITY: Contains 1 ricin B-type lectin domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```

```

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AL391251; CA616189.1; -.
DR FAK; J35697; J35697. Glyco_hydro_62.
DR InterPro: IPR00123; Glyco_hydro_62.
DR InterPro: IPR00123; Ricin B lectin.
DR Pfam: PF00652; Glyco_hydro_62.
DR Pfam: PF00652; Ricin B lectin; 3.
DR SMART: SM00458; Ricin B lectin; 1.
DR PROSITE: PS00231; Ricin B lectin; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
KW Complete proteome.
FT SIGNAL 1 37
FT CHAIN 38 475 ALPHA-L-ARABINOFURANOSIDASE.
FT DOMAIN 169 166 RICHIN B-TYPE LECTIN.
SQ SEQUENCE 475 AA; 50045 MW; 47E107F834C6D0 CRC64;

Query Match
Best local similarity 24.1%; Score 115.5; DB 1; Length 475;
Matches 52; Conservative 35; Mismatches 104; Indels 25; Gaps 10;

QY 6 SASPTVRIYGRNKRVDYDDPHDQGIQIWPFSKSNDDNQLTIKRDGTIRSN;SC 64
DB 37 AAGSGALRAGSNRC-LDVGSGSDGALQLQIDCWGRT--NQQMTSTDTGRLTYGDKC 93
QY 65 LTYGYTA--GVYVIFDCNTAVRNPITQIWDNGTIIINPSNLYI--AASG--IKETTL 120
DB 94 LVTGKATRTGRTVQIWSGAGANQ--WRVNSDSTGVYSGCLDANGANSTANFTV 151
QY 121 VQTLDTYTLGGW 132
DB 152 LVTGSGNQTWGLTGPPTDGLCPSTYRSGSTVLAQKSGWALXKDTFTYHNH 211
QY 175 MALYCDGS-----IRKKNDDCITSGRSVS 201
DB 212 HLYVGTSGSGSYSNVFSPTNMSDMSAQQNN 247

RESULT 10
ID E13B_ARTSP STANDARD; PRT; 546 AA.
AC 059146; 1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) (1->3)-beta-
DE glucan endohydrolase (1->3)-beta-glucanase).
GN Actinobacter sp. (strain YCM03).
OC Bacteria; Actinobacteri; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Actinobacter.
OX NCBI_TaxID:1667;
OX (1)
RE SEQUENCE FROM N.A.
RX Submitted (DEC-1993) to the EMBL/Genbank/DBJ databases.
RA Natanabe T., Hasegawa H., Tanaka H., Doi A., Doi K.;
RA FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
CC IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS (BY
CC SIMILARITY).
CC -1 CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
CC in 1,3-beta-D-glucans.
CC -1 SUBCELLULAR LOCATION: periplasmic (by similarity).
CC -1 PATHWAY: BELONGS TO FAMILY 64 OF GLYCOSYL_HYDROLASES.
CC -1 SUBCELLULAR LOCATION: secreted.
CC -1 SIMILARITY: Contains 1 ricin B-type lectin domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

```

```

Cc      Pfam: PF00652; Ricin B Lectin; 3
Cc      DR SMART: SMO0458; RCLIN_1.
Cc      KW PROSITE: PS02031; RICIN B LECTIN; 1.
Cc      KR HYDROLASE; Glycosidase; Signal; Peptidase; Cell wall; Lectin.
Cc      FT SIGNAL 37 548 POTENTIAL.
Cc      FT CHAIN 1 36 GLUTAMINE-ENDORIBIN-GLUCOSIDASE.
Cc      FT DOMAIN 422 436 POSSIBLE BETA-GLUCANASE ACTIVITY, BUT IS
Cc      FT DOMAIN 37 430 UNABLE TO LYSE VIABLE CELLS.
Cc      FT DOMAIN 472 548 ESSENTIAL FOR THE LYTIC ACTIVITY, BUT NOT
Cc      FT FOR THE BETA-GLUCANASE FUNCTION.
Cc      SO SEQUENCE 548 AA; 5808 MW; 412B5A4A2AC049D CRC64;
Cc      Qy Query Match 8.3%; Score 114; DB 1; Length 548;
Cc      Bc Best Local Similarity 31.3%; Pred. No. 0.0261; Gaps 7;
Cc      Dc Matches 41; Conservative 18; Mismatches 52; Indels 20; Gaps 7;
Cc      Db 422 GGALRISTSLCTLDIPADPDFTQVLT -ATGSGNAAGTGRGDIVRALSKLDAVAR 479
Cc      Qy 16 GENCMRI-----DTADDPHHQGLCLMPKSNDDPVOITLRGGTGNSGC--TI 67
Cc      Db 440 SCETDGAGWAVLYCNGTGAOKXT-----YDSATFALRNPSGSCDLAAGSAPLPDPOXVL 535
Cc      Qy 122 CTLDYTLGGW 132
Cc      Db 536 WCHNDEEAKRW 546
Cc      RESULT 12
Cc      AAPP_STRLI STANDARD; PRT; 475 AA.
Cc      ID _AAPP_STRLI STANDARD; PRT; 475 AA.
Cc      AC P96463;
Cc      DT 15-DEC-1998 [Ref. 37, Created]
Cc      DT 15-DEC-1998 [Ref. 37, Last sequence update]
Cc      DT 28-FEB-2003 [Ref. 41, Last annotation update]
Cc      DE Alpha-D-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).
Cc      OS Arabidopsis thaliana.
Cc      OC Eukaryota; Viridiplantae; Angiosperms; Streptomycetes lividans;
Cc      OC Bacteria; Actinobacteriae; Actinomycetales; Actinomycetaceae;
Cc      OC Streptomycetes; Streptomycetaceae; Streptomycetes.
Cc      NC NCB1_TaxId=1916;
Cc      RN [1]
Cc      RX SEQUENCE FROM N.A.
Cc      RC STRAIN=66 / 1326;
Cc      RA MEDLINE=97220396; PubMed=9148759;
Cc      RA "Lincent, F., Sharrock, F., Dupont, C., Morgesani, R., Kluepfel, D.;
Cc      WT "Arabidopsis thaliana strain ATCC 49246. Streptomycetes lividans:
Cc      RT cloning and DNA sequence of the ald5 gene and characterization of the
Cc      RL enzyme".
Cc      RL Biochem. J. 322:845-851(1997).
Cc      RN [2]
Cc      RP REVISIONS.
Cc      RC STRAIN=66 / 1326;
Cc      RA Sharrock F.;
Cc      DT Submitted (OCT-1998) to the EMBL/GenBank/DDBB databases
Cc      DT -1. FULL-LENGTH cDNA SPECIFIC FOR STREPTOMYCETACEAE ACTIVITY ON
Cc      DT ARABINOSIDE AND RELATED SUBSTRATES. SPECIFICALLY WITH THE CYTOSIDES AND
Cc      DT BINDS SPECIFICALLY TO XYLANS. FROM SMALL ARABINOXYLO-OLIGOSIDES,
Cc      DT IT LIBERATES ARABINOSE AND, AFTER PROLONGED INCUBATION, THE
Cc      DT PURIFIED ENZYME EXHIBITS SOME XYLANOLYTIC ACTIVITY AS WELL.
Cc      DT -1. CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-
Cc      DT arabinofuranoside residues in alpha-L-arabinoxylans.
Cc      DT -1. PATHWAY: xylan degradation.
Cc      DT -1. SUBCELLULAR LOCATION: Secreted.
Cc      DT -1. SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
Cc      DT -1. SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.
Cc      CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
Cc      CC between the Swiss Institute of Bioinformatics and the EMBL consortium.
Cc      CC The European Bioinformatics Institute. There are no restrictions on its
Cc      CC use by non-profit institutions as long as its content is in no way

```

```
CC modified and this statement is not removed. Usage by end user for commercial/
CC entities requires a license agreement (See http://www.isdb-sib.ch/about/license/)
CC or send an email to license@isdb-sib.ch).
CC -----
DR EMBL; M64551; AAC65824.1; .
DR InterPro; IPR005193; Glyco_hydro_62.
DR InterPro; IPR00772; Rcin_B_Lectin.
DR Pfam; PF00664; Glyco_hydro_62; 1.
DR SMART; SMO0619; Lectin_I-lectin; 3.
DR PROSITE; PS00231; RCIN B LECTIN; 1.
DR Kxylan degradation; Hydrolase; Glycosidase; Signal; Lectin.
FT SIGNAL 1 37
FT CHAIN 38 475 ALPHA-L-RABINOMUNOGENOSIDASE.
FT DOMAIN 39 166 RCIN B-TYPE LECTIN.
SO SEQUENCE 475 AA; 50369 MW; C3DBJ4SEBTFP85AD CRC64;
Query Match Similarity 7.9%; Score 112.5; DB 1; Length 475;
Meet Local 52; PctIdent 24.1%; PctId Mc 0.029;
Matches 52; Conservative 35; HSPCIndels 104; Indels 25; Gaps 10
Cc -----
Qy 6 SAPEPTAYGVGNMNVVRRDPPDFDNOCIGMSKSNNDNLTWIKRGTYSNG--SC 64
Db 37 AASGALRGAGSNN-C LVVGSSODGALLQLYXCKGEF--NQWTSTDTGLTVYGDKC 93
Qy 65 LYTYGYTA-GYYVMFDCTAVREATITWINDGIINPSMYLV-AASSCI-KGITLLT 120
Db 94 LDYPVKAKAPGRVQVQSISGGSGNQ-Q-WRVNSDIIVGVSLSCLSLKADQRTMGYNQ 151
Qy 121 VQRLYLTLAQMGLANDVPAPEVT-----LYGPDLCHENSGSGSVETCD-SQQKKK 174
Db 152 LWTCGGCGNKVTELGTPFLDTCALFEYSMTSGVAOPRSYGSVALVDFTTHNR 211
Qy 175 WALYGDQS-----TRPXNQDQCITSGRSDVS 201
Db 212 HLVIYSTSSGSSGVSWVPPTPMDSMASGGMAN 247
Cc -----
RESULT 13
AC ID SPI RAAPA STANDARD; PROT; 525 AA.
RC Q05308;
RA MEDLINE=91955 (Rel. 31, Created)
RA Q01-FEB-1995 (Rel. 31, Last sequence update)
RA Q01-FEB-1995 (Rel. 31, Last annotation update)
RA Q28-FEB-2003 (Rel. 41, Last annotation [Rpt]).
RA Serine protease I precursor (BC 3.4.21.-*) (Rpt).
RA Racobacter faecitabidus.
CA O6 Racobacter faecitabidus.
CS Actinobacteria; Actinobacteridae; Actinomycetales;
CX NCBI_TaxID=13243.
CY NCBI_TaxID=13243.
RA RESEQUENCE FROM N.A., AND SEQUENCE OF 212-222; 224-238 AND 240-244.
RC STRAIN=YLM-50;
RA MEDLINE=9304226; PubMed=1339445;
RA ShimoI H.; Imura Y.; Ohata T.; Tadenuma M.;
RT "Molecular structure of Racobacter faecitabidus protease I. A yeast-lytic serine protease having mannose-binding activity.";
CU Biol. Chem. 287(25):95-25195(1992).
PU J. BIOCHEM. CHEM. 287(25):95-25195(1992).
RD SEQUENCE OF 212-247.
RA MEDLINE=9218668; PubMed=1778983;
RA ShimoI H.; Tadenuma M.;
RT "Characterization of Racobacter faecitabidus protease I, a yeast-lytic serine protease having mannose-binding activity.";
CU Blochm. 110:608-613(1991).
CC -1. FUNCTION: MAJOR SERINE PROTEASE EXHIBITING LYTIC ACTIVITY TOWARD LIVING YEAST CELLS. SIMILAR TO ELASTASE IN ITS SUBSTRATE SPECIFICITY AND HAS A LECTIN-LIKE AFFINITY FOR MANNOSE.
CC -1. SUBCELLULAR LOCATION: SECRETORY PATHWAY.
CC -1. SIMILARITY: BELONGS TO PEPTIDASE FAMILY 52A.
CC -1. SIMILARITY: Contains 1 rcin b-type lectin domain.
CC -----
```

CC	This SMS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.jdb-sdb.ch/about/consume/) or send an email to license@sbs-stb.ch .
CC	
DR	EMBL D10753; P8A01385.1; ..
DR	P8A01385.1; ..
DR	HSPF; A45053; A45053.
DR	MEROPO; S01.276; ..
DR	InterPro: IPR004236; AL protease.
DR	InterPro: IPR001316; hmdcp1as62n.
DR	InterPro: IPR000772; Rcin B_lectin.
DR	InterPro: IPR01254; Ser.protease_Try.
DR	Pfam: PF02883; AL.protease; ..
DR	Pfam: PF06923; RcinB_lectin; 3.
DR	Pfam: PF00681; ALyticPASE.
DR	PRINTS: PR00681; ALyticPASE.
DR	SMART: SM00458; RCIN; 1.
DR	PROSITE: PS00134; TRYPSIN_HIS; 1.
DR	PROSITE: PS00135; TRYPSIN_SER; 1.
DR	Hydroxylase, serine protease, Nannose-binding, signal; Zymogen, Lectin.
KW	SIGNAL
FT	CHAIN 1 32
FT	DISULFD 3 12
FT	DISULFD 3 12
FT	DOMAIN 212 525
FT	DOMAIN 396 525
FT	DOMAIN 401 525
FT	
FT	DISULFD 223 239
FT	DISULFD 310 320
FT	DISULFD 346 376
FT	DISULFD 412 431
FT	DISULFD 442 461
FT	DISULFD 486 512
FT	ACT_SITE 238 238
FT	ACT_SITE 270 270
FT	ACT_SITE 352 352
SO	SEQUENCE 525 AA; 55654 MW; DA3BCFFD330EB61 CRC64;
Query Match	7.8%; Score 111; DB 1; Length 525;
Best Local Similarity	31.1%; Pred. No. 0.044;
Matches	33; Conservative 17; Mismatches 46; Indels 12; Gaps 5
Oy	2 DUTCASAEPTVAVICNGKVRDPDQDQICLAPSSANNDDGATIRGGTISN 61
Dy	339 DVT-----TSVGYNQNNCIDVPNSDFDKGLQLWNVCNGNR-AQKVSFPHPGTILRN 450
Oy	62 GSCL-TTYGRT-AGGVYWIPECNTRVEERTIMQIWMNSTIGNISRSN 105
Dy	451 GKLDARAWHTHNTITVLNRCNGHI--AQKFLINGRDLVNVAHN 494
RESULT 14	
RHS3_CABE	
ID _PAC3 CABE	STANDARD; PROT; 612 AA.
AC P34676; Q9U003;	
DT 01-FEB-1994 (Rel. 28, Created)	
DT 28-FEB-2003 (Rel. 41, Last sequence update)	
DT 28-FEB-2003 (Rel. 41, Last annotation update)	
DE Poly(peptide-N-acetylglucosaminyltransferase 3 (EC 2.4.1.41))	
(Protein-UDP-acetylglucosaminyltransferase) (UniProtKB/Swiss-Prot)	
DE N-acetylgalactosaminyltransferase (GalNAc-T1) [pgpaatase 3].	
GN GLY-3 OR ZK689.8	
OS Caenorhabditis elegans	
OC Phylum: Metazoa; Class: Chordata; Subphylum: Vertebrata; Order: Osteichthyes; Family: Cyprinidae; Genus: Carassius; Species: Koi; Strain: Common Goldfish	
NCBI_TaxId=6239;	
RE SEQUENCE FROM N.A.	

FT	CAREBHD	131	131	N-LINKED (GLNAC..)	(POTENTIAL).
FT	CAREBHD	211	211	N-LINKED (GLNAC..)	(POTENTIAL).
FT	CAREBHD	363	363	N-LINKED (GLNAC..)	(POTENTIAL).
FT	CAREBHD	444	444	N-LINKED (GLNAC..)	(POTENTIAL).
50	SEQUENCE	545 AA;	60;46 MW;	2DCSN1L0CE935D9C	GNCA4;
Query Match		7.1%;	Score 100.5;	Db 1;	Length 545;
Best Local Similarity		19.9%;	Pred. No 0.36;		
Matches	46;	Conservative	43;	Mismatches	97;
				Indels	45;
				Gaps	8;
CY	22	VYRQDDPFDHQIQUMSSKSNDDPNQVLTIKEDPTINSNGCTTYGTA-----	72		
Db	342	LIDILRSLANDRHLIVAKNGNT-----TVNRIDVQGLQLETFDITDILADMDSKQV	395		
CY	73	-----GVWIPKCNKTVLEATIQ-----TWDPGIIINPSNVLAASSGKQITLVLT	124		
Db	356	KISDIKIEELASHVITVFRSLSPQSSVYFPGVIVTASNSGLOKAS-----NSVSFQSC	452		
CY	125	DYTLQGLAAGNDAPRATVITFYFDLCIENSGSSVWETCTSSQAGSKMALIDGSRIR	184		
Db	453	NBSRQIQVLSGVAPRVS-----PTQDCALDNGVLVAGVADSTSDQGVITPVYRGLK	509		
CY	185	PRONQDQCTSRSGVSTVINYVSGASQSRVETVTSAGIINKKGLAM	235		
Db	510	NKTDGCGILTRSS-----VQKSS-----LVEDQGVETGSGVQL	544		

Search completed: December 11, 2003, 14:09:04
Job time : 4.6201 secs

Thu Dec 11 16:10:05 2003

us-09-601-667c-7.rept

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18 ; Search time 20.3487 Seconds
(without alignments)

3347.915 Million cell updates/sec

Title: US-09-601-667C-7

Perfect score: 1418

Sequence: 1 DDVTCASAEPTVRIWRSNGM.....RRITVPATKRNQMLPYF 264

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting first 45 summaries

Database:

SPRMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_orchanelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_viridiplanete:*
14: sp_viridiplanete:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1316.5	92.8	531	10	ORXK36
2	1125.5	79.4	263	10	ORXK2
3	1112.5	78.5	565	10	ORW23
4	1091.5	77.0	263	10	ORXK2
5	1005	70.9	266	10	ORXK2
6	909.5	64.1	541	10	ORXK2
7	877	61.8	260	10	ORXK2
8	876	61.8	260	10	ORXK2
9	876	61.8	260	10	ORXK2
10	830.5	58.6	549	10	ORXK2
11	830.5	58.6	549	10	ORXK2
12	764	53.9	528	10	ORXK2
13	750.5	52.9	382	10	ORXK2
14	750	52.9	547	10	ORXK2
15	679.5	47.9	573	10	ORXK2
16	679.5	47.9	592	10	ORXK2

17	577	40.7	570	10	ORXK2	ORXK2
18	566.5	40.0	316	10	ORXK2	ORXK2
19	565.5	39.9	316	10	ORXK2	ORXK2
20	564.5	39.8	316	10	ORXK2	ORXK2
21	561.5	39.6	564	10	ORXK2	ORXK2
22	547.5	38.6	563	10	ORXK2	ORXK2
23	543	38.3	570	10	ORXK2	ORXK2
24	537.5	37.9	320	10	ORXK2	ORXK2
25	537.5	37.9	320	10	ORXK2	ORXK2
26	533	37.6	604	10	ORXK2	ORXK2
27	528.5	37.3	563	10	ORXK2	ORXK2
28	528	37.2	603	10	ORXK2	ORXK2
29	527.5	37.2	320	10	ORXK2	ORXK2
30	515	36.3	307	10	ORXK2	ORXK2
31	515	36.3	565	10	ORXK2	ORXK2
32	512	36.1	566	10	ORXK2	ORXK2
33	499	31.7	569	10	ORXK2	ORXK2
34	482.5	12.9	223	10	ORXK2	ORXK2
35	472	10.0	422	10	ORXK2	ORXK2
36	472	10.0	422	10	ORXK2	ORXK2
37	472	10.0	422	10	ORXK2	ORXK2
38	472	10.0	422	10	ORXK2	ORXK2
39	472	10.0	422	10	ORXK2	ORXK2
40	472	10.0	422	10	ORXK2	ORXK2
41	472	10.0	422	10	ORXK2	ORXK2
42	472	10.0	422	10	ORXK2	ORXK2
43	472	10.0	422	10	ORXK2	ORXK2
44	472	10.0	422	10	ORXK2	ORXK2
45	472	10.0	422	10	ORXK2	ORXK2

ALIGNMENTS

RESULT 1

ID ORXK36 PRELIMINARY: PRT: 531 AA.

AC ORXK36: 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DT 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

DE 01-JUN-2002 (TREMUR21, 21, Last sequence update)

Matches 247; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 DDTVCASSEPTVAVRNGKMGVVDVDDDPHDGNOIQLPKSKSNNDPNQMTIKEDGTIR 60
 DB 269 DDTVCASSEPTVAVRNGKMGVVDVDDDPHDGNOIQLPKSKSNNDPNQMTIKEDGTIR 328
 QY 61 NSGCLTGYTAGYVWIPDCNTAVREATINQINDGTTINPSNLYLAASSGKGTILT 120
 DB 329 NSGCLTGYTAGYVWIPDCNTAVREATINQINDGTTINPSNLYLAASSGKGTILT 388
 QY 121 VOTLDYTLGGWLAGNDIAPREVTIYGRDLQMSNGSVVETGDSQKQKMAIYGD 180
 DB 389 VOTLDYTLGGWLAGNDIAPREVTIYGRDLQMSNGSVVETGDSQKQKMAIYGD 447
 QY 181 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVAQA 240
 DB 448 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVQAS 507
 QY 241 NPKLRILIIYPATGKPNQWMLPV 263
 DB 508 NPKLRILIIYPATGKPNQWMLPV 530

RESULT 2

Q8LKQ2 PRELIMINARY; PRT; 263 AA.
 AC Q8LKQ2;
 DT 01-OCT-2002 (TRENBLREL. 22, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 OS Viscum album subsp. coloratum 2 (Fragment).
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA. INACTIVATING PROTEIN FAMILY.
 DB EMBL: AF508918; GenBank: AF508918; RefSeq: NP000072; Rfam: PF00652; Rfam: B.1.lectin.
 CC Eukaryotes; Viscum album; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Santalales; Viscaceae; Viscum.
 CX NCBI_Taxid:159976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.-K.;
 RA cDNA cloning and sequence analysis of the lectin genes of the Korean
 RT mistletoe (Viscum album coloratum).
 RT M1. Cells 121215-220(2002).
 RN [2]. Cells 121215-220(2002).
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.-K.;
 RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF508918; GenBank: AF508918; RefSeq: NP000072; Rfam: PF00652; Rfam: B.1.lectin.
 DR Interpro: IPR000772; Rfam: B.1.lectin.5.
 DR Pfam: PF00652; Rfam: B.1.lectin.5.
 DR SMART: SM00458; Rfam: B.1.lectin.2.
 DR PROSITE: PS50231; Rfam: B.1.lectin.2.
 DR PROSITE: PS50231; Rfam: B.1.lectin.2.
 FT NON_TER
 FT 263
 SQ SEQUENCE 263 AA; 29150 MW; B685BDB7C19C8D1F CRC64;

Query Match 79.4%; Score 1125.5; DB 10; Length 263;
 Best Local Similarity 79.5%; Pred. No. 2.4e-86;
 Matches 209; Conservative 21; Mismatches 32; Indels 1; Gaps 1;

QY 1 DDTVCASSEPTVAVRNGKMGVVDVDDDPHDGNOIQLPKSKSNNDPNQMTIKEDGTIR 60
 DB 1 DDTVCASSEPTVAVRNGKMGVVDVDDDPHDGNOIQLPKSKSNNDPNQMTIKEDGTIR 60
 QY 61 NSGCLTGYTAGYVWIPDCNTAVREATINQINDGTTINPSNLYLAASSGKGTILT 120
 DB 61 NSGCLTGYTAGYVWIPDCNTAVREATINQINDGTTINPSNLYLAASSGKGTILT 120
 QY 121 VOTLDYTLGGWLAGNDIAPREVTIYGRDLQMSNGSVVETGDSQKQKMAIYGD 180
 DB 121 VOTLDYTLGGWLAGNDIAPREVTIYGRDLQMSNGSVVETGDSQKQKMAIYGD 180
 QY 241 NPKLRILIIYPATGKPNQWMLPV 263
 DB 241 NPKLRILIIYPATGKPNQWMLPV 263

QY 181 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVAQA 240
 DB 180 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVAQA 239
 QY 241 NPKLRILIIYPATGKPNQWMLPV 263
 DB 240 NPKLRILIIYPATGKPNQWMLPV 262

RESULT 3

Q8W243 PRELIMINARY; PRT; 565 AA.
 AC Q8W243;
 DT 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-OCT-2002 (TRENBLREL. 23, Last annotation update)
 OS Viscum album subsp. coloratum.
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA. INACTIVATING PROTEIN FAMILY.
 DB EMBL: AF508918; GenBank: AF508918; RefSeq: NP000072; Rfam: PF00652; Rfam: B.1.lectin.
 CC Eukaryotes; Viscum album; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Santalales; Viscaceae; Viscum.
 CX NCBI_Taxid:159976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Park W.-B., Lyu S.-I.
 RA Cloning of Viscum album subsp. coloratum (Korean mistletoe).
 RT Biochem. Biophys. Res. Commun. 0:0-0(2002).
 CC -1- CATALYTIC ACTIVITY: ENDOPOLYMERASE OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA. INACTIVATING PROTEIN FAMILY.
 DB EMBL: AF508918; GenBank: AF508918; RefSeq: NP000072; Rfam: PF00652; Rfam: B.1.lectin.
 CC Interpro: IPR001574; Rfam: B.1.lectin.
 DR Pfam: PF00652; Rfam: B.1.lectin.6.
 DR Pfam: PF00652; Rfam: B.1.lectin.6.
 DR PRINTS: PRO0396; SMART: SMART.
 DR SMART: SM00458; Rfam: B.1.lectin.2.
 DR PROSITE: PS50231; Rfam: B.1.lectin.2.
 KW Hydrolase; Signal; Toxin.
 FT SIGNAL
 FT 1
 FT 22
 FT CHAIN 23
 FT 272
 FT 39
 FT 565
 SQ SEQUENCE 565 AA; 62401 MW; 59153994DN005F11 CRC64;

Query Match 78.5%; Score 112.5; DB 10; Length 565;
 Best Local Similarity 80.6%; Pred. No. 7.6e-85;
 Matches 212; Conservative 15; Mismatches 31; Indels 5; Gaps 2;

QY 1 DDTVCASSEPTVAVRNGKMGVVDVDDDPHDGNOIQLPKSKSNNDPNQMTIKEDGTIR 60
 DB 307 DDTVCASSEPTVAVRNGKMGVVDVDDDPHDGNOIQLPKSKSNNDPNQMTIKEDGTIR 362
 QY 61 NSGCLTGYTAGYVWIPDCNTAVREATINQINDGTTINPSNLYLAASSGKGTILT 120
 DB 363 NSGCLTGYTAGYVWIPDCNTAVREATINQINDGTTINPSNLYLAASSGKGTILT 422
 QY 121 VOTLDYTLGGWLAGNDIAPREVTIYGRDLQMSNGSVVETGDSQKQKMAIYGD 180
 DB 423 VOTLDYTLGGWLAGNDIAPREVTIYGRDLQMSNGSVVETGDSQKQKMAIYGD 481
 QY 181 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVAQA 240
 DB 482 GSIRPKONQDCLTSGRDSVTVINIVSCGASGSGQWVFTNEGALINLKNGLAMDVAQA 541
 QY 241 NPKLRILIIYPATGKPNQWMLPV 263
 DB 542 NPKLRILIIYPATGKPNQWMLPV 564


```
AC Q8LXQ1;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Lectin chain B isoform 3 (fragment).
DS [2]
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21566752; PubMed=1170524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT "CDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RN 121. Cells 12:215-220(2001).
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508919; AA46937.1;
DR Interpro: IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
FT NON-TER 1
FT NON-TER 263
SQ SEQUENCE 263 AA; 25071 MW; 3F9CADA860F061D CRC64;
Query Match 77.0%; Score 1091.5; DB 10; Length 263;
Best Local Similarity 77.6%; Pred. No. 1,7e-83;
Matches 204; Conservative 22; Mismatches 36; Indels 1; Gaps 1;
QY 1 DVTCTGASPTVYRIGNRKRVDDPDHGNQIOLMPSKSNDDPNQMTIRKDGTR 60
DB 1 DVTCTGSEPTVYRIGNRKRVDDPDHGNQIOLMPSKSNDDPNQMTIRKDGTR 60
QY 1 DVTCTGSEPTVYRIGNRKRVDDPDHGNQIOLMPSKSNDDPNQMTIRKDGTR 60
DB 1 DVTCTGSEPTVYRIGNRKRVDDPDHGNQIOLMPSKSNDDPNQMTIRKDGTR 60
QY 61 NSCLTGYGTAGVYVIFPCNTAVREATTIQQIWDNGTIIIPNSNVLAASSGIKQTLT 120
DB 61 NSCLTGYGTAGVYVIFPCNTAVREATTIQQIWDNGTIIIPNSNVLAASSGIKQTLT 120
QY 121 VQTLDTLDTAGGMLAGNDPAPREVTYGFPLDCLMSNGSVWETDSSQKQGMALVGD 180
DB 121 VQTLDTLDTAGGMLAGNDPAPREVTYGFPLDCLMSNGSVWETDSSQKQGMALVGD 180
QY 121 VQTLDTLDTAGGMLAGNDPAPREVTYGFPLDCLMSNGSVWETDSSQKQGMALVGD 180
DB 121 VQTLDTLDTAGGMLAGNDPAPREVTYGFPLDCLMSNGSVWETDSSQKQGMALVGD 180
QY 181 GSIRPKQNDQCLTSGRDSVYIVIVSCSGSGSGRWFFNKGALINLKNGLANDVQA 240
DB 181 GSIRPKQNDQCLTSGRDSVYIVIVSCSGSGSGRWFFNKGALINLKNGLANDVQA 240
QY 180 GSIRPKQNDQCLTSGRDSVYIVIVSCSGSGSGRWFFNKGALINLKNGLANDVQA 239
DB 180 GSIRPKQNDQCLTSGRDSVYIVIVSCSGSGSGRWFFNKGALINLKNGLANDVQA 239
QY 241 NPELRLIIIVPATKGNQMWLPV 263
DB 241 NPELRLIIIVPATKGNQMWLPV 263
DB 240 NPELRLIIIVPATKGNQMWLPV 262
RESULT 5
Q8LXQ3;
AC Q8LXQ3;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Lectin chain B isoform 1 (fragment).
DS [2]
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21566752; PubMed=1170524;
```

```
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT "CDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RN 121. Cells 12:215-220(2001).
RP SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508917; AA46935.1;
DR Interpro: IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 5.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
FT NON-TER 1
FT NON-TER 266
SQ SEQUENCE 266 AA; 4451473G7B94C73 CRC64;
Query Match 70.9%; Score 1005; DB 10; Length 266;
Best Local Similarity 69.9%; Pred. No. 3e-76;
Matches 166; Conservative 31; Mismatches 45; Indels 4; Gaps 2;
QY 1 DVTCTGASPTVYRIGNRKRVDDPDHGNQIOLMPSKSNDDPNQMTIRKDGTR 60
DB 1 DVTCTGSEPTVYRIGNRKRVDDPDHGNQIOLMPSKSNDDPNQMTIRKDGTR 60
QY 1 DVTCTGSEPTVYRIGNRKRVDDPDHGNQIOLMPSKSNDDPNQMTIRKDGTR 60
DB 1 DVTCTGSEPTVYRIGNRKRVDDPDHGNQIOLMPSKSNDDPNQMTIRKDGTR 60
QY 61 NSCLTGYGTAGVYVIFPCNTAVREATTIQQIWDNGTIIIPNSNVLAASSGIKQTLT 117
DB 61 NSCLTGYGTAGVYVIFPCNTAVREATTIQQIWDNGTIIIPNSNVLAASSGIKQTLT 120
QY 118 TLTQTLDTLDTAGGMLAGNDPAPREVTYGFPLDCLMSNGSVWETDSSQKQGMALV 177
DB 118 TLTQTLDTLDTAGGMLAGNDPAPREVTYGFPLDCLMSNGSVWETDSSQKQGMALV 179
QY 121 VQTLDTLDTAGGMLAGNDPAPREVTYGFPLDCLMSNGSVWETDSSQKQGMALVGD 179
DB 121 VQTLDTLDTAGGMLAGNDPAPREVTYGFPLDCLMSNGSVWETDSSQKQGMALVGD 179
QY 178 YEDDSRRPKQNDQCLTSGRDSVYIVIVSCSGSGSGRWFFNKGALINLKNGLANDV 237
DB 178 YEDDSRRPKQNDQCLTSGRDSVYIVIVSCSGSGSGRWFFNKGALINLKNGLANDV 239
QY 180 YEDDSRRPKQNDQCLTSGRDSVYIVIVSCSGSGSGRWFFNKGALINLKNGLANDV 239
DB 180 YEDDSRRPKQNDQCLTSGRDSVYIVIVSCSGSGSGRWFFNKGALINLKNGLANDV 239
QY 238 AQANPELRLIIIVPATKGNQMWLPV 263
DB 238 AQANPELRLIIIVPATKGNQMWLPV 263
DB 240 AASNPFLRLIIIVPATKGNQMWLPV 265
RESULT 6
Q8L174;
AC Q8L174;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Protocin A chain (EC 3.2.2.22) (RVA N-glycosidase)
DS [2]
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Santalales; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9238377; PubMed=1633111;
RA Roberts L.M., Tregear J.M., Lord J.M.;
RT "Molecular cloning of ricin.";
RT Targeted Diagn. Ther. 7:81-97(1992).
CC -1- CATALYTIC ACTIVITY: ENDOTHERYLIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC AMINOACIDS ON THE 28S RRNA.
CC -1- STRUCTURE: BINDS TO THE KINOSOME-INACTIVATING PROTEIN FAMILY.
DB EMBL; AF02992; AA2382.1;
DR Interpro: IPR000772; Ricin_B_lectin.
DR Interpro: IPR001574; RIP.
DR Interpro: IPR001400; SomaCorrpin.
DR Pfam; PF00652; Ricin_B_lectin; 6;
```

DR Pfam: PF00161; R1P; 1.
DR PRINTS: PRO0396; SHIGA.RICIN.
DR SMART: SM00458; R1CIN; 2.
DR PROSITE: PS0231; R1CIN_B.LECTIN; 2.
DR PROSITE: PS00275; SHIGA_R1CIN; 1.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
FM Hydrolase; Toxin.
FT NON-TER 1
SC SEQUENCE 541 AA; 60261 MW; 2878205E1F239D9 CRC64;
Query Match 54.1%; Score 909.5; DB 10; Length 541;
Best Local Similarity 63.8%; Pred. No. 7,1e-68;
Matches 166; Conservative 34; Mismatches 59; Indels 1; Gaps 1;

QY 5 CSASEPTVRIYGRNGKRVVDVDDPHGNDIQLPKSKNDPVQLATIKRGGTIRNSGC 64
DB 283 CNDPEPIYRIYGRNGLCVDVDRFHNGNAIQLPCKSNPDANQLMLKENDITIRNSGC 342
QY 65 LITVGTAGYVWIPDCTAVREATIQTQINDGIIINRSNVLAAASGIKGTLITVOTL 124
DB 343 LITVGSQGVWVIDDRAADATRETIYGRDLCKESNGSVVETCDSSQKQKALYADSSIR 402
QY 125 DYLGGQMLAGNDAPRETIYGRDLCKESNGSVVETCDSSQKQKALYADSSIR 184
DB 403 IYVSGQMLPNTPTPTTIVGLXGLCTQNSQGVWIDEC-TSEKAEQVALYADSSIR 461
QY 185 PRONQDCLTSGRDSVSTVIVSGASGSGQGVFTNKGALINLKNGLANDVQAAMP 244
DB 462 PQNRNDCLTIDNKTGKVIKLSGPPSSQGVWFRNDGTLINLGLVLDVRSDPS 521
QY 245 LRRITVPATKNGQMLPVF 264
DB 522 KQITIVHPRNDINQIWLVPF 541

RESULT 7
Q41143 PRELIMINARY; FRT; 263 AA.
ID Q41143
AC 01-NOV-1996 (TRENBERG). 01, Created
DT 01-NOV-1996 (TRENBERG). 01, Last sequence update
DT 01-MAR-2003 (TRENBERG). 23, Last annotation update
DE R1CIN B beta chain (fragment).
GN R1CIN B BETA CHAIN (fragment).
GC Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
NE [1]
RF SEQUENCE FROM N.A.
KA Latin B.F., Murray E.E., Halling A.C., Halling K.C., Tikakaze N.,
RA R1CIN B.F., Murray E.E., Halling A.C., Halling K.C., Tikakaze N.,
RT "CH"=S.L., TRENBERG L.L., Weaver R.F., R1CIN B, a hybrid ricin-Ricinus
RT communis agglutinin gene from
RL Plant Mol. Biol. 9:287-295 (1997).
DR EMBL: M17631; AA65306.1; -
DR HSSP: P02879; 2AAL.
DR InterPro: IPR000772; R1CIN_B.Lectin.
DR InterPro: IPR004400; Somatotropic.
DR Pfam: PF00652; R1CIN_B.Lectin; 6.
DR SMART: SM00458; R1CIN; 2.
DR PROSITE: PS0231; R1CIN_B.LECTIN; 2.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
FT NON-TER 1
SC SEQUENCE 263 AA; 29134 MW; A3880FDD1D1E144 CRC64;
Query Match 61.8%; Score 877; DB 10; Length 263;
Best Local Similarity 61.7%; Pred. No. 1.5e-65;
Matches 161; Conservative 37; Mismatches 61; Indels 2; Gaps 2;

DB 4 CNDPEPIYRIYGRNGLCVDVDRFHNGNAIQLPCKSNPDANQLMLKENDITIRNSGC 63
QY 65 LITVGTAGYVWIPDCTAVREATIQTQINDGIIINRSNVLAAASGIKGTLITVOTL 124
DB 64 LITVGSQGVWVIDDRAADATRETIYGRDLCKESNGSVVETCDSSQKQKALYADSSIR 123
QY 125 DYLGGQMLAGNDAPRETIYGRDLCKESNGSVVETCDSSQKQKALYADSSIR 184
DB 124 IYVSGQMLPNTPTPTTIVGLXGLCTQNSQGVWIDEC-TSEKAEQVALYADSSIR 182
QY 185 PRONQDCLTSGRDSVSTVIVSGASGSGQGVFTNKGALINLKNGLANDVQAAMP-R 243
DB 183 PQNRNDCLTIDNKTGKVIKLSGPPSSQGVWFRNDGTLINLGLVLDVRSDPS 242
QY 244 LRRITVPATKNGQMLPVF 264
DB 243 LKQITIVHPRNDINQIWLVPF 263

RESULT 8
Q948W4 PRELIMINARY; FRT; 580 AA.
ID Q948W4
AC 01-DEC-2001 (TRENBERG). 19, Created
DT 01-DEC-2001 (TRENBERG). 19, Last sequence update
DT 01-MAR-2003 (TRENBERG). 23, Last annotation update
DE Type 2 ribosome-inactivating protein cinnamomin II precursor
DE (NC 3.2.2.22) (rRNA N-glycosidase).
GC Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
NE [1]
RF SEQUENCE FROM N.A.
KA Yang O. Gong Z.Z., Liu X.Y.;
RA "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns".
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AY039802; AKR2459.1; -
DR InterPro: IPR000772; R1CIN_B.Lectin.
DR InterPro: IPR004400; Somatotropic.
DR Pfam: PF00652; R1CIN_B.Lectin; 6.
DR Pfam: PF00161; R1P; 1.
DR PRINTS: PRO0396; SHIGA.RICIN.
DR SMART: SM00458; R1CIN; 2.
DR PROSITE: PS0231; R1CIN_B.LECTIN; 2.
FM Hydrolase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
SC SEQUENCE 580 AA; 64285 MW; 37E4298CECCE0CFP CRC64;
Query Match 61.8%; Score 976; DB 10; Length 580;
Best Local Similarity 63.3%; Pred. No. 5e-65;
Matches 167; Conservative 33; Mismatches 63; Indels 2; Gaps 2;

QY 1 DDVTCASAPTVRIYGRNGKRVVDVDDPHGNDIQLPKSKNDPVQLATIKRGGTIRNSGC 60
DB 317 NQDCTADEPVIISGNGGLCVDVDRFHNGNAIQLPCKSNPDANQLMLKENDITIRNSGC 376
QY 61 NSGCLTIVGTAGYVWIPDCTAVREATIQTQINDGIIINRSNVLAAASGIKGTLITL 120
DB 377 NSGCLTIVGTAGYVWIPDCTAVREATIQTQINDGIIINRSNVLAAASGIKGTLITL 120
QY 121 VQTLDTLTCQMLAANTAPRETIYGRDLCKESNGSVVETCDSSQKQKALYADSSIR 180
DB 437 VQNLVIAARQWIAKNTIPFTSIVGRNDCKQNDQWVYECSSDAEQ-KNALTPD 495
QY 181 GSIRPQNDQCLTS-GRDSVSTVIVSGASGSGQGVFTNKGALINLKNGLANDVQA 239

```
Db 496 GSIRPHODRCLITSDHNSGSIITSSCSPESSGQSWFWFMDQTLINLNGLVMDVKG 555
QY 240 ANPLKRLITIPATKRNQMLPY 263
Db 556 SPSLHQIILIPATKRNQMLPY 579

RESULT 9
ID Q94BW3 PRELIMINARY; PRT; 580 AA.
AC Q94BW3 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR 01-DEC-2001 (TREMBLrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin III precursor
DB (EC 3.2.2.2) (rRNA N-6)
OS Cinnamomum camphora (Camphor tree)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxId=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDORHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 26S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AY039803; AKK2460.1; -.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; R1P_1.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; R1P; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; R1CIN; 2.
DR PROSITE; PS50231; R1CIN_B_LECTIN; 2.
DR HYDROLASE; Signal; 1; 32.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN III
SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7F8558 CRC64;

Query Match 61.3%; Score 869; DB 10; Length 580;
Best Local Similarity 62.9%; Pred. No. 1.9e-64;
Matches 166; Conservative 33; Mismatches 63; Indels 2; Gaps 2;

QY 1 DDTTCASAEPTVAVENKRVYRDDPHDQICLMPKSNNDQWLTKDGTGS 60
Db 317 NDTCADPEPTVAVISGNLQCDVHCKRKNRNPIDLMFCQNSDYNQDLTKDGTGS 376
QY 61 NSCLITNGYSAGDYVWIDYCRFTVPAISVQFMANGTIINQALVLSASGNERITLT 120
Db 377 NGCLITNGYSAGDYVWIDYCRFTVPAISVQFMANGTIINQALVLSASGNERITLT 436
QY 121 VQTLDTYLAGQMLAGNDIAPREVTIYGRDLCNSNSGSAWYETCCSSQKQKVALYGD 180
Db 437 VQDLTYASQKQMLAGNDIAPREVTIYGRDLCNSNSGSAWYETCCSSQKQKVALYGD 495
QY 181 GSIRPHODRCLITSDHNSGSIITSSCSPESSGQSWFWFMDQTLINLNGLVMDVKG 239
Db 496 GSIRPHODRCLITSDHNSGSIITSSCSPESSGQSWFWFMDQTLINLNGLVMDVKG 555
QY 240 ANPLKRLITIPATKRNQMLPY 263
Db 556 SPSLHQIILIPATKRNQMLPY 579

RESULT 10
ID Q94VZ2 PRELIMINARY; PRT; 549 AA.
AC Q94VZ2 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DR 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Type II ribosome-inactivating protein cinnamomin IEC 3.2.2.22 (rRNA
DB N-glycosidase) (fragment)
OS Cinnamomum camphora (Camphor tree)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxId=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Xie L., Wang E.-D.;
RT Molecular cloning of cinnamomin A-, B-chain and the expression,
RT purification, characterization and mutagenesis of the A-chain.
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDORHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 26S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; P02873; 2A1.
DR HSPB; P02873; 2A1.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; R1P_1.
DR Pfam; PF00652; Ricin_B_lectin; 5.
DR Pfam; PF00161; R1P; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; R1CIN; 2.
DR PROSITE; PS50231; R1CIN_B_LECTIN; 2.
DR HYDROLASE; Toxin; 1.
FT NON-TER 1
FT SIGNAL 1 1
SQ SEQUENCE 549 AA; 60648 MW; 02607BE607C44B0 CRC64;

Query Match 58.6%; Score 830.5; DB 10; Length 549;
Best Local Similarity 60.0%; Pred. No. 3e-61;
Matches 159; Conservative 32; Mismatches 71; Indels 3; Gaps 2;

QY 1 DDTTCASAEPTVAVENKRVYRDDPHDQICLMPKSNNDQWLTKDGTGS 60
Db 285 NDTCADPEPTVAVISGNLQCDVHCKRKNRNPIDLMFCQNSDYNQDLTKDGTGS 344
QY 61 NSCLITNGYSAGDYVWIDYCRFTVPAISVQFMANGTIINQALVLSASGIERITLT 120
Db 345 NGCLITNGYSAGDYVWIDYCRFTVPAISVQFMANGTIINQALVLSASGIERITLT 404
QY 121 VQTLDTYLAGQMLAGNDIAPREVTIYGRDLCNSNSGSAWYETCCSSQKQKVALYGD 180
Db 405 VQNLTYASQKQMLAGNDIAPREVTIYGRDLCNSNSGSAWYETCCSSQKQKVALYGD 463
QY 181 GSIRPHODRCLITSDHNSGSIITSSCSPESSGQSWFWFMDQTLINLNGLVMDVKG 238
Db 464 GSIRPHODRCLITSDHNSGSIITSSCSPESSGQSWFWFMDQTLINLNGLVMDVKG 523
QY 239 ANPLKRLITIPATKRNQMLPY 263
Db 524 SPSLHQIILIPATKRNQMLPY 548

RESULT 11
ID Q94BW5 PRELIMINARY; PRT; 581 AA.
AC Q94BW5 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR 01-DEC-2001 (TREMBLrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin I precursor
DB (EC 3.2.2.2) (rRNA N-6)
OS Cinnamomum camphora (Camphor tree)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxId=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
```

RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomoin proteins and study of their expression
RT patterns "J. Biol. Chem. 278:10411-10416, 2003."
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AY039801; AKS2458.1; -.
DR InterPro: IPR001572; Ricin_B_lectin.
DR Pfam: PF00161; Ricin_B_lectin; 5.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
KM Hydrolase; Signal; Toxin.
FT SIGNAL 1 32 POTENTIAL.
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CHAIN 33 581 CINNAMOIN I.
SQ SEQUENCE 581 AA; 64215 MW; 6885F88F8A3D196 CRC64;
Query Match 581 AA; Score 830.5; DB 10; Length 581;
Best Local Similarity 54.8%; Pred No. 1e-55; Indels 3; Gaps 2;
Matches 159; Conservative 32; Mismatches 71;
QY 1 DPTVCSAEPYRIVAGNRGVDDDDPHQNOQLMPKSNNDPQWLTIKROGTIRNS 60
DB 317 NDDTADPEPTVIRISGRNGCDVDYDCKTNKNGFIQLMPKQNSDVQWLTIKROGTIRNS 376
QY 61 NSCLTYGYTAGVYVMIIPDCTVAREATVQIWDNGTINFRSNLVLAASSGIKOTLT 120
DB 377 NKKCLTNGISASGVYVMIIPDCTVAREATVQIWDNGTINFRSNLVLAASSGIKOTLT 436
QY 121 VQTLDTAGCGHLAGDTPRATVYGRDLCNMGSGSVYVTCGSGQKQKALVQ 180
DB 437 VQNTVYASRQGLASGNTPEPTGISVGFNDLQMGAGMWTREBSSEKASQ KVALTP 495
QY 181 GSIRPKQND--QCLTSGRDSVSVINIVSCGASGQWFTNMGALINIKNGLANDVA 238
DB 496 GSIRPHODPGPACPLDNRHOGSIIIISSCSPSGSRHWYPMVDGYVNLKNGLVNDVA 555
QY 239 QANPLERILLIYPATGKNGMMLVP 263
DB 556 GSNVSHQIILIPATGKNGMMLVP 580

RESULT 12

Q06076 PRELIMINARY; PRT; 528 AA.
AC Q06076;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Abtin-d (BC 3.2.2.22) (rRNA N-glycosidase) (fragment).
OS Abtus precacotus (Indian Iicorice) (Crab's eye).
OC Sukariya; Vitidiplanetes; Streptophyta; Embryophyta; Tracheophyta;
OC Baktaryas; Vitidiplanetes; Streptophyta; Embryophyta; Tracheophyta;
OC eucoides I. Fabales; Fabaceae; Papilionoideae; Asteae; Abrus.
OC NCBI_Taxid:3816;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=3132798; PubMed=8421313;
RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
RT "Primary structure of three distinct isobutins determined by cDNA
RT sequencing: conservation and significance";
RL J. Mol. Biol. 229:263-267(1999).
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: N93346; AA3266.1; -.
DR HSEF; P1140; 1ABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.

DR Pfam: PF00652; Ricin_B_lectin; 6.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KM Hydrolase; Toxin.
FT NON_TER 1 1
FT NON_TER 528 528
SQ SEQUENCE 528 AA; 58870 MW; 62ED42F88F8E0F8 CRC64;
Query Match 528 AA; Score 764; DB 10; Length 528;
Best Local Similarity 54.8%; Pred No. 1e-55; Indels 2; Gaps 2;
Matches 143; Conservative 45; Mismatches 71;
QY 5 CSAS-EPYRIVAGNRGVDDDDPHQNOQLMPKSNNDPQWLTIKROGTIRNS 63
DB 269 CSRYEPYRIVAGNRGVDDYDGHNGRIAMKCKRLERQWLTKSDILIRNSK 328
QY 64 CLTYGYTAGVYVMIIPDCTVAREATVQIWDNGTINFRSNLVLAASSGIKOTLT 123
DB 329 CLTIRGAPENYVMIIPDCTVAREATVQIWDNGTINFRSNLVLAASSGIKOTLT 388
QY 124 LDPTLAGCGHLAGDTPRATVYGRDLCNMGSGSVYVTCGSGQKQKALVQ 183
DB 389 NEVLAMQGMWNTSPFTGISVGRDLCNMGSGSVYVTCGSGQKQKALVQ 447
QY 184 RPKNDQCLTSGRDSVSVINIVSCGASGQWFTNMGALINIKNGLANDVAQANR 243
DB 448 RSVQNTNCLTSGRDSVSVINIVSCGASGQWFTNMGALINIKNGLANDVAQANR 507
QY 244 LRLIIPATGKNGMMLVP 264
DB 508 LKQIILIPATGKNGMMLVP 528

RESULT 13

Q8SA43 PRELIMINARY; PRT; 382 AA.
AC Q8SA43;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Abtin isoform G (BC 3.2.2.22) (rRNA N-glycosidase)
OS Abtus precacotus (Indian Iicorice) (Crab's eye).
OC Sukariya; Vitidiplanetes; Streptophyta; Embryophyta; Tracheophyta;
OC Baktaryas; Vitidiplanetes; Streptophyta; Embryophyta; Tracheophyta;
OC eucoides I. Fabales; Fabaceae; Papilionoideae; Asteae; Abrus.
OC NCBI_Taxid:3816;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Leaf;
RA Cook J.P., Roberts L.M., Lord M.;
RT "New isoform of Abtin - Abtin G";
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: A479626; A47743.1; -.
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; Ricin_B_lectin; 5.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KM Hydrolase; Toxin.
FT NON_TER 1 1
FT NON_TER 382 382
SQ SEQUENCE 382 AA; 42743 MW; B08AB341813AD2EE CRC64;

Query Match 52.98, Score 750.5, DB 10, Length 382,
Best Local Similarity 54.38, Pred. No. 9,4e-55,
Matches 139, Conservative 42, Mismatches 74, Indels 1, Gaps 1,
QY 9 EPTVRIYVNGKGVDDPHDNDGQIQAPSSNDPQWITKPGTISNSGCTTY 68
DB 128 EPTVRIYVNGKGVDDPHDNDGQIQAPSSNDPQWITKPGTISNSGCTTY 187
QY 69 GTTAYVYVIMPCNTAVRBAKTIWQINDGTIIPRSNLYAASSGKGTLYOTDYL 128
DB 188 GTPGVYVIMIDCTSAPEBAKTIWQINDGTIIPRSKALVSSSSMAGKLTVOANDYK 247
QY 129 GQVLAQNDTPAETVITVGRDLCSSNGSVWETCDSSQKQKVALYQDSIRPKQ 188
DB 248 GQVLAQNDTPAETVITVGRDLCSSNGSVWETCDSSQKQKVALYQDSIRPKQ 306
QY 189 QDQCTSGSDSVYVINSQSGASQGVWFTFTEALIKLNGLANDYQANPELARI 248
DB 307 TNGCTISQKHQGSTIVLWGSNGASQGVWFTFTEALIKLNGLANDYQANPELARI 366
QY 249 IYPAKPKPQWMLPVF 264
DB 367 IYPAKPKPQWMLPVF 382
PRT; 547 AA.
RESULT 14
QY 10 Q9M288 PRELIMINARY; PRT; 547 AA.
AC Q9M288
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Preproa9glutinin (EC 3.2.2.22) (rRNA N-glycosidase).
GN AAG.
OS Abrys precatorius (Indian licoice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Adrue.
NCBI_taxid=3816;
RA 111
RP SEQUENCE FROM N.A.
RX MEDLINE:20102702, PubMed:10636890.
RA Liu C.T., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Huang M.T.,
Lin J.Y.,
RT "Primary Structure and Function Analysis of the Abrys precatorius
RT Agglutinin A Chain by Site-directed Mutagenesis: Pro199 of Amphiphilic
RT alpha-Helix H Impacts Protein Synthesis Inhibitory Activity.",
RL J. Biol. Chem. 275:1897-1901(2000).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DB EMBL: AF190173, AF28309.1, -.
DB HSBP: P11140, IABR.
DR InterPro: IPR000772, Rictin_B_lectin.
DR InterPro: IPR001574, RIP.
DR Pfam: PF00652, Rictin_B_lectin. 6.
DR Pfam: PF00161, RIP; 1.
DR PRINTS: PR00396, SHIGARICIN.
DR SMART: SM00458, RICTIN. 2.
DR PROSITE: PS00231, RICTIN_B_LECTIN; 2.
DR PROSITE: PS00275, SHIGARICTIN; 1.
DB PROSITE: Toxin.
SQ SEQUENCE 547 AA, 61248 MW, 3554326C354A1BD CRC64;
Query Match 52.98, Score 750.5, DB 10, Length 547,
Best Local Similarity 54.08, Pred. No. 1,6e-54,
Matches 141, Conservative 41, Mismatches 77, Indels 2, Gaps 2,
QY 5 CSAS-EPTVRIYVNGKGVDDPHDNDGQIQAPSSNDPQWITKPGTISNSG 63
DB 288 CSAS-EPTVRIYVNGKGVDDPHDNDGQIQAPSSNDPQWITKPGTISNSG 347

QY 64 CLTGYTAQVYVIMPCNTAVRBAKTIWQINDGTIIPRSNLYAASSGKGTLYOT 123
DB 348 CLTGYTAQVYVIMPCNTAVRBAKTIWQINDGTIIPRSKALVSSSSMAGKLTVO 407
QY 124 LDYTLAQGLAQNTPAETVITVGRDLCSSNGSVWETCDSSQKQKVALYQDSI 183
DB 408 NDRKQGMKRTSNTDTSVYVINSQSGASQGVWFTFTEALIKLNGLANDYQANPE 466
QY 184 PPKMOCCTSGSDSVYVINSQSGASQGVWFTFTEALIKLNGLANDYQANPE 243
DB 467 PPKMOCCTSGSDSVYVINSQSGASQGVWFTFTEALIKLNGLANDYQANPE 526
QY 244 LRRTIYPAKPKPQWMLPVF 264
DB 527 LRRTIYPAKPKPQWMLPVF 547
PRT; 573 AA.
RESULT 15
QY 10 Q9M288 PRELIMINARY; PRT; 573 AA.
AC Q9M288
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribosome-inactivating protein IRAR (EC 3.2.2.22) (rRNA N-glycosidase).
GN LECTINAR.
OS Iris hollandica (Dutch iris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
OC Irid.
NCBI_taxid=35876;
RA Van Damme E.J.M., Pennans M.J.,
RP SEQUENCE FROM N.A.
RX 1 iris (iris hollandica var. Professor Blaauw) plants express both type
RX 1 and type 2 ribosome-inactivating proteins in bulb tissue.",
RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DB EMBL: AF256184, AF155093.1, -.
DB InterPro: IPR000772, Rictin_B_lectin.
DB InterPro: IPR001574, RIP.
DR Pfam: PF00652, Rictin_B_lectin. 6.
DR Pfam: PF00161, RIP; 1.
DR PRINTS: PR00396, SHIGARICIN.
DR SMART: SM00458, RICTIN. 2.
DR PROSITE: PS00231, RICTIN_B_LECTIN; 2.
DR PROSITE: PS00275, SHIGARICTIN; 1.
DB PROSITE: Toxin.
SQ SEQUENCE 573 AA, 63759 MW, 1414A3B9A2CD4F5C CRC64;
Query Match 47.98, Score 679.5, DB 10, Length 573,
Best Local Similarity 50.24, Pred. No. 1,4e-48,
Matches 139, Conservative 40, Mismatches 89, Indels 3, Gaps 3,
QY 1 DQVTSSEPTVRIYVNGKGVDDPHDNDGQIQAPSSNDPQWITKPGTISNSG 60
DB 311 DQVTSSEPTVRIYVNGKGVDDPHDNDGQIQAPSSNDPQWITKPGTISNSG 370
QY 61 NSGCTTYGYTAYVYVIMPCNTAVRBAKTIWQINDGTIIPRSNLYAASSGKGTLY 120
DB 371 NSGCTTYGYTAYVYVIMPCNTAVRBAKTIWQINDGTIIPRSKALVSSSSMAGKLT 429
QY 121 VQTLAYTLQGLAQNTPAETVITVGRDLCSSNGSVWETCDSSQKQKVALYQ 179
DB 430 MQVTHASQGMKRTSNTDTSVYVINSQSGASQGVWFTFTEALIKLNGLANDYQ 488
QY 180 DSGIRPKQNDCTSGSDSVYVINSQSGASQGVWFTFTEALIKLNGLANDYQ 239
DB 489 DSGIRPKQNDCTSGSDSVYVINSQSGASQGVWFTFTEALIKLNGLANDYQ 548

PT Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants

XX
 XX
 PS Claim 9, Fig 8b; 78pp; German.

XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and its
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B1 protein.

XX
 SQ Sequence 264 AA;

Query Match 100.0%; Score 1418; DB 20; Length 264;
 Best Local Similarity 100.0%; Pred. No. 1.9e-131;
 Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDVTCASAEPTVATVGRNGKRVVDHDDPHGNOQLMPKSKNDPNQMLTTRKDGTRRS 60
 DB 1 DDVTCASAEPTVATVGRNGKRVVDHDDPHGNOQLMPKSKNDPNQMLTTRKDGTRRS 60
 QY 61 NSGCLTFTGAGTAVYVAFPCNTAVRKAATWQIMDNGTIIINRSNLYLAASGIGKTTT 120
 DB 61 NSGCLTFTGAGTAVYVAFPCNTAVRKAATWQIMDNGTIIINRSNLYLAASGIGKTTT 120
 QY 121 VQTLDDYTLGGMLAGNDAPRAETVYGFPRDLCMSNGSVWETCDSSQKQKALYGD 180
 DB 121 VQTLDDYTLGGMLAGNDAPRAETVYGFPRDLCMSNGSVWETCDSSQKQKALYGD 180
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSQKRWFTNBSAIIINLKGILANDVQA 240
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSQKRWFTNBSAIIINLKGILANDVQA 240
 QY 241 NPKLRRIITYPATCKRQNMMLPVF 264
 DB 241 NPKLRRIITYPATCKRQNMMLPVF 264

RESULT 2
 AAY25992
 ID AAY25992 standard; Protein; 265 AA.
 AC AAY25992;
 XX 18-OCT-1999 (first entry)
 XX Mistletoe lectin B1 variant protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B1.

OS Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.

PI Morris P, Stiefel T, Voelster W, Walters P.
 XX WJL; 1999-44535/38.
 DR N-PSDB: AA609116.

XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and its
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B1 protein.

XX
 SQ Sequence 265 AA;

Query Match 100.0%; Score 1418; DB 20; Length 265;
 Best Local Similarity 100.0%; Pred. No. 1.9e-131;
 Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDVTCASAEPTVATVGRNGKRVVDHDDPHGNOQLMPKSKNDPNQMLTTRKDGTRRS 60
 DB 1 DDVTCASAEPTVATVGRNGKRVVDHDDPHGNOQLMPKSKNDPNQMLTTRKDGTRRS 60
 QY 61 NSGCLTFTGAGTAVYVAFPCNTAVRKAATWQIMDNGTIIINRSNLYLAASGIGKTTT 120
 DB 61 NSGCLTFTGAGTAVYVAFPCNTAVRKAATWQIMDNGTIIINRSNLYLAASGIGKTTT 120
 QY 121 VQTLDDYTLGGMLAGNDAPRAETVYGFPRDLCMSNGSVWETCDSSQKQKALYGD 180
 DB 121 VQTLDDYTLGGMLAGNDAPRAETVYGFPRDLCMSNGSVWETCDSSQKQKALYGD 180
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSQKRWFTNBSAIIINLKGILANDVQA 240
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSQKRWFTNBSAIIINLKGILANDVQA 240
 QY 241 NPKLRRIITYPATCKRQNMMLPVF 264
 DB 241 NPKLRRIITYPATCKRQNMMLPVF 264

RESULT 3
 AAY25988
 ID AAY25988 standard; Protein; 264 AA.
 AC AAY25988;
 XX 18-OCT-1999 (first entry)
 XX Mistletoe lectin B3 protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B3.

OS Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelker W, Welters P;
 XX WPI: 1999-44535/38.
 XX N-PSDB: AA209112.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Claim 9; Fig 10B; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (MA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX free from toxins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a mistletoe lectin B3 protein.
 XX Sequence 264 AA;
 XX
 XX Query Match 99.6%; Score 1412; D5 20; Length 264;
 XX Best Local Similarity 99.6%; Pred. No. 7.3e-131;
 XX Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DDTCSASEPTVRIYVGNKRWVDVDDPHDQNOIQWPSKSNDDPQWLTKIKEDTIRS 60
 DB 1 DDTCSASEPTVRIYVGNKRWVDVDDPHDQNOIQWPSKSNDDPQWLTKIKEDTIRS 60
 QY 61 NSGCTTGYTGAGYVWIMFPCNTVBEATVQIWNQGTINFRSNVLAASGIGKTTLT 120
 DB 61 NSGCTTGYTGAGYVWIMFPCNTVBEATVQIWNQGTINFRSNVLAASGIGKTTLT 120
 QY 121 VQTLDTYTLGGWLAGNDTAPREVTYVGFRLQMSNGSGVWETCSSQKQKALYGD 180
 DB 121 VQTLDTYTLGGWLAGNDTAPREVTYVGFRLQMSNGSGVWETCSSQKQKALYGD 180
 QY 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRWVFVFNKGLINKGLANDVQA 240
 DB 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRWVFVFNKGLINKGLANDVQA 240
 QY 241 NPKRLRIITVPAKGKQKQMLPFV 264
 DB 241 NPKRLRIITVPAKGKQKQMLPFV 264
 XX
 XX RESULT 4
 XX AA25994
 XX ID AA25994 standard; Protein; 265 AA.
 XX
 XX AA25994;
 XX
 XX 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin B3 variant protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform; lectin B3.
 XX
 XX Viscum album.

XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX Morris P, Stiefel T, Voelker W, Welters P;
 XX WPI: 1999-44535/38.
 XX N-PSDB: AA209118.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 16B; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (MA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX free from toxins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a variant mistletoe lectin B3 protein.
 XX Sequence 265 AA;
 XX
 XX Query Match 99.6%; Score 1412; D5 20; Length 265;
 XX Best Local Similarity 99.6%; Pred. No. 7.3e-131;
 XX Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DDTCSASEPTVRIYVGNKRWVDVDDPHDQNOIQWPSKSNDDPQWLTKIKEDTIRS 60
 DB 1 DDTCSASEPTVRIYVGNKRWVDVDDPHDQNOIQWPSKSNDDPQWLTKIKEDTIRS 60
 QY 61 NSGCTTGYTGAGYVWIMFPCNTVBEATVQIWNQGTINFRSNVLAASGIGKTTLT 120
 DB 61 NSGCTTGYTGAGYVWIMFPCNTVBEATVQIWNQGTINFRSNVLAASGIGKTTLT 120
 QY 121 VQTLDTYTLGGWLAGNDTAPREVTYVGFRLQMSNGSGVWETCSSQKQKALYGD 180
 DB 121 VQTLDTYTLGGWLAGNDTAPREVTYVGFRLQMSNGSGVWETCSSQKQKALYGD 180
 QY 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRWVFVFNKGLINKGLANDVQA 240
 DB 181 GSIRPKQNDQCLTSGRDSVSTVINIVSCGASGSGRWVFVFNKGLINKGLANDVQA 240
 QY 241 NPKRLRIITVPAKGKQKQMLPFV 264
 DB 241 NPKRLRIITVPAKGKQKQMLPFV 264
 XX
 XX RESULT 5
 XX AA25989
 XX ID AA25989 standard; Protein; 264 AA.
 XX
 XX AA25989;
 XX
 XX 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin B4 protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX

KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 cancer; cytotoxicity; antigen; isoform; lectin B4.
 XX
 XX Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI; 1999-445335/38.
 XX N-P8DE; AA209113.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Claim 9; Fig 11b; 78pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly of the
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen production of the
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B4 protein.
 CC
 CC Sequence 264 AA;
 CC
 CC Query Match 99.1%; Score 1405; DB 20; Length 264;
 CC Best Local Similarity 99.2%; Pred. No. 3,6e-130;
 CC Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 QY 1 DDTVTSASPTVAVIVGNKGVAVYVDDPDHNOQLMPKSNMNDPQQLATIKKIDGTRIS 60
 DB 1 DDTVTSASPTVAVIVGNKGVAVYVDDPDHNOQLMPKSNMNDPQQLATIKKIDGTRIS 60
 QY 61 NGSCLTITGTTAGVYVWIPDCNTAVENATIMQINDGNTINRSMNVLAASSGIKKITT 120
 DB 61 NGSCLTITGTTAGVYVWIPDCNTAVENATIMQINDGNTINRSMNVLAASSGIKKITT 120
 QY 121 VQILDVTLGGMLANGDTAPREVTIYGFDDCHESNGSVWVETCDSSQKQKVALYGD 180
 DB 121 VQILDVTLGGMLANGDTAPREVTIYGFDDCHESNGSVWVETCDSSQKQKVALYGD 180
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTNEGAILNLKGPAMDVAQA 240
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTNEGAILNLKGPAMDVAQA 240
 QY 241 NPKLRRLITTPATGKPNQWLEVP 264
 DB 241 NPKLRRLITTPATGKPNQWLEVP 264

XX Mistletoe lectin B4 variant protein fragment.
 DE
 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MLA; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B4.
 XX
 XX Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI; 1999-445335/38.
 XX N-P8DE; AA209113.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 17b; 78pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly of the
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen production of the
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B4 protein.
 CC
 CC Sequence 265 AA;
 CC
 CC Query Match 99.1%; Score 1405; DB 20; Length 265;
 CC Best Local Similarity 99.2%; Pred. No. 3,6e-130;
 CC Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 QY 1 DDTVTSASPTVAVIVGNKGVAVYVDDPDHNOQLMPKSNMNDPQQLATIKKIDGTRIS 60
 DB 1 DDTVTSASPTVAVIVGNKGVAVYVDDPDHNOQLMPKSNMNDPQQLATIKKIDGTRIS 60
 QY 61 NGSCLTITGTTAGVYVWIPDCNTAVENATIMQINDGNTINRSMNVLAASSGIKKITT 120
 DB 61 NGSCLTITGTTAGVYVWIPDCNTAVENATIMQINDGNTINRSMNVLAASSGIKKITT 120
 QY 121 VQILDVTLGGMLANGDTAPREVTIYGFDDCHESNGSVWVETCDSSQKQKVALYGD 180
 DB 121 VQILDVTLGGMLANGDTAPREVTIYGFDDCHESNGSVWVETCDSSQKQKVALYGD 180
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTNEGAILNLKGPAMDVAQA 240
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTNEGAILNLKGPAMDVAQA 240
 QY 241 NPKLRRLITTPATGKPNQWLEVP 264
 DB 241 NPKLRRLITTPATGKPNQWLEVP 264

ID AAY25990 standard; Protein; 264 AA.
XX
AC AAY25990;
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B5 protein fragment.
DE
XX Mistletoe lectin; antitumor; immunostimulant; B-chain; MIA; immunity;
XX ribosome; 28S subunit; non-cytotoxic; T-cell activation; immune response;
KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.
XX
XX Viscum album.
OS
XX DE19804210-A1.
FN
XX 12-AUG-1999.
PD
XX 03-FEB-1998; 98DE-1004210.
PF
XX 03-FEB-1998; 98DE-1004210.
XX
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
PA
XX Morris P, Stiefel T, Voelter W, Welters P;
PI WPI; 1999-445335/38.
XX
XX N-PSDB; AA209114.
DR
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 9; Fig 12b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumor-associated, bacterial or viral). The method allows production of
CC recombinant products, particularly in yeast, and its individual isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a mistletoe lectin B5 protein.
XX
SQ Sequence 264 AA;
Query Match 98.9%; Score 1403; DB 20; Length 264;
Best Local Similarity 98.9%; Pred. No. 5,6e-130;
Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 DDTGCSAEPFTRIVGRNGKRVDDDFHGNQIQIOWPFSKSNDDPQWLTIXEDGTRIS 60
DB 1 DDTGCSAEPFTRIVGRNGKRVDDDFHGNQIQIOWPFSKSNDDPQWLTIXEDGTRIS 60
QY 61 NSGCLTGYTAGYVWIPDCNTARVBAKTIQIMNGTIIIPRSNIVLAASGKKTITL 120
DB 61 NSGCLTGYTAGYVWIPDCNTARVBAKTIQIMNGTIIIPRSNIVLAASGKKTITL 120
QY 121 VQTLDDYTLGGWLAGNDIAPREVITVGRFDLCESNGSVAWETDSSQNGKMAIYGD 180
DB 121 VQTLDDYTLGGWLAGNDIAPREVITVGRFDLCESNGSVAWETDSSQNGKMAIYGD 180
QY 181 GSIRKONODCLTSGDSVSTVINIVSCGASGSGQWFTFNGALINLKNGLAMVDQA 240
DB 181 GSIRKONODCLTSGDSVSTVINIVSCGASGSGQWFTFNGALINLKNGLAMVDQA 240
QY 241 NPKLRITITVPATGKPNQWMLPVE 264
DB 241 NPKLRITITVPATGKPNQWMLPVE 264

DB 241 NPKLRITITVPATGKPNQWMLPVE 264
RESULT 8
ID AAY25996 standard; Protein; 265 AA.
XX
XX AAY25996;
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B5 variant protein fragment.
DE
XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX ribosome; 28S subunit; non-cytotoxic; T-cell activation; immune response;
KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.
XX
XX Viscum album.
OS
XX DE19804210-A1.
FN
XX 12-AUG-1999.
PD
XX 03-FEB-1998; 98DE-1004210.
PF
XX 03-FEB-1998; 98DE-1004210.
XX
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
PA
XX Morris P, Stiefel T, Voelter W, Welters P;
PI WPI; 1999-445335/38.
XX
XX N-PSDB; AA209120.
DR
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Disclosure; Fig 18b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumor-associated, bacterial or viral). The method allows production of
CC recombinant products, particularly in yeast, and its individual isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a variant mistletoe lectin B5 protein.
XX
SQ Sequence 265 AA;
Query Match 98.9%; Score 1403; DB 20; Length 265;
Best Local Similarity 98.9%; Pred. No. 5,7e-130;
Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 DDTGCSAEPFTRIVGRNGKRVDDDFHGNQIQIOWPFSKSNDDPQWLTIXEDGTRIS 60
DB 1 DDTGCSAEPFTRIVGRNGKRVDDDFHGNQIQIOWPFSKSNDDPQWLTIXEDGTRIS 60
QY 61 NSGCLTGYTAGYVWIPDCNTARVBAKTIQIMNGTIIIPRSNIVLAASGKKTITL 120
DB 61 NSGCLTGYTAGYVWIPDCNTARVBAKTIQIMNGTIIIPRSNIVLAASGKKTITL 120
QY 121 VQTLDDYTLGGWLAGNDIAPREVITVGRFDLCESNGSVAWETDSSQNGKMAIYGD 180
DB 121 VQTLDDYTLGGWLAGNDIAPREVITVGRFDLCESNGSVAWETDSSQNGKMAIYGD 180
QY 181 GSIRKONODCLTSGDSVSTVINIVSCGASGSGQWFTFNGALINLKNGLAMVDQA 240
DB 181 GSIRKONODCLTSGDSVSTVINIVSCGASGSGQWFTFNGALINLKNGLAMVDQA 240

Db 181 GSIRPRKONODCLTSRSDSVSTVINIVSCGASGSGRWVETNEGAILINKSLAVDVAQA 240

Qy 241 NPKLRRIIYPATGKPNQWMLPVF 264

Db 241 NPKLRRIIYPATGKPNQWMLPVF 264

RESULT 9

AAZ5987

ID AAZ5987 standard; Protein; 264 AA.

AC AAZ5987;

XX 18-OCT-1999 (first entry)

DT 18-OCT-1999 (first entry)

DE Mistletoe lectin B2 protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

XX Mistletoe 268 subunit; non-cytotoxic; T-cell activation; immune response;

KW lymphokine-producing macrophages; so stimulate growth (particularly

KW cancer; cytotoxicity; antigen; isoform; lectin B2.

XX Viscum album.

OS Viscum album.

XX DB19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

PA Morris P, Stiefel T, Voelter W, Welters P;

PI WPI; 1999-445335/38.

DR N-PSDB; AA209111.

XX Preparation of mistletoe lectins in heterologous systems,

XX particularly for use as anticancer agents and immunostimulants

XX Claim 9; Fig 9B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments

XX which have antitumour and immunostimulatory activity. The A-chain (MIA)

XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of

XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and its

XX lymphokine-producing macrophages, so stimulate growth (particularly

XX fragments are used to treat uncontrolled cell growth (particularly

XX cancers) and if they lack cytotoxicity, to increase the strength of the

XX immune response, particularly to a co-administered antigen

XX (tumour-associated, bacterial or viral). The method allows production of

XX mistletoe lectin and its individual chains, in many different isoforms

XX and on a large scale, at any time of the year. Recombinant products are

XX free from toxins present in natural mistletoe extracts. This sequence

XX represents a fragment of a mistletoe lectin B2 protein.

XX Sequence 264 AA;

Qy Query Match 97.2%; Score 1379; DB 20; Length 264;

Db Best Local Similarity 97.7%; Pred. No. 1.3e-127;

Matches 256; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DDVTCASAEPTVRIYGRSGRWVDRDDPHDGNQIQLPKSNNDPNQMLTKIKDNTIRS 60

Db 1 DDVTCASAEPTVRIYGRSGRWVDRDDPHDGNQIQLPKSNNDPNQMLTKIKDNTIRS 60

Qy 61 NGSCLTITTYGTAGVYVAFPCDNVAREKTIWQIMDNGTINPRSNLVLAASGKIKTTLT 120

Db 61 NGSCLTITTYGTAGVYVAFPCDNVAREKTIWQIMDNGTINPRSNLVLAASGKIKTTLT 120

Qy 121 VQTLDTLTLGGCMLAAGNPTAPREVITVGPRLCMEANGSGSVWETCDSSGKRNQKNAALYGD 180

Db 121 VQTLDTLTLGGCMLAAGNPTAPREVITVGPRLCMEANGSGSVWETCDSSGKRNQKNAALYGD 180

Qy 181 GSIRPRKONODCLTSRSDSVSTVINIVSCGASGSGRWVETNEGAILINKSLAVDVAQA 240

Db 181 GSIRPRKONODCLTSRSDSVSTVINIVSCGASGSGRWVETNEGAILINKSLAVDVAQA 240

Qy 241 NPKLRRIIYPATGKPNQWMLPVF 264

Db 241 NPKLRRIIYPATGKPNQWMLPVF 264

RESULT 10

AAZ5993

ID AAZ5993 standard; Protein; 265 AA.

AC AAZ5993;

XX 18-OCT-1999 (first entry)

DT 18-OCT-1999 (first entry)

DE Mistletoe lectin B2 variant protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

XX Mistletoe 268 subunit; non-cytotoxic; T-cell activation; immune response;

KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;

KW cancer; cytotoxicity; antigen; isoform; lectin B2.

XX Viscum album.

OS Viscum album.

XX DB19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

PA Morris P, Stiefel T, Voelter W, Welters P;

PI WPI; 1999-445335/38.

DR N-PSDB; AA209111.

XX Preparation of mistletoe lectins in heterologous systems,

XX particularly for use as anticancer agents and immunostimulants

XX Disclosure; Fig 15B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments

XX which have antitumour and immunostimulatory activity. The A-chain (MIA)

XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of

XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its

XX lymphokine-producing macrophages, so stimulate growth (particularly

XX fragments are used to treat uncontrolled cell growth (particularly

XX cancers) and if they lack cytotoxicity, to increase the strength of the

XX immune response, particularly to a co-administered antigen

XX (tumour-associated, bacterial or viral). The method allows production of

XX mistletoe lectin and its individual chains, in many different isoforms

XX and on a large scale, at any time of the year. Recombinant products are

XX free from toxins present in natural mistletoe extracts. This sequence

XX represents a fragment of a variant mistletoe lectin B2 protein.

XX Sequence 265 AA;

Qy Query Match 97.2%; Score 1379; DB 20; Length 265;

Db Best Local Similarity 97.7%; Pred. No. 1.3e-127;

Matches 256; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DDVTCASAEPTVRIYGRSGRWVDRDDPHDGNQIQLPKSNNDPNQMLTKIKDNTIRS 60

Db 1 DDVTCASAEPTVRIYGRSGRWVDRDDPHDGNQIQLPKSNNDPNQMLTKIKDNTIRS 60

QY 61 NSCLTGYTAVYAGVYVWIFDQNTAVREATIQTWNGTIIINPSNLVLAASSGIGKOTTLF 120
 DB 61 NSCLTGYTAVYAGVYVWIFDQNTAVREATIQTWNGTIIINPSNLVLAASSGIGKOTTLF 120
 QY 121 VQTDYTLGQWLAAGNDTAPREVTIYGFEDLCWESNGSYYWETCSQKQKQKALYGD 180
 DB 121 VQTDYTLGQWLAAGNDTAPREVTIYGFEDLCWESNGSYYWETCSQKQKQKALYGD 180
 QY 181 GSIRPKONODCLTGRDSYSTVINIVSCGASGSGQWFTNEGALILNKAGLADYVQA 240
 DB 181 GSIRPKONODCLTGRDSYSTVINIVSCGASGSGQWFTNEGALILNKAGLADYVQA 240
 QY 241 NPELRRIITYPATGKKNQWMLPVF 264
 DB 241 NPELRRIITYPATGKKNQWMLPVF 264

RESULT 11
 AAY25985
 AAY25985 standard; Protein; 263 AA.
 AC AAY25985;
 DT 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin B protein fragment.
 XX
 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B.
 OS Viscum album.
 XX
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
 PA Morris F, Stiefel T, Voelter W, Walters P;
 PI WPI; 1999-445335/38.
 DR N-PSDB; RAZ09109.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 9; Fig 7B; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumor-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B protein.
 SO Sequence 263 AA;
 Query Match 94.5%; Score 1339.5; DS 20; Length 263;
 Best Local Similarity 95.8%; Pred. No. 1e-123;

Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
 QY 1 DDTVCASAEPTVAIVGNNGKAVDVRDDPFDGNGQIQIAPSKSNNDPNQIWTIKEDGTTIS 60
 DB 1 DDTVCASAEPTVAIVGNNGKAVDVRDDPFDGNGQIQIAPSKSNNDPNQIWTIKEDGTTIS 60
 QY 61 NSCLTGYTAVYAGVYVWIFDQNTAVREATIQTWNGTIIINPSNLVLAASSGIGKOTTLF 120
 DB 61 NSCLTGYTAVYAGVYVWIFDQNTAVREATIQTWNGTIIINPSNLVLAASSGIGKOTTLF 120
 QY 121 VQTDYTLGQWLAAGNDTAPREVTIYGFEDLCWESNGSYYWETCSQKQKQKALYGD 180
 DB 121 VQTDYTLGQWLAAGNDTAPREVTIYGFEDLCWESNGSYYWETCSQKQKQKALYGD 180
 QY 181 GSIRPKONODCLTGRDSYSTVINIVSCGASGSGQWFTNEGALILNKAGLADYVQA 240
 DB 181 GSIRPKONODCLTGRDSYSTVINIVSCGASGSGQWFTNEGALILNKAGLADYVQA 240
 QY 241 NPELRRIITYPATGKKNQWMLPVF 263
 DB 241 NPELRRIITYPATGKKNQWMLPVF 263

RESULT 12
 AAY25991
 AAY25991 standard; Protein; 264 AA.
 AC AAY25991;
 DT 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin B variant protein fragment.
 XX
 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B.
 OS Viscum album.
 XX
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
 PA Morris F, Stiefel T, Voelter W, Walters P;
 PI WPI; 1999-445335/38.
 DR N-PSDB; RAZ09115.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 XX Disclosure; Fig 13b; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumor-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B protein.

XX Sequence 264 AA;
SQ Query Match 94.5%; Score 1339.5; DB 20; Length 264;
Best Local Similarity 95.8%; Pred. No. 1e-123;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 DDVTGASBPPTVAIVGNKRGKRVDDPRDGNQIOLMPKSNNDPNQMLTIKROGTRIS 60
DB 1 DDVTGASBPPTVAIVGNKRGKRVDDPRDGNQIOLMPKSNNDPNQMLTIKROGTRIS 60

QY 61 NSCLTGYTAGVYVWIPDCNTAVREKTIWQIMNGTIIIPRSNLVLAASSGKKTLLT 120
DB 61 NSCLTGYTAGVYVWIPDCNTAVREKTIWQIMNGTIIIPRSNLVLAASSGKKTLLT 120

QY 121 VQTLDTYLQGMALANDTAPEVITVGFRLCWSNGSVWVETCDSSQKQKMAVGD 180
DB 121 VQTLDTYLQGMALANDTAPEVITVGFRLCWSNGSVWVETCDSSQKQKMAVGD 180

QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTMGALIMKGLANDVAQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTMGALIMKGLANDVAQA 240

QY 241 NPKLRRIIYPATGKPNQMLPV 263
DB 241 NPKLRRIIYPATGKPNQMLPV 263

QY 263 240 NPKLRRIIYPATGKPNQMLPV 262

RESULT 13
AAV25979
ID AAV25979 standard; Protein; 531 AA.
XX AAV25979;
XX 18-OCT-1999 (first entry)
XX Mistletoe lectin I protein fragment.
XX Mistletoe lectin I protein fragment.
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin I.
XX Viscum album.
XX DEL9804210-AL.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelker W, Welters P;
XX MPI; 1999-445335/38.
XX N-PSDB; AA209106.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 7; Fig 1b; 79pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MIA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a mistletoe lectin I protein fragment.
XX Sequence 531 AA;
SQ Query Match 94.5%; Score 1339.5; DB 20; Length 531;
Best Local Similarity 95.8%; Pred. No. 2e-123;
Matches 252; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 DDVTGASBPPTVAIVGNKRGKRVDDPRDGNQIOLMPKSNNDPNQMLTIKROGTRIS 60
DB 269 DDVTGASBPPTVAIVGNKRGKRVDDPRDGNQIOLMPKSNNDPNQMLTIKROGTRIS 328

QY 61 NSCLTGYTAGVYVWIPDCNTAVREKTIWQIMNGTIIIPRSNLVLAASSGKKTLLT 120
DB 329 NSCLTGYTAGVYVWIPDCNTAVREKTIWQIMNGTIIIPRSNLVLAASSGKKTLLT 388

QY 121 VQTLDTYLQGMALANDTAPEVITVGFRLCWSNGSVWVETCDSSQKQKMAVGD 180
DB 389 VQTLDTYLQGMALANDTAPEVITVGFRLCWSNGSVWVETCDSSQKQKMAVGD 447

QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTMGALIMKGLANDVAQA 240
DB 448 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWVFTMGALIMKGLANDVAQA 507

QY 241 NPKLRRIIYPATGKPNQMLPV 263
DB 508 NPKLRRIIYPATGKPNQMLPV 530

RESULT 14
AAV25982
ID AAV25982 standard; Protein; 532 AA.
XX AAV25982;
XX 18-OCT-1999 (first entry)
XX Mistletoe lectin I (variant) protein fragment.
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin I.
XX Viscum album.
XX DEL9804210-AL.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelker W, Welters P;
XX MPI; 1999-445335/38.
XX N-PSDB; AA209106.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Disclosure; Fig 4b; 79pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MIA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of

ribosome. Non-cytotoxic forms of (I) activate T-cells and lymphokine-producing macrophages, so stimulate immunity. (I) and its fragments are used to treat uncontrolled cell growth (particularly cancer), to suppress the immune response, particularly to a co-administered antigen (tumour-associated, bacterial or viral). The method allows production of mastocyte lectin, and its individual chains, in many different isofoms and on a large scale, at any time of the year. Recombinant products are used to treat allergic diseases. (I) is also used to produce a vaccine that represents a fragment of a mastocyte lectin I protein variant.

Sequence 532 AA.

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.rapb

Page 2

QY 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCEBNSGSGVWFTCDSSQKQKALYGD 180
DB 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCEBNSGSGVWFTCDSSQKQKALYGD 179
QY 181 GSIRPKONODCLTSGSDSVSTVINIVSCSGASGSGORWFTNEGALINKKGLADVAQA 240
DB 180 GSIRPKONODCLTSGSDSVSTVINIVSCSGASGSGORWFTNEGALINKKGLADVAQA 239
QY 241 NPKLRITIIYPATGKPKQWMLFV 263
DB 240 NPKLRITIIYPATGKPKQWMLFV 262

RESULT 2
US-09-347-064-4
Sequence 4, Application US/09347064A
Sequence 10, US2003018165A1
GENERAL INFORMATION:
APPLICANT: Eck, Jürgen
APPLICANT: Zinke, Arno
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
TITLE OF INVENTION: album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: ECT/EP98/00009
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: BE 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 267
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-4

Query Match 94.0%; Score 1333.5; DB 9; Length 267;
Best local Similarity 95.4%; Pred. No. 6, 9e-128;
Matches 251; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
QY 1 DDTVCASEPTVIVGNKGVYDVEDDFDNGIOQLMPSKSNDDNQLTIRKDTIRIS 60
DB 1 DDTVCASEPTVIVGNKGVYDVEDDFDNGIOQLMPSKSNDDNQLTIRKDTIRIS 60
QY 61 NNSCLTYGTAGVWIFPCNIVAEATWQJWNGTINPRSNLYLAASGIGTTLT 120
DB 61 NNSCLTYGTAGVWIFPCNIVAEATWQJWNGTINPRSNLYLAASGIGTTLT 120
QY 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCEBNSGSGVWFTCDSSQKQKALYGD 180
DB 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCEBNSGSGVWFTCDSSQKQKALYGD 179
QY 181 GSIRPKONODCLTSGSDSVSTVINIVSCSGASGSGORWFTNEGALINKKGLADVAQA 240
DB 180 GSIRPKONODCLTSGSDSVSTVINIVSCSGASGSGORWFTNEGALINKKGLADVAQA 239
QY 241 NPKLRITIIYPATGKPKQWMLFV 263
DB 240 NPKLRITIIYPATGKPKQWMLFV 262

RESULT 3
US-10-083-336A-1
Sequence 1, Application US/10083336A
Publication No. US2003018165A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Miliard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Mannemacher, Robert W

QY 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCEBNSGSGVWFTCDSSQKQKALYGD 180
DB 121 VOTLDYTLGGWLAGNDTAPREVTYIGFRDLCEBNSGSGVWFTCDSSQKQKALYGD 179
QY 181 GSIRPKONODCLTSGSDSVSTVINIVSCSGASGSGORWFTNEGALINKKGLADVAQA 240
DB 180 GSIRPKONODCLTSGSDSVSTVINIVSCSGASGSGORWFTNEGALINKKGLADVAQA 239
QY 241 NPKLRITIIYPATGKPKQWMLFV 263
DB 240 NPKLRITIIYPATGKPKQWMLFV 262

RESULT 4
US-10-137-077-17
Sequence 17, Application US/10137077
Publication No. US20030092109A1
GENERAL INFORMATION:
APPLICANT: Goldstein, Irwin J.
APPLICANT: Kueger, Robert P.
TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom
FILE REFERENCE: US-07124
CURRENT APPLICATION NUMBER: US/10/137,077
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 60/288,596
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/354,322
PRIOR FILING DATE: 2002-05-02
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 44
TYPE: PRT
ORGANISM: Reticularia communis
US-10-137-077-17

Query Match 13.1%; Score 186; DB 15; Length 44;
Best local Similarity 77.3%; Pred. No. 9, 7e-12;
Matches 34; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 12 VRTVGNKGVYDVEDDFDNGIOQLMPSKSNDDNQLTIRKDTIRIS 55
DB 1 VRTVGNKGVYDVEDDFDNGIOQLMPSKSNDDNQLTIRKDTIRIS 54

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.rapb

Publication No. US20020142426A1
GENERAL INFORMATION:
APPLICANT: Olanet, Peter J.
APPLICANT: Meyers, Rachel B.
APPLICANT: Galvin, Katherine A.
APPLICANT: Millennium Pharmaceuticals Inc.
TITLE OF INVENTION: 33945, A Human Glycosyltransferase and
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: MP12001-0181RCP(M)
CURRENT FILING DATE: 2002-02-12
PRIORITY FILING DATE: 2001-05-30
PRIORITY FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SOFTWARE: FASTSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 145
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus
US-10-074-527-5

Query Match 12.3%; Score 174.5; DB 14; Length 145;
Best Local Similarity 35.8%; Pred. No. 7.4e-10;
Matches 43; Conservative 20; Mismatches 46; Indels 11; Gaps 5;

OY 154 ESNQSGVWVETDSSQNGKAL---YDGSIRKQNDGCTGRSVTVINIVSC- 209
DB 25 ESDGNQVQVWVCHSNPKNQKWSLTDSDGELBSVYNDKCLTVNNSGSEYKALQCD 84
OY 210 SGASGSGRWVFNTEGAL----LNLKN-GLADVQAKNPKL-RRITVYATKRNQWMP 262
DB 85 SATSDNQKMLNDBLGNKILNLVNTGLVDYKSGDTONGTKLHLYTSGSGNQWMP 144

RESULT 6
US-10-156-761-14970
Sequence 14970, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-23
PRIORITY FILING DATE: 2001-05-23
PRIORITY FILING DATE: 2001-05-30
PRIORITY FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14970
LENGTH: 420
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-14970

Query Match 10.9%; Score 155; DB 15; Length 420;
Best Local Similarity 31.2%; Pred. No. 3.1e-07;
Matches 44; Conservative 19; Mismatches 63; Indels 10; Gaps 5;

OY 1 DD--VYCSASEPTFRIYGNMGMVDVDDPDHGNQIQWPSKNNDPQLWTIKDGTI 58
DB 284 DDVQVYVTSSSGAPITGLAKCVVAGSSSSANAPVLY--DCNGTTAQKQTVASDGL 341
OY 59 RSNQSGCL--TVYGTAGVYVWIFDGNVAVKATWQIMQNTIIPRSN--LVLAASGCI 114

DB 342 RALGKCLDVTENGTAAGSTQVWMDGSGSANOK--WVTAAGDIYPOAKCLDVTGNNSA 399
OY 115 KGTIVTVQTLIDVTLQGGWLAG 135
DB 400 NGRILQVWCSGSAANQKWKYG 420

RESULT 7
US-10-156-761-9724
Sequence 9724, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-23
PRIORITY FILING DATE: 2001-05-23
PRIORITY FILING DATE: 2001-05-30
PRIORITY FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9724
LENGTH: 658
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-9724

Query Match 9.8%; Score 139.5; DB 15; Length 658;
Best Local Similarity 32.1%; Pred. No. 2.8e-05;
Matches 44; Conservative 17; Mismatches 57; Indels 19; Gaps 7;

OY 11 TYR-IVERNKERV-----DYRDDDFHGNQIQWPSKNNDPQLWT-IRKDPGIR 58
DB 523 TYRPLPQVWVAVTGKSGSCADINNTITNGTQVLEW--DCNGSPQSWTYSRKEVYL 580
OY 60 SNQSGCLTY--GTVAGVYVWIFDGNVAVKATWQIMQNTIIPRSN-VLA--SSGIR 115
DB 581 YANKKIDANLCTTNGTAVIVDNCQANQK--WNINSDGITTWVNAAGCLDANNAAN 638
OY 116 GTTIVTVQTLIDVTLQGGW 132
DB 639 GTSIVMSQGTGDNQKW 655

RESULT 8
US-10-156-761-8170
Sequence 8170, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-23
PRIORITY FILING DATE: 2001-05-23
PRIORITY FILING DATE: 2001-05-30
PRIORITY FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8170

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.rapb

Page 4

LENGTH: 536
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-8170

Query Match 9.4%; Score 134; DB 15; Length 536;
Best Local Similarity 30.1%; Pred. No. 66-05;

Matches 40; Conservative 18; Mismatches 59; Indels 16; Gaps 6;

Cy 14 IYGRNR-VPRDDPFDHNOGCMKSKNDNDQATIKDGTISNG-SCITTY--68
Db 409 LVGASNRKCLDAYNQTAFGKLEIMDC--GGANQVITIRAGSLRLVGTGCLAYDN 465
Cy 69 GYTAQVYVWFEDCTAVREATIWMQNDGIIINPSRLV-----PSSGKGTLLVQ 122
Db 466 GTTSGKYVLYTCNGANCK-NSINPQVTVGTGSLCLDVTGSDQKSGVNGTALIEW 523
Cy 123 TLDTYLTGQWLAG 135
Db 524 TCNGANQWRLG 536

RESULT 9

US-10-137-077-18

Sequence 18; Application US/10137077

Publication No. US20030092109A1

GENERAL INFORMATION:

APPLICANT: Goldstein, Irwin J.

APPLICANT: Winter, Harry C.

APPLICANT: Kruger, Robert C.

TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin

FILE REFERENCE: US-0714

CURRENT FILING DATE: 2002-05-02

PRIOR FILING DATE: 2001-05-03

PRIOR APPLICATION NUMBER: 60/288,596

PRIOR FILING DATE: 2002-02-04

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patent version 3.1

SEQ ID NO 18

LENGTH: 41

TYPE: PRT

ORGANISM: Ricinus communis

US-10-137-077-18

Query Match 9.4%; Score 133; DB 15; Length 41;
Best Local Similarity 56.1%; Pred. No. 2.3e-06;

Matches 23; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Cy 224 GAILNKLNGLADYVACANFKRRIITVPATGKPNQMLFV 264
Db 1 GTILNYSGLVIDVPASDPSIKQIILYELHGPQIWELEP 41

RESULT 10

US-09-973-457-5

Sequence 5; Application US/09973457

Patent No. US20020164746A1

GENERAL INFORMATION:

APPLICANT: Kapeller-Liebermann, Rosana

TITLE OF INVENTION: 47174, A NOVEL HUMAN GLYCOSYLTRANSFERASE

FILE REFERENCE: 10448-099001

CURRENT FILING DATE: 2001-10-09

PRIOR FILING DATE: 2000-10-06

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows version 4.0

SEQ ID NO 5

LENGTH: 135

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match 9.1%; Score 129; DB 10; Length 135;
Best Local Similarity 28.1%; Pred. No. 3e-05;

Matches 41; Conservative 19; Mismatches 38; Indels 48; Gaps 9;

Cy 145 IYGRDLCHESNGSASVWETCDSCQVQCK---WALY-----DGSIRPKQ 187
Db 7 IGRNTSLDVG-----NSESIDQNPQVLDCHGGMQMLTINESDGLR--I 56
Cy 188 NDDGLTSGRDSVTVINIVSCG--ASGSQVFTNBSGAILNLKN-----GLADY 237
Db 57 NSDGLT-----VNGTVLISCDGTGRKNDQVWVNDGTRFKSKKGVDSGLD 111
Cy 238 AQANPKRRIITVPATGK-PNQMWL 261
Db 112 KQGN---RVQLWTGNSDAPQWMI 133

RESULT 11

US-10-074-527-6

Sequence 6; Application US/1074527

Publication No. US20020142426A1

GENERAL INFORMATION:

APPLICANT: Olandt, Peter J.

APPLICANT: Meyers, Rachel E.

APPLICANT: Galvin, Katherine A.

TITLE OF INVENTION: 33945, A Human Glycosyltransferase and

FILE REFERENCE: US-0714

CURRENT FILING DATE: 2002-02-12

PRIOR FILING DATE: 2001-02-15

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSeq for Windows version 4.0

SEQ ID NO 6

LENGTH: 135

TYPE: PRT

ORGANISM: Artificial Sequence

US-10-074-527-6

Query Match 9.1%; Score 129; DB 14; Length 135;
Best Local Similarity 28.1%; Pred. No. 3e-05;

Matches 41; Conservative 19; Mismatches 38; Indels 48; Gaps 9;

Cy 145 IYGRDLCHESNGSASVWETCDSCQVQCK---WALY-----DGSIRPKQ 187
Db 7 IGRNTSLDVG-----NSESIDQNPQVLDCHGGMQMLTINESDGLR--I 56

RESULT 12

US-10-156-761-10246

Sequence 10246; Application US/10156761

Patent No. US2003013018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: ISHIKAWA, JUN

APPLICANT: ISHIKAWA, JUN

APPLICANT: ISHIKAWA, JUN

APPLICANT: ISHIKAWA, JUN

APPLICANT: ISHIKAWA, JUN

APPLICANT: ISHIKAWA, JUN

APPLICANT: ISHIKAWA, JUN

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.rapb

Page 5

APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIMA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKA
APPLICANT: MATSUDA, HISASHIMA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO: 4246
SEQ ID NO: 4247
SEQ ID NO: 4248
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-10246

Query Match 8.9% Score 126; DB 15; Length 647;
Best Local Similarity 26.3%; Pred. NO. 0.00051;
Matches 45; Conservative 20; Mismatches 60; Indels 46; Gaps 8;

Qy 9 EPTVIRGKNGRVYDDDDHQQIQIWPESKSNPQQLMTIKRDTIRSNSSCL--T 66
Db 520 DQGSFVELAGKIDVASSSSANNAVGLY--DCKSTQKMTVADSVQAGKIDVT 577
Qy 67 TGYTRCYVMTFQNTANREKATITQIWDNGITINPASHVLAASSGKQTLITVQTLDY 126
Db 578 SASTADGKICQIDCN-----GTAQMSYN-----ASTGVNTADKCLDV 620
Qy 127 TLGGWLAGNDTAPREVTYVGFIDLOMSNGSGVWETCDSSQKQKQWAL 177
Db 621 T-----GNSSA-----NGRAAQIWSCTGAANQ-KWTL 646

RESULT 13

US-09-770-621-4

Sequence 4, Application US/09770621

Patent No. US2001002481SAI

GENERAL INFORMATION:

APPLICANT: M nyl, Arja

APPLICANT: Vehmanper m, Richard

APPLICANT: Fagerster m, Richard

APPLICANT: Lantto, Raija

APPLICANT: Palohelmo, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Laitinen, Tarja

NUMBER OF SEQUENCES: 39

TITLE OF INVENTION: Production and Secretion of Proteins of

CORRESPONDENCE ADDRESS:

ADDRESSER: STEINER, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N.W. Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/770,621

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/590,563

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/332,412

FILING DATE: 31-OCT-1994

CLASSIFICATION:
Prior APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-770-621-4

Query Match 8.8% Score 124.5; DB 9; Length 492;
Best Local Similarity 20.8%; Pred. NO. 0.00051;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

Qy 23 DVREDDHGNQIQIWPESKSNPQQLMTIKRDTIRSNSSCLTGY----- 70
Db 168 DVVNAEAFDSNGSRCDENIORTND---MIEVAFRTAQGPBALCYNDVITENNA 223
Qy 71 --TAQYVNI-----EDCNTRVEXTTQIMDNGITINPASHVLAASSGKQTL 119
Db 224 AKQAVNHWDFRSGVPLDC---VGRQSHFNSGNVNNFRTTLQGFAL-GVDV 276
Qy 120 TQQLDYLTLGGKLAANDRPRP-----ATVGRFD-----LC 152
Db 277 EVTELDI-----ENAPQYASVIRCLANDRCGTITWGVHSDMSYGNPL 326
Qy 133 MESN-----GGSVW-----ET 164
Db 327 FNNKNKQAVYAVDALNCSDDGSGPSPVPPPGGSGQIRGVASNCIDVNGNT 386
Qy 165 CDSGQ-----KNGKRALYDGSIFPKQNDQCLTSGRDSVSTVINTVSGSAGS 215
Db 387 ADRVQVQLDCHSGSNQ--QNTTSSGSRIFGN--KCLDGGSSNGAVVQLTSCWGA-R 442
Qy 216 QKVTNTEGAILNKKRYGLAND-VQANPRLRIITVPTGRKQW 260
Db 443 QKWEIRADQTVVWGGCLDAVGGGTGNGRRLQVTSQNGANNQW 488

RESULT 14

US-09-770-621-7

Sequence 7, Application US/09770621

Patent No. US2001002481SAI

GENERAL INFORMATION:

APPLICANT: M nyl, Arja

APPLICANT: Vehmanper m, Richard

APPLICANT: Fagerster m, Richard

APPLICANT: Lantto, Raija

APPLICANT: Palohelmo, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Laitinen, Tarja

NUMBER OF SEQUENCES: 39

TITLE OF INVENTION: Production and Secretion of Proteins of

CORRESPONDENCE ADDRESS:

ADDRESSER: STEINER, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N.W. Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.rapb

Page 6

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 5,08650.0340003
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDEDNESS: NO. US20010024815A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
THICKNESS/SEGMENT: AM50
US-09-770-621-7

Query Match      8.8%; Score 124.5; DB 9; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.0005;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

QY 23 DVRRDDPHDGNQIOLMPS---KSNNDPQNLWIKEDGTR---SNASCLTYGY-----70
DB 168 DVVNEAFEDNSGRCDNSLQRTGND---MIEVAFRTAQGPSAKLCYNDYNIEMNNA 223
QY 71 --TAGYVYNI-----FQCTAVRENTIQINDGIIINPSNVLTAASGIKGTLL 119
DB 224 AKQAVYINRYDPRKSGVPLD-----VGFQSHFNSGNPYNPFTLLQGFAL-GVDV 276
QY 120 TVQCLDYTLGGQWLAGNDAPR-----VTYGRPD-----LC 152
DB 277 EYTELDI-----ENAPQTVASYIRDLAVDRCTGTYWGVDSDEMSYQNPLL 326
QY 153 MESN-----GGSVWV-----ET 164
DB 327 FDNNGKKAQYAVVLDALNEDSGDGSFNSPVPSPGSSGQIRGVASNRCDIVPNSGT 386
QY 165 CDSGQ-----KNGKMAIYGDSIRPKQNDQCLTSGRDSVYINITYSGASGS 215
DB 387 AGDTYQVLDGSGSNQ-QWYTSSEPRIFGN-KILDGSSSNQAVVQYSGWGA-N 442
QY 216 QRAWFTNEGAILNLKNGLAMD-VQANPKLRRIIYIPATGKPNQW 260
DB 443 QKWELEADGTIVGVSGELDLAVGGGTGNGTRLOLYSCWGNQKX 488
```

RESULT 15
US-0-286-993-4
Sequence 41 Application US/10286993
Publication No. US20030146453A1
GENERAL INFORMATION:
APPLICANT: Mantyla, Arja
APPLICANT: Palotieimo, Marja
APPLICANT: Lantto, Raija

```
APPLICANT: Pagersstrom, Richard
APPLICANT: Lantto, Raija
APPLICANT: Suomenen, Rirkko
APPLICANT: Vehmaampere, Jari
TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
FILE REFERENCE: 1716.034004
CURRENT FILING DATE: 2002-08-13
PRIOR FILING DATE: 1998-07-23/09/120, 804
PRIOR APPLICATION NUMBER: PCT/FI97/00037
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: US 08/590,563
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 492
TYPE: PRT
ORGANISM: Actinobacteria flexuosa
US-10-286-993-4

Query Match      8.8%; Score 124.5; DB 12; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.0005;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

QY 23 DVRRDDPHDGNQIOLMPS---KSNNDPQNLWIKEDGTR---SNASCLTYGY-----70
DB 168 DVVNEAFEDNSGRCDNSLQRTGND---MIEVAFRTAQGPSAKLCYNDYNIEMNNA 223
QY 71 --TAGYVYNI-----FQCTAVRENTIQINDGIIINPSNVLTAASGIKGTLL 119
DB 224 AKQAVYINRYDPRKSGVPLD-----VGFQSHFNSGNPYNPFTLLQGFAL-GVDV 276
QY 120 TVQCLDYTLGGQWLAGNDAPR-----VTYGRPD-----LC 152
DB 277 EYTELDI-----ENAPQTVASYIRDLAVDRCTGTYWGVDSDEMSYQNPLL 326
QY 153 MESN-----GGSVWV-----ET 164
DB 327 FDNNGKKAQYAVVLDALNEDSGDGSFNSPVPSPGSSGQIRGVASNRCDIVPNSGT 386
QY 165 CDSGQ-----KNGKMAIYGDSIRPKQNDQCLTSGRDSVYINITYSGASGS 215
DB 387 AGDTYQVLDGSGSNQ-QWYTSSEPRIFGN-KILDGSSSNQAVVQYSGWGA-N 442
QY 216 QRAWFTNEGAILNLKNGLAMD-VQANPKLRRIIYIPATGKPNQW 260
DB 443 QKWELEADGTIVGVSGELDLAVGGGTGNGTRLOLYSCWGNQKX 488

Search completed: December 11, 2003, 14:48:49
Job time : 18.0129 secs
```

Tue Dec 11 16:10:03 2003

us-09-601-667c-7.ram

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:55:54 / Search time 130.432 seconds
(without alignments)
1841.713 Million cell updates/sec

Title: US-09-601-667C-7

Perfect score: 1418
Sequence: 1 DVTGSAEPTFRIVGNGM.....RIIIIVATGHWQWLPVP 264

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Pending Parents: AA Main.*
1: /cgm2_6/prodata/1/paa/PCTUS_COMB.pep.*
2: /cgm2_6/prodata/1/paa/US06_COMB.pep.*
3: /cgm2_6/prodata/1/paa/US07_COMB.pep.*
4: /cgm2_6/prodata/1/paa/US08_COMB.pep.*
5: /cgm2_6/prodata/1/paa/US09_COMB.pep.*
6: /cgm2_6/prodata/1/paa/US092_COMB.pep.*
7: /cgm2_6/prodata/1/paa/US093_COMB.pep.*
8: /cgm2_6/prodata/1/paa/US094_COMB.pep.*
9: /cgm2_6/prodata/1/paa/US095_COMB.pep.*
10: /cgm2_6/prodata/1/paa/US096_COMB.pep.*
11: /cgm2_6/prodata/1/paa/US097_COMB.pep.*
12: /cgm2_6/prodata/1/paa/US098_COMB.pep.*
13: /cgm2_6/prodata/1/paa/US099_COMB.pep.*
14: /cgm2_6/prodata/1/paa/US0992_COMB.pep.*
15: /cgm2_6/prodata/1/paa/US0993_COMB.pep.*
16: /cgm2_6/prodata/1/paa/US0994_COMB.pep.*
17: /cgm2_6/prodata/1/paa/US0995_COMB.pep.*
18: /cgm2_6/prodata/1/paa/US0996_COMB.pep.*
19: /cgm2_6/prodata/1/paa/US0997_COMB.pep.*
20: /cgm2_6/prodata/1/paa/US0998_COMB.pep.*
21: /cgm2_6/prodata/1/paa/US0999_COMB.pep.*
22: /cgm2_6/prodata/1/paa/US09992_COMB.pep.*
23: /cgm2_6/prodata/1/paa/US09993_COMB.pep.*
24: /cgm2_6/prodata/1/paa/US09994_COMB.pep.*
25: /cgm2_6/prodata/1/paa/US09995_COMB.pep.*
26: /cgm2_6/prodata/1/paa/US100_COMB.pep.*
27: /cgm2_6/prodata/1/paa/US101_COMB.pep.*
28: /cgm2_6/prodata/1/paa/US102_COMB.pep.*
29: /cgm2_6/prodata/1/paa/US103_COMB.pep.*
30: /cgm2_6/prodata/1/paa/US104_COMB.pep.*
31: /cgm2_6/prodata/1/paa/US105_COMB.pep.*
32: /cgm2_6/prodata/1/paa/US106_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1418	100.0	264	20	US-09-601-667B-7
					Sequence 7, Appl1

2	1418	100.0	264	20	US-09-601-667C-7	Sequence 7, Appl1
3	1418	100.0	264	22	US-09-791-537-111174	Sequence 111174, Appl1
4	1412	99.6	264	20	US-09-601-667B-9	Sequence 9, Appl1
5	1412	99.6	264	20	US-09-601-667C-9	Sequence 9, Appl1
6	1407.5	98.1	264	20	US-09-601-667C-10	Sequence 10, Appl1
7	1407.5	98.1	264	20	US-09-601-667C-11	Sequence 11, Appl1
8	1405	98.1	264	20	US-09-601-667C-10	Sequence 10, Appl1
9	1403	98.9	264	20	US-09-601-667C-11	Sequence 11, Appl1
10	1403	98.9	264	20	US-09-601-667C-11	Sequence 11, Appl1
11	1379	97.2	264	20	US-09-601-667C-8	Sequence 8, Appl1
12	1379	97.2	264	20	US-09-601-667C-8	Sequence 8, Appl1
13	1339.5	94.5	263	20	US-09-601-667B-6	Sequence 6, Appl1
14	1339.5	94.5	263	20	US-09-601-667C-6	Sequence 6, Appl1
15	1339.5	94.5	263	20	US-09-601-667C-4	Sequence 4, Appl1
16	1339.5	94.5	263	20	US-09-601-667C-4	Sequence 4, Appl1
17	1333.5	94.0	263	17	US-09-347-064-10	Sequence 10, Appl1
18	1333.5	94.0	263	17	US-09-347-064-10	Sequence 10, Appl1
19	1333.5	94.0	263	17	US-09-347-064-10	Sequence 10, Appl1
20	1333.5	94.0	263	17	US-09-347-064-10	Sequence 10, Appl1
21	1333.5	94.0	263	17	US-09-347-064-10	Sequence 10, Appl1
22	1333.5	94.0	267	17	US-09-347-064-4	Sequence 4, Appl1
23	1333.5	94.0	267	17	US-09-347-064-4	Sequence 4, Appl1
24	1333.5	94.0	267	17	US-09-347-064-4	Sequence 4, Appl1
25	1333.5	94.0	267	17	US-09-347-064-4	Sequence 4, Appl1
26	1290	91.0	264	20	US-09-601-667C-3	Sequence 3, Appl1
27	1290	91.0	264	20	US-09-601-667C-3	Sequence 3, Appl1
28	1290	91.0	264	20	US-09-601-667C-1	Sequence 1, Appl1
29	1290	91.0	264	20	US-09-601-667C-1	Sequence 1, Appl1
30	1290	91.0	264	20	US-09-601-667C-1	Sequence 1, Appl1
31	1199.5	84.6	263	20	US-09-601-667B-10	Sequence 10, Appl1
32	1199.5	84.6	263	20	US-09-601-667B-10	Sequence 10, Appl1
33	1125.5	79.4	263	20	US-09-627-165B-10	Sequence 10, Appl1
34	1125.5	79.4	263	20	US-09-627-165B-10	Sequence 10, Appl1
35	1091.5	77.0	263	20	US-09-627-165B-12	Sequence 12, Appl1
36	1091.5	77.0	263	20	US-09-627-165B-12	Sequence 12, Appl1
37	1091.5	77.0	263	20	US-09-627-165B-12	Sequence 12, Appl1
38	1091.5	77.0	263	20	US-09-627-165B-12	Sequence 12, Appl1
39	1005	70.9	266	20	US-09-627-165B-8	Sequence 8, Appl1
40	1005	70.9	266	20	US-09-627-165B-8	Sequence 8, Appl1
41	908.5	64.1	262	22	US-09-791-537-15464	Sequence 15464, Appl1
42	908.5	64.1	262	22	US-09-791-537-15464	Sequence 15464, Appl1
43	907.5	64.0	262	22	US-09-791-537-21007	Sequence 21007, Appl1
44	907.5	64.0	262	22	US-09-791-537-21007	Sequence 21007, Appl1
45	907.5	64.0	576	1	PCT-US02-05722A-1	Sequence 1, Appl1

ALIGNMENTS

US-09-601-667B-7
Sequence Application US/09601667B
APPLICANT: Morris, Peter
APPLICANT: Stiefel, Thomas
APPLICANT: Voelkers, Wolfgang
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT FILING DATE: 2000-10-06
PRIORITY FILING DATE: 1999-02-03
PRIORITY FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 7
LENGTH: 264
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: mistletoe lectin 1 (match)
US-09-601-667B-7

Query Match 100.0%; Score 1418; DB 20; Length 264;
Best Local Similarity 100.0%; Pred. No. 7,66-142;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVTCASAEPTVAVRNKNGRVVDDDDPHDNGQIQLMPSKSNDDPNQMLTKKIDGTTIS 60
DB 1 DVVTCASAEPTVAVRNKNGRVVDDDDPHDNGQIQLMPSKSNDDPNQMLTKKIDGTTIS 60
QY 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
DB 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
QY 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
DB 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
QY 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
DB 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
QY 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
DB 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQKRWFTNEGAILINKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQKRWFTNEGAILINKGLANDVQA 240
QY 241 NPKLRRIITYPATKPKQKQMLPVF 264
DB 241 NPKLRRIITYPATKPKQKQMLPVF 264

RESULT 2

US-09-601-667C-7
Sequence 7, Application US/09601667C

GENERAL INFORMATION:

APPLICANT: Morris, Peter
APPLICANT: Stetzel, Thomas
APPLICANT: Stetzel, Wolfgang
APPLICANT: Weisler, Peter
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601,667C
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/EP99/00696
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: D 198 04 210.8
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 1
SEQ ID NO 2
TYPE: PRT
FEATURE:
ORGANISM: Artificial Sequence

US-09-601-667C-7
OTHER INFORMATION: mistletoe lectin 1 (match)

Query Match

US-09-601-667B-9
Sequence 9, Application US/09601667B
Best Local Similarity 100.0%; Pred. No. 7,66-142;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVTCASAEPTVAVRNKNGRVVDDDDPHDNGQIQLMPSKSNDDPNQMLTKKIDGTTIS 60
DB 1 DVVTCASAEPTVAVRNKNGRVVDDDDPHDNGQIQLMPSKSNDDPNQMLTKKIDGTTIS 60
QY 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
DB 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
QY 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
DB 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
QY 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
DB 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
QY 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
DB 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQKRWFTNEGAILINKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQKRWFTNEGAILINKGLANDVQA 240
QY 241 NPKLRRIITYPATKPKQKQMLPVF 264
DB 241 NPKLRRIITYPATKPKQKQMLPVF 264

DB 241 NPKLRRIITYPATKPKQKQMLPVF 264

RESULT 3

US-09-791-537-111174
Sequence 111174, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Biomolx, Inc.
APPLICANT: Decker, Joseph
APPLICANT: Decker, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEM
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patent version 3.0
SEQ ID NO 111174
LENGTH: 264
TYPE: PRT
FEATURE:
ORGANISM: viscum album

US-09-791-537-111174

Query Match 100.0%; Score 1418; DB 22; Length 264;
Best Local Similarity 100.0%; Pred. No. 7,66-142;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVTCASAEPTVAVRNKNGRVVDDDDPHDNGQIQLMPSKSNDDPNQMLTKKIDGTTIS 60
DB 1 DVVTCASAEPTVAVRNKNGRVVDDDDPHDNGQIQLMPSKSNDDPNQMLTKKIDGTTIS 60
QY 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
DB 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
QY 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
DB 61 NSCCTTYGTAAGYVWIPDCNTRVREATTIWMONGTIIINRSNVLAASSGKGTTLT 120
QY 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
DB 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
QY 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
DB 121 VQTLDTYLGQGLAGNDTAPREVITYGFRDLQMESNGSVWVETCDSSQKQKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQKRWFTNEGAILINKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQKRWFTNEGAILINKGLANDVQA 240
QY 241 NPKLRRIITYPATKPKQKQMLPVF 264
DB 241 NPKLRRIITYPATKPKQKQMLPVF 264

RESULT 4

US-09-601-667B-9
Sequence 9, Application US/09601667B

GENERAL INFORMATION:

APPLICANT: Morris, Peter
APPLICANT: Stetzel, Thomas
APPLICANT: Stetzel, Wolfgang
APPLICANT: Weisler, Peter
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601,667B
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/EP99/00696
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: D 198 04 210.8
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 1
SEQ ID NO 2
TYPE: PRT
FEATURE:
ORGANISM: Artificial Sequence

US-09-601-667B-9
OTHER INFORMATION: mistletoe lectin B3 (match)

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.rapm

Query Match
Best Local Similarity 99.6%; Score 1412; DB 20; Length 264;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DVTCSASEPTVAVGNKRVVDDPHDNGOIQLPKSKNDPQWLTKKDGITRS 60
DB 1 DVTCSASEPTVAVGNKRVVDDPHDNGOIQLPKSKNDPQWLTKKDGITRS 60
QY 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKATITL 120
DB 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKATITL 120
QY 121 VQTLDTLGGWLAGNDTPREVTIYGFEDLCMSNGSVWETTCSSQKQKALYGD 180
DB 121 VQTLDTLGGWLAGNDTPREVTIYGFEDLCMSNGSVWETTCSSQKQKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSRWFTNKGALINLKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSRWFTNKGALINLKGLANDVQA 240
QY 241 NPKLRRIITYPATGKPNQWMLPVF 264
DB 241 NPKLRRIITYPATGKPNQWMLPVF 264

RESULT 5
US-09-601-667c-9
Sequence 9, Application US/0960167C
GENERAL INFORMATION:
APPLICANT: Morris, Peter
APPLICANT: Stiefel, Thomas
APPLICANT: Voelter, Wolfgang
APPLICANT: Welte, Peter
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601, 667C
CURRENT FILING DATE: 2000-10-06
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: D 358 04 210.8
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 9
LENGTH: 264
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: mistletoe lectin B3 (match)
US-09-601-667c-5

Query Match
Best Local Similarity 99.6%; Score 1412; DB 20; Length 264;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DVTCSASEPTVAVGNKRVVDDPHDNGOIQLPKSKNDPQWLTKKDGITRS 60
DB 1 DVTCSASEPTVAVGNKRVVDDPHDNGOIQLPKSKNDPQWLTKKDGITRS 60
QY 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKATITL 120
DB 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKATITL 120
QY 121 VQTLDTLGGWLAGNDTPREVTIYGFEDLCMSNGSVWETTCSSQKQKALYGD 180
DB 121 VQTLDTLGGWLAGNDTPREVTIYGFEDLCMSNGSVWETTCSSQKQKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSRWFTNKGALINLKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSRWFTNKGALINLKGLANDVQA 240
QY 241 NPKLRRIITYPATGKPNQWMLPVF 264
DB 241 NPKLRRIITYPATGKPNQWMLPVF 264

RESULT 6
US-09-791-537-11176
Sequence 10, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biocomatrix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEM
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patent version 3.0
SEQ ID NO 11176
LENGTH: 265
TYPE: PRT
ORGANISM: Viscum album
US-09-791-537-11176

Query Match
Best Local Similarity 99.3%; Score 1407.5; DB 22; Length 265;
Matches 264; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 DVTCSASEPTVAVGNKRVVDDPHDNGOIQLPKSKNDPQWLTKKDGITRS 60
DB 1 DVTCSASEPTVAVGNKRVVDDPHDNGOIQLPKSKNDPQWLTKKDGITRS 60
QY 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKATITL 120
DB 61 NSCLTITGTYGAVYVMIPEKNAVREKATIQWMDGIIIPRSNLVLAASGKATITL 120
QY 121 VQTLDTLGGWLAGNDTPREVTIYGFEDLCMSNGSVWETTCSSQKQKALYGD 180
DB 121 VQTLDTLGGWLAGNDTPREVTIYGFEDLCMSNGSVWETTCSSQKQKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSRWFTNKGALINLKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSRWFTNKGALINLKGLANDVQA 240
QY 241 NPKLRRIITYPATGKPNQWMLPVF 264
DB 241 NPKLRRIITYPATGKPNQWMLPVF 265

RESULT 7
US-09-601-667b-10
Sequence 10, Application US/0960167B
GENERAL INFORMATION:
APPLICANT: Morris, Peter
APPLICANT: Stiefel, Thomas
APPLICANT: Voelter, Wolfgang
APPLICANT: Welte, Peter
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601, 667B
CURRENT FILING DATE: 2000-10-06
PRIOR FILING DATE: PCT/EP99/00696
PRIOR APPLICATION NUMBER: D 198 04 210.8
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 10
LENGTH: 264
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: mistletoe lectin B4 (match)
US-09-601-667b-10

Query Match
Best Local Similarity 99.1%; Score 1405; DB 20; Length 264;

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.rapm

Page 4

Best Local Similarity 99.2%; Pred. No. 1.9e-140;
Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMLTKKIDGTIS 60
Db 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMLTKKIDGTIS 60
Qy 61 NSGCLTYGYTAGYVYMI FDCNVAVEATIIWOIMNGTIIIPRSNLYAASGKIGTLLT 120
Db 61 NSGCLTYGYTAGYVYMI FDCNVAVEATIIWOIMNGTIIIPRSNLYAASGKIGTLLT 120
Qy 121 VQTLDTYLAGQGLAGNDTAPREVITYGFRDLQMSNGSVMWETCDSSQXQKXALYGD 180
Db 121 VQTLDTYLAGQGLAGNDTAPREVITYGFRDLQMSNGSVMWETCDSSQXQKXALYGD 180
Qy 181 GSIRPKQNDQCLTSGRDSVSTVINYSGSGASQSQRWFTNEGAILNLKGLAMDVQA 240
Db 181 GSIRPKQNDQCLTSGRDSVSTVINYSGSGASQSQRWFTNEGAILNLKGLAMDVQA 240
Qy 241 NPKLRRIIIPATGKPNQMLPVF 264
Db 241 NPKLRRIIIPATGKPNQMLPVF 264

RESULT 8
US-09-601-667c-10
; Sequence 10, Application US/09601667c
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/3636
; CURRENT APPLICATION NUMBER: US/09/601,667c
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 10
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mistletoe lectin B4 (match)
US-09-601-667c-10

Query Match 99.1%; Score 1405; DB 20; Length 264;
Best Local Similarity 99.2%; Pred. No. 1.9e-140;
Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMLTKKIDGTIS 60
Db 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMLTKKIDGTIS 60
Qy 61 NSGCLTYGYTAGYVYMI FDCNVAVEATIIWOIMNGTIIIPRSNLYAASGKIGTLLT 120
Db 61 NSGCLTYGYTAGYVYMI FDCNVAVEATIIWOIMNGTIIIPRSNLYAASGKIGTLLT 120
Qy 121 VQTLDTYLAGQGLAGNDTAPREVITYGFRDLQMSNGSVMWETCDSSQXQKXALYGD 180
Db 121 VQTLDTYLAGQGLAGNDTAPREVITYGFRDLQMSNGSVMWETCDSSQXQKXALYGD 180
Qy 181 GSIRPKQNDQCLTSGRDSVSTVINYSGSGASQSQRWFTNEGAILNLKGLAMDVQA 240
Db 181 GSIRPKQNDQCLTSGRDSVSTVINYSGSGASQSQRWFTNEGAILNLKGLAMDVQA 240
Qy 241 NPKLRRIIIPATGKPNQMLPVF 264
Db 241 NPKLRRIIIPATGKPNQMLPVF 264

RESULT 9
US-09-601-667b-11
; Sequence 11, Application US/09601667b
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/3636 US/09/601,667b
; CURRENT APPLICATION NUMBER: US/09/601,667b
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 11
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mistletoe lectin B5 (match)
US-09-601-667b-11

Query Match 99.9%; Score 1403; DB 20; Length 264;
Best Local Similarity 99.9%; Pred. No. 3e-140;
Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMLTKKIDGTIS 60
Db 1 DVTCSASEPTVRIYGNKRVYRDDPHDQNOQLMPKSNNDPNQMLTKKIDGTIS 60
Qy 61 NSGCLTYGYTAGYVYMI FDCNVAVEATIIWOIMNGTIIIPRSNLYAASGKIGTLLT 120
Db 61 NSGCLTYGYTAGYVYMI FDCNVAVEATIIWOIMNGTIIIPRSNLYAASGKIGTLLT 120
Qy 121 VQTLDTYLAGQGLAGNDTAPREVITYGFRDLQMSNGSVMWETCDSSQXQKXALYGD 180
Db 121 VQTLDTYLAGQGLAGNDTAPREVITYGFRDLQMSNGSVMWETCDSSQXQKXALYGD 180
Qy 181 GSIRPKQNDQCLTSGRDSVSTVINYSGSGASQSQRWFTNEGAILNLKGLAMDVQA 240
Db 181 GSIRPKQNDQCLTSGRDSVSTVINYSGSGASQSQRWFTNEGAILNLKGLAMDVQA 240
Qy 241 NPKLRRIIIPATGKPNQMLPVF 264
Db 241 NPKLRRIIIPATGKPNQMLPVF 264

RESULT 10
US-09-601-667c-11
; Sequence 11, Application US/09601667c
; GENERAL INFORMATION:
; APPLICANT: Morris, Peter
; APPLICANT: Stiefel, Thomas
; APPLICANT: Voelter, Wolfgang
; TITLE OF INVENTION: Recombinant Mistletoe Lectins
; FILE REFERENCE: 29841/3636
; CURRENT APPLICATION NUMBER: US/09/601,667c
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: PCT/EP99/00696
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: D 198 04 210.8
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 11
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.rapm

Page 5

OTHER INFORMATION: mismatch lectin B2 (match)
US-09-601-667c-11

Query Match 98.9%; Score 1403; DB 20; Length 264;
Best Local Similarity 98.9%; Pred. No. 3a-140; 2; Mismatches 21; Conservative 1; Indels 0; Gaps 0;

QY 1 DVTCSASBPYVAVGNKGVVDVDDPHDQNOIQLPKSKNDPNQMTIKKIDTIRS 60
DB 1 DVTCSASBPYVAVGNKGVVDVDDPHDQNOIQLPKSKNDPNQMTIKKIDTIRS 60
QY 61 NSGCLTYGYTAGVYVWIPDCNVAKEATWQIMNGTIIINPSNVLAASSGIGKTTLT 120
DB 61 NSGCLTYGYTAGVYVWIPDCNVAKEATWQIMNGTIIINPSNVLAASSGIGKTTLT 120
QY 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQNGKALYGD 180
DB 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQNGKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGAILNKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGAILNKGLANDVQA 240
QY 241 NPKLRRIIIVPAKGRKNQMLPVF 264
DB 241 NPKLRRIIIVPAKGRKNQMLPVF 264

RESULT 11

US-09-601-667b-8
Sequence 8, Application US/09601667b

GENERAL INFORMATION:
APPLICANT: Morris, Peter
APPLICANT: Stiefel, Thomas
APPLICANT: Voelter, Wolfgang
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601,667b
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/EP99/00696
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: D 198 04 210.8
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 8

LENGTH: 264

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:

OTHER INFORMATION: mismatch lectin B2 (match)
US-09-601-667b-8

Query Match 97.2%; Score 1379; DB 20; Length 264;
Best Local Similarity 97.7%; Pred. No. 1.1e-137;

Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVTCSASBPYVAVGNKGVVDVDDPHDQNOIQLPKSKNDPNQMTIKKIDTIRS 60
DB 1 DVTCSASBPYVAVGNKGVVDVDDPHDQNOIQLPKSKNDPNQMTIKKIDTIRS 60
QY 61 NSGCLTYGYTAGVYVWIPDCNVAKEATWQIMNGTIIINPSNVLAASSGIGKTTLT 120
DB 61 NSGCLTYGYTAGVYVWIPDCNVAKEATWQIMNGTIIINPSNVLAASSGIGKTTLT 120
QY 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQNGKALYGD 180
DB 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQNGKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGAILNKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGAILNKGLANDVQA 240

QY 241 NPKLRRIIIVPAKGRKNQMLPVF 264
DB 241 NPKLRRIIIVPAKGRKNQMLPVF 264

RESULT 12

US-09-601-667c-8
Sequence 8, Application US/09601667c

GENERAL INFORMATION:
APPLICANT: Morris, Peter
APPLICANT: Stiefel, Thomas
APPLICANT: Voelter, Wolfgang
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601,667c
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/EP99/00696
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: D 198 04 210.8
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 8

LENGTH: 264

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:

OTHER INFORMATION: mismatch lectin B2 (match)
US-09-601-667c-8

Query Match 97.2%; Score 1379; DB 20; Length 264;
Best Local Similarity 97.7%; Pred. No. 1.1e-137;

Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVTCSASBPYVAVGNKGVVDVDDPHDQNOIQLPKSKNDPNQMTIKKIDTIRS 60
DB 1 DVTCSASBPYVAVGNKGVVDVDDPHDQNOIQLPKSKNDPNQMTIKKIDTIRS 60
QY 61 NSGCLTYGYTAGVYVWIPDCNVAKEATWQIMNGTIIINPSNVLAASSGIGKTTLT 120
DB 61 NSGCLTYGYTAGVYVWIPDCNVAKEATWQIMNGTIIINPSNVLAASSGIGKTTLT 120
QY 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQNGKALYGD 180
DB 121 VQTLDTYLLQGMLAGNDTAPREVITYGFRDLCHESNGSGVWETCDSSQNGKALYGD 180
QY 181 GSIRPKONODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGAILNKGLANDVQA 240
DB 181 GSIRPKONODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGAILNKGLANDVQA 240
QY 241 NPKLRRIIIVPAKGRKNQMLPVF 264
DB 241 NPKLRRIIIVPAKGRKNQMLPVF 264

RESULT 13

US-09-601-667b-6
Sequence 6, Application US/09601667b

GENERAL INFORMATION:
APPLICANT: Morris, Peter
APPLICANT: Stiefel, Thomas
APPLICANT: Voelter, Wolfgang
TITLE OF INVENTION: Recombinant Mistletoe Lectins
FILE REFERENCE: 29841/36636
CURRENT APPLICATION NUMBER: US/09/601,667b
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/EP99/00696
PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: D 198 04 210.8
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 6

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.rai

Page 2

RESULT 2
 US-08-776-059-33
 / Sequence 33, Application US/087760598
 / Patent No. 6271368
 / GENERAL INFORMATION:
 / APPLICANT: LENTZEN, Hans
 / APPLICANT: KIST, Jürgen
 / APPLICANT: BAUM, Hans
 / APPLICANT: ZINKE, Holger
 / TITLE OF INVENTION: RECOMBINANT MISTUSTOF LECTIN (RML)
 / FILE REFERENCE: 674503-2003
 / CURRENT APPLICATION NUMBER: US/08/776, 0598
 / CURRENT FILING DATE: 1999-06-19
 / EARLIER APPLICATION NUMBER: PCT/EP96/02273
 / EARLIER FILING DATE: 1996-06-25
 / EARLIER PCT NO.: PCT/EP96/02273
 / EARLIER FILING DATE: 1996-06-26
 / NUMBER OF SEQ ID NOS: 56
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 33
 / LENGTH: 264
 / TYPE: PRT
 / ORGANISM: Vesicum album
 US-08-776-059-33

[illegible]

RESULT 3
US-08-776-059-35
Sequence 35, Application US/08760598
GENERAL INFORMATION:
APPLICANT: LEITZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (ROL)
CURRENT PILING DATE: 1995-06-15
CURRENT PILING DATE: 1995-06-15
CURRENT PILING DATE: 1995-06-15
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95103949.8
EARLIER FILING DATE: 1995-06-26
PUBLISHED SEQ ID NOS: 56
SEQUENCE LENGTH VER. 2.0
SEQ ID NO 35
LENGTH: 564
TYPE: PRF
ORGANISM: Viscum album

[illegible]

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

```

? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US-08/378,761A
? INVENTOR: 26-JAN-1995
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: BORDUCKI, ANDREA T
? REGISTRATION NUMBER: 33651
? REFERENCE/DOCKET NUMBER: 38272B
? TELECOMMUNICATION INFORMATION:
? TELEPHONE NO.: 313-751-4846
? FAX NO.: 313-751-4846
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS: 77:
? LENGTH: 540 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? OS=08-378-761A-77
?
Query Match          55.3%; Score 783.5; DB: 1; Length 540;
Basic Similarity     56.2%; Pred.No.3.9e-73;
Matches 146; Conservative 41; Mismatches 72; Indels      1; Gaps       1

```

QY 5 CAAEPTVAVKNGKRVYVADDDPHDNGIQIOLMPKSNNDPNQIATIKRDTIRNSGSC 64
DB 282 CMDEPFIYAVKNGKLCVYVGEFFPDGNPIQLMPCKSNNTDWNQIATIKRDTIRNSGKC 341
QY 65 LITVGYTAGVYVIMFDCNTAREATTIWOJMDNGTIINPSNVLAAASGIGTLLTVQTL 124
DB 342 LITKSSPRQGVYVINCSTATVGTATRMQIMNRTIINPSGLVLAATSGNSGKTLVQTN 401
QY 125 DYTLAGQGLANDTAPREVITVGPADLCMESNGSVWTCDSQKXQKXALYGGGSR 184
DB 402 IYAVSQGLPTNNTPFVITIVGLYKMLQNSGKYLEDC-TSEKAEQOVALYADGSIR 460
QY 185 PKQNDQCLTSGRDSVSTVINIVSGSGASGSRWFTEBSALLINKGLAMDVQAQPKL 244
DB 461 PQRNDQCLTTPDANKIGTIVKILSCGPASGSRWFFQNDGTLINLYGLVDVRSDBSL 520
QY 245 RRIIYVATKRNQNMPLPVF 264
DB 521 KQIIVHPFHNANQIWLEPLF 540

RESULT 5

US-08-485-286-77
/ Sequence 77, Application US/08485286
/ Patent No. 5646026
/ Patent No. 5646119
/ GENERAL INFORMATION:
/ APPLICANT: WALSH, TERENCE A
/ APPLICANT: HEY, TIMOTHY D
/ TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
/ TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
/ NUMBER OF SEQUENCES: 81
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ANDREA T. BORUCKI
/ STREET: 9330 ZIONSVILLE ROAD
/ CITY: INDIANAPOLIS
/ STATE: IN
/ COUNTRY: US
/ ZIP: 46268
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485-286
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIORITY INFORMATION DATA:
/ APPLICATION NUMBER: US 08/379761
/ FILING DATE: 26-JAN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BORUCKI, ANDREA T
/ REGISTRATION NUMBER: 33651
/ REFERENCE/DOCKET NUMBER: 38272B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (317) 337-4846
/ INFORMATION FOR SEQ ID NO: 77:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 540
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-485-286-77

Query Match 55.3%, Score 783.5, DB 1, Length 540,
Best Local Similarity 56.2%, Pred. No. 3,9e-73,
Matches 146, Conservative 41, Mismatches 72, Indels 1, Gaps 1,

QY 5 CAAEPTVAVKNGKRVYVADDDPHDNGIQIOLMPKSNNDPNQIATIKRDTIRNSGSC 64
DB 282 CMDEPFIYAVKNGKLCVYVGEFFPDGNPIQLMPCKSNNTDWNQIATIKRDTIRNSGKC 341
QY 65 LITVGYTAGVYVIMFDCNTAREATTIWOJMDNGTIINPSNVLAAASGIGTLLTVQTL 124
DB 342 LITKSSPRQGVYVINCSTATVGTATRMQIMNRTIINPSGLVLAATSGNSGKTLVQTN 401
QY 125 DYTLAGQGLANDTAPREVITVGPADLCMESNGSVWTCDSQKXQKXALYGGGSR 184
DB 402 IYAVSQGLPTNNTPFVITIVGLYKMLQNSGKYLEDC-TSEKAEQOVALYADGSIR 460
QY 185 PKQNDQCLTSGRDSVSTVINIVSGSGASGSRWFTEBSALLINKGLAMDVQAQPKL 244
DB 461 PQRNDQCLTTPDANKIGTIVKILSCGPASGSRWFFQNDGTLINLYGLVDVRSDBSL 520
QY 245 RRIIYVATKRNQNMPLPVF 264
DB 521 KQIIVHPFHNANQIWLEPLF 540

RESULT 6

US-09-512-342-14
/ Sequence 14, Application US/09512342
/ Patent No. 6388068
/ GENERAL INFORMATION:
/ APPLICANT: SATOH, SHINGO
/ APPLICANT: KASUDA, SUSUMU
/ TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT
/ TITLE OF INVENTION: FOREIGN POLYPEPTIDE FLUID
/ FILING DATE: 08/13/01
/ CURRENT APPLICATION NUMBER: US/09/512,342
/ CURRENT FILING DATE: 2000-02-24
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 293
/ TYPE: PRT
/ ORGANISM: Cucumis sativus
US-09-512-342-14

Query Match 12.9%, Score 182.5, DB 4, Length 293,
Best Local Similarity 28.1%, Pred. No. 7.1e-11,
Matches 63, Conservative 31, Mismatches 91, Indels 39, Gaps 10,

QY 14 IYGNKMGVYVADDDPHDNGIQIOLMPKSNNDPNQIATIKRDTIRNSGSC 59
DB 41 LVGSDCLTEHNSP-----WYKPAGINFPRSCCEKQOTQIATVDDTIRPM 89
QY 60 SNQCLT---VYTAGVYVIMFDCNTAREATTIWOJMDNGTIINPSNVLAAASGIGK 116
DB 90 NKRCLAAVFGVAVIN--KAVVSCGKXSPKMKWTOKNDGTLAVDSRWMLTGLDLY-- 145
QY 117 TITVGYTAGVYVIMFDCNTAREATTIWOJMDNGTIINPSNVLAAASGIGTLLTVQTL 124
DB 146 --VTLASKRTPSQEMVYESLSMWNANIELMNLCLGSTDSSHGGLNCNTDKNQK 202
QY 175 NALVSGSIRPKQNDQCLTSGRDSVSTVINIVSGSGASGSRWFTEBSALLINKGLAMDVQAQPKL 244
DB 203 NALVADGRTIQRHVNANCLTSPDQFRRV--VVSKEDEXPRQEW 244

RESULT 7

US-09-159-106-15
/ Sequence 15, Application US/09159106
/ Patent No. 6281503
/ GENERAL INFORMATION:
/ APPLICANT: FERRER, PAU
/ APPLICANT: DIERS, IVAN
/ APPLICANT: HEDEGARD, LARSBERG
/ TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
/ TITLE OF INVENTION: Activity

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.raii

Page 4

```

? FILE REFERENCE: 4693.204-US
? CURRENT APPLICATION NUMBER: US/09/159,106
? CURRENT FILING DATE: 1998-09-23
? EARLIER FILING DATE: 1998-04-21/96
? EARLIER FILING DATE: 1998-12-04
? EARLIER APPLICATION NUMBER: 0885/96
? EARLIER FILING DATE: 1996-08-23
? EARLIER APPLICATION NUMBER: ECT/D97/00160
? EARLIER FILING DATE: 1997-04-11
? NUMBER OF SEQ ID NOS: 15
? SOURCE: SEQ ID NOS 1-15
? SEQ ID NOS 1-15: Abstract for: Windows Version 3.0
? LENGTH: 132
? TYPE: prt
? ORGANISM: Oerskovia xanthineolytica
? OS-09-159-106-15

```

Query Match	9.6%	Score 136	DB 3	Length 132
Best Local Similarity	36.3%	Pred. No. 1.56-06		
Matches	45	Conservative	11	Mismatches 52
				Indels 16
				Gaps 6
QY	18	NGMRVDRDDDEHNSQIQMPKSNNDPNQATIKEDTIRKNSGLTITV--GTTAGV	75	
Db	14	NGNSPVPKPRADPDHNSQVQIVTISGN--AAQVTKRSQSDVSLAKLQVDRSGSTIRKAA	71	
QY	76	WIPNCQVRAEATIKQVIT--IDMR--IINPSNVILAAASG--KCTTLVQVGLDTL	128	
Db	72	VQVYTC-----GTGAGMAVDAGSKALRNPGSLCLPRTQAFAPDQGNQLQVTCNGT	136	
QY	129	GGGW	132	
Db	127	AGGW	130	

RESULT 8
 US-09-159-106-11
 Sequence 11, Application US/09159106
 Patent No. 6284509
 GENERAL INFORMATION:
 INVENTOR: Heller, Paul
 APPLICANT: Heller, Paul
 APPLICANT: Halkier, Toibon
 APPLICANT: Hedegaard, Libbeth
 TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
 TITLE OF INVENTION: Activity
 FILE REFERENCE: 4693.204-US
 CURRENT APPLICATION NUMBER: US/09/159.106
 EARLIER APPLICATION NUMBER: US/09/159.106
 EARLIER FILING DATE: 1996-12-04
 EARLIER APPLICATION NUMBER: 06427/96
 EARLIER FILING DATE: 1996-12-04
 EARLIER APPLICATION NUMBER: 0885/96
 EARLIER FILING DATE: 1996-08-23
 EARLIER APPLICATION NUMBER: PCT/D97/00160
 EARLIER FILING DATE: 1997-04-14
 NUMBER OF SEQ ID NOS: 15
 SOURCE: Genbank
 SEQ ID NO. 1: FASTSEQ For Windows Version 3.0
 LENGTH: 435
 TYPE: FRT
 ORGANISM: Oerskovia xanthineolytica
 US-09-159-106-11

Query MatchScore 9.64; Score 136; DB 3; Length 435;
 Best Local Similarity 36.34; Pred. No. 8.9e-06;
 Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6

CY 18 NGRADYADDDHFGAGCIGLTPKRSNSNDPQGLMTIKEDITRSNSGICLLY--GTPYGY 7
 DB 317 NGRADYADDDHFGAGCIGLTPKRSNSNDPQGLMTIKEDITRSNSGICLLY--GTPYGY 374
 317 NGRADYADDDHFGAGCIGLTPKRSNSNDPQGLMTIKEDITRSNSGICLLY--GTPYGY 374

OY 76 VMFPEFPAVEATKQVLR--DMGK--LIPNSNVLVAASGSI--KRTTLVGTQIDYLL 128
 DB 375 VQVWVNC-----GAGAKNAIDAGSGALRNRPQSGICLIDTQAGAPLRDQGLTQVNCNGIT 429

QY	129	GQGW	132
Db	430	AQGW	433

RESULT 9
 US-08-468-812-4
 Sequence 4, Application US/0846832
 Patent No. 595836
 GENERAL INFORMATION:
 APPLICANT: Menander, Jari
 APPLICANT: Pasi
 APPLICANT: Pasanen m Richard
 APPLICANT: Iatito, Raija
 APPLICANT: Paloheimo, Marja
 APPLICANT: Suominen, Pirkko
 APPLICANT: Laitinen, Tarja
 APPLICANT: Kristo, Paula
 TITLE OF INVENTION: Actionadura Xyl'anase Sequences and Method^os
 TITLE OF INVENTION: of Use
 NUMBER OF CLAIMS: 25
 CORRESPONDENCE ADDRESS
 ADDRESSEE: STEVEN KESSLER, GOLSTEIN & FOX
 STREET: 1100 New York Ave., N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.

```

1      COMPUTER READABLE FORM:
2      MEDIUM TYPE: Floppy disk
3      COMPUTER: IBM PC compatible
4      OPERATING SYSTEM: PC-DOS/MS-DOS
5      SOFTWARE: PatentIn Release #1.0, Version #1.30
6      CURRENT APPLICATION DATA/08/468, 812
7      FILING DATE: 06-JUN-1995
8      CLASSIFICATION: 435
9      PRIORITY APPLICATION DATA:
10     APPLICATION NUMBER: US 08/352,412
11     FILING DATE: 31-OCT-1994
12     CLASSIFICATION: 435
13     PRIORITY APPLICATION DATA:
14     APPLICATION NUMBER: US 08/282,001
15     FILING DATE: 29-JUL-1994
16     CLASSIFICATION: 435
17     ATTORNEY/AGENT INFORMATION:
18     NAME: Bugalsky, Larry B.
19     REGISTRATION NUMBER: 35,066
20     REFERENCE/DOCKET NUMBER: 1050.0340002
21     TELECOMMUNICATION INFORMATION:
22     TELEPHONE: 202-371-2600
23     TELEFAX: 202-371-2540
24     INFORMATION FOR SEQ ID NO.: 4:
25     SEQUENCE CHARACTERISTICS:
26     TYPE: amino acid
27     LENGTH: 497 amino acids
28     TOPOLOGY: linear
29     MOLECULE TYPE: protein
30     US-08-468-812-4

```

Query Match 8.8%; Score 124.5; DB 2; Length 492;
 Best Local Similarity 20.8%; Pred. No. 0.00017;
 Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 170

QY DYADDDFDHGNQIDMPG---KSNQNPOLYTKRDKGTR---SNGSCLTYYGY----- 70
 DB DYADDDFDHGNQIDMPG---KSNQNPOLYTKRDKGTR---SNGSCLTYYGY----- 70
 QY 168 DYADDDFDHGNQIDMPG---KSNQNPOLYTKRDKGTR---SNGSCLTYYGY----- 70
 DB 168 DYADDDFDHGNQIDMPG---KSNQNPOLYTKRDKGTR---SNGSCLTYYGY----- 70

QY 71 -TAQVWVI-----PPCTATREMTIWMQNTQITNPSRLYLAASGICGTL 119
 DB 71 -TAQVWVI-----PPCTATREMTIWMQNTQITNPSRLYLAASGICGTL 119

QY 224 AKTQAVVNNVDFEKSFGYIDC---VGQSPFSPGSENVNENRTLTQGFAL-GTV 276
 DB 224 AKTQAVVNNVDFEKSFGYIDC---VGQSPFSPGSENVNENRTLTQGFAL-GTV 276

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.rat

Page 5

QY 120 TVQTLDTYLGQGMKAGNTPARE-----VTYGFED-----LC 152
Db 277 EYTHLDI-----ENKPKQYASVIRDCIADVRCCTGIIYWGVRDSDNSRYGNPL 326
QY 153 MESN-----GGSVWV-----ET 164
Db 327 FNNNGKQAYAVLALNKGSDGGSNPPVSPPGGSGQIRGVASNRCTDVNGNT 386
QY 165 CDSGQ-----KNGCKMALYGDGSIKPKQNDQCTGSRDVSSTVINIVSCGASG 215
Db 387 ADGTQVQLYDCHSGSNQ-QWTYSSGFRIFGN--KCLDAGSSNGAVQVYISCWGGA-N 442
QY 216 QRWYTFNGAILNKNGLAND-VQAMPKLRRIIIPATKKNQW 260
Db 443 QKMLRADGTVGVSGCLDVGAGTGNGTRLDJSCWGNQK 488

RESULT 10

US-08-468-812-7

Sequence 7, Application US/08468812

Patent No. 5935836

GENERAL INFORMATION:

APPLICANT: Vennaemper, Jari

APPLICANT: M nyl, Arja

APPLICANT: Fagerstr m, Richard

APPLICANT: Paloheimo, Ralf

APPLICANT: Suontinen, Pirkko

APPLICANT: Lahninen, Taina

APPLICANT: Kistio, Paula

TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods

NUMBER OF INVENTIONS: 25

CORRESPONDENCE ADDRESS:

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,812

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA: US 08/332,412

STATE: D.C.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/282,001

FILING DATE: 29-JUL-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

NAME: Bugalsky, Larry B.

REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 1050,0340002

TELEPHONE: 202-371-2500

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 492 amino acids

TYPE: amino acid

STANDARDS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

POSITION IN GENOME:

CHROMOSOME/SEGMENT: AM50

US-08-468-812-7

Query Match 8.88; Score 124.5; DB 2; Length 492;
Best Local Similarity 20.88; Pred. No. 0.00017;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

QY 23 DYRDDPFHDSNOLMPS---KSNDPQWLMTIKSDGTR---SNGSLTGY-----70
Db 168 DIVVAEFLDNGSGRCDSNLOFTGND---WIEVAFTRQGDPSAKCYNDINEMMA 223
QY 71 --TAGYVYWI-----FDCNVAFRANTIQWIDGTTIPPSRLVLAASGKIKYTL 119
Db 224 AKTVAYVNVKDFKSRGVPIDC-----VGFOSHNSGNVPYFRTLLQGFAL-GVD 276
QY 120 TVQTLDTYLGQGMKAGNTPARE-----VTYGFED-----LC 152
Db 277 EYTHLDI-----ENKPKQYASVIRDCIADVRCCTGIIYWGVRDSDNSRYGNPL 326
QY 153 MESN-----GGSVWV-----ET 164
Db 327 FNNNGKQAYAVLALNKGSDGGSNPPVSPPGGSGQIRGVASNRCTDVNGNT 386
QY 165 CDSGQ-----KNGCKMALYGDGSIKPKQNDQCTGSRDVSSTVINIVSCGASG 215
Db 387 ADGTQVQLYDCHSGSNQ-QWTYSSGFRIFGN--KCLDAGSSNGAVQVYISCWGGA-N 442
QY 216 QRWYTFNGAILNKNGLAND-VQAMPKLRRIIIPATKKNQW 260
Db 443 QKMLRADGTVGVSGCLDVGAGTGNGTRLDJSCWGNQK 488

RESULT 11

US-08-590-563-4

Sequence 4, Application US/08590563

Patent No. 6100114

GENERAL INFORMATION:

APPLICANT: Vennaemper, Jari

APPLICANT: M nyl, Arja

APPLICANT: Fagerstr m, Richard

APPLICANT: Paloheimo, Ralf

APPLICANT: Suontinen, Pirkko

APPLICANT: Lahninen, Taina

TITLE OF INVENTION: Production and Secretion of Proteins of

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

STREET: 1100 New York Ave., N.W. Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/590,563

FILING DATE: 26-JAN-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/332,412

FILING DATE: 31-OCT-1994

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

NAME: Bugalsky, Larry B.

REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 1050,0340002

TELEPHONE: 202-371-2500

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 492 amino acids

TYPE: amino acid

STANDARDS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

POSITION IN GENOME:

CHROMOSOME/SEGMENT: AM50

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.fai

Page 6

ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-590-563-4

Query Match
Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00017;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

DB 23 DVADEPDHNGNOLMPS--KSNNDPNOLWTIKEDGTR---SNGSLTITVGY-----70
DB 168 DVNAPEDSGNSGRCDNQLRTND---WIVAFRTAGDPSAKLINDIEMNNA 223
QY 71 --TAGYVWI-----FDCTAVREATIQWINDGTTINPESNLVLAASGIRKFTL 119
DB 224 AKTOAVYNNVADPKSRGVPIDC-----VGFQSHNSGSPVNNPRTTLOQFAL-GVDV 276
QY 120 TVQTLDTLGGWLANDTAPRE-----VITVGFED-----LC 152
DB 277 EYTELDI-----ENAPQVYASVIRDCIATVWGRDSDMSYQNEL 326
QY 153 MESN-----GGSVWV-----ET 164
DB 327 FDRNGKKQAYVALDLNEDSGDGPSPNPVSPGSSQIRGVASNRCIDVPMNT 386
QY 165 CDSQ-----KQSKMALVDSGISPPKXNDQCLTSGDVSVTIINVCSSGSS 215
DB 387 ADQTVQVLDYCHSGSNQ--QWTTSSSEFRIRPN--KCLDAGSSNAGVQVYSCWGA-N 442
QY 216 QRWVPTMEGAILNKNGLANL-VQANPKIRIIIVATGPKPNQW 260
DB 443 QKVELRADGTVVQSGCLDAVGGGTNGTGLQVYSCWGNQKW 488

RESULT 12
US-08-590-563-7
Sequence 7, Application US/08590563
Patent No. 6300114
GENERAL INFORMATION:
APPLICANT: M ncy1, Arja
APPLICANT: Vehmanner, Jari
APPLICANT: Pasterst m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahti, Raita
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-08-590-563-7

Query Match
Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00017;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

DB 23 DVADEPDHNGNOLMPS--KSNNDPNOLWTIKEDGTR---SNGSLTITVGY-----70
DB 168 DVNAPEDSGNSGRCDNQLRTND---WIVAFRTAGDPSAKLINDIEMNNA 223
QY 71 --TAGYVWI-----FDCTAVREATIQWINDGTTINPESNLVLAASGIRKFTL 119
DB 224 AKTOAVYNNVADPKSRGVPIDC-----VGFQSHNSGSPVNNPRTTLOQFAL-GVDV 276
QY 120 TVQTLDTLGGWLANDTAPRE-----VITVGFED-----LC 152
DB 277 EYTELDI-----ENAPQVYASVIRDCIATVWGRDSDMSYQNEL 326
QY 153 MESN-----GGSVWV-----ET 164
DB 327 FDRNGKKQAYVALDLNEDSGDGPSPNPVSPGSSQIRGVASNRCIDVPMNT 386
QY 165 CDSQ-----KQSKMALVDSGISPPKXNDQCLTSGDVSVTIINVCSSGSS 215
DB 387 ADQTVQVLDYCHSGSNQ--QWTTSSSEFRIRPN--KCLDAGSSNAGVQVYSCWGA-N 442
QY 216 QRWVPTMEGAILNKNGLANL-VQANPKIRIIIVATGPKPNQW 260
DB 443 QKVELRADGTVVQSGCLDAVGGGTNGTGLQVYSCWGNQKW 488

RESULT 13
US-09-770-621-4
Sequence 4, Application US/09770621
Patent No. 6506593
GENERAL INFORMATION:
APPLICANT: M ncy1, Arja
APPLICANT: Vehmanner, Jari
APPLICANT: Pasterst m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahti, Raita
TITLE OF INVENTION: Production and Secretion of Proteins of

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.ra1

Page 7

NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIORITY INFORMATION DATA:
PRIORITY NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIORITY INFORMATION DATA:
PRIORITY NUMBER: 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIORITY INFORMATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
PRIORITY INFORMATION DATA:
PRIORITY NUMBER: 35,086
FILING DATE:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-770-621-4
Query Match 8.8%; Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00017;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;
DB 23 DYRDDPHDNGQIOWPSS---KSNNDPMQMTIKRDGTIR---SNSGLTGY-----70
DB 168 DVNAEFEDNSGRCDNSLQRTGND---WISVAFRTAQDPSAKLCYNDVNIEMNNA 223
DB 71 --TAGTYVNI-----FDGNTAVRATVQINDGTIIPRSNLIYLAASGIGKTTLL 119
DB 224 AKTQAVYNNVYRDKSRGVPLD-----VGQSHNSGNPNYVFRFTLLQOPFAL-GVDV 276
DB 120 TVQTLDTYTLGGQMLAGNDTAPRE-----VTIYGRFD-----LC 152
DB 277 EYVELDI-----ENAPQVASYIRDLCLAVDRCTGIYVGVGDSDWSRYONFL 326
DB 153 MESN-----GGSVW-----ET 164
DB 327 FDNNGNKQATYVADALNBSDDGGSPNPSPSPGSSGQIGVYASNRCDIVPMNT 386
DB 165 CASSQ-----XNGKXALYGGISIRPKNODQCLTSGRDSYVINYISGASGS 215
DB 387 ADGTVOYLDCHSGSNQ-QWYTSAGSFIRPGN-KCLDAGSSNAGVQIYISCKWGR-N 442
DB 216 QWVFTNKAALINLKNGLAND-VAQANPKRRIIYIPATGPKPNQW 260
DB 443 QKWELRADGTIVGVSGLCIDAVGGGTGNGTGLQLYSCMGNNQW 488

RESULT 14
US-09-770-621-7
Sequence 7, Application US/09770621
Patent No. 6506593
GENERAL INFORMATION:
APPLICANT: M etyl, Arja
APPLICANT: Remaunper, Richard
APPLICANT: Lantio, Rajja
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Taina
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIORITY INFORMATION DATA:
PRIORITY NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIORITY INFORMATION DATA:
PRIORITY NUMBER: 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIORITY INFORMATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
PRIORITY INFORMATION DATA:
PRIORITY NUMBER: 35,086
FILING DATE:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM60
US-09-770-621-7
Query Match 8.8%; Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00017;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;
DB 23 DYRDDPHDNGQIOWPSS---KSNNDPMQMTIKRDGTIR---SNSGLTGY-----70
DB 168 DVNAEFEDNSGRCDNSLQRTGND---WISVAFRTAQDPSAKLCYNDVNIEMNNA 223
DB 71 --TAGTYVNI-----FDGNTAVRATVQINDGTIIPRSNLIYLAASGIGKTTLL 119
DB 224 AKTQAVYNNVYRDKSRGVPLD-----VGQSHNSGNPNYVFRFTLLQOPFAL-GVDV 276
DB 120 TVQTLDTYTLGGQMLAGNDTAPRE-----VTIYGRFD-----LC 152

Thu Dec 11 16:10:03 2003

us-09-601-667c-7.tai

Page 8

Db 277 EYELDI-----ENAPQYASVIRDCIAYDSCTGITVGVNRDSDMSYQNFLL 326
QY 153 MSN-----GGSVWV-----ST 164
Db 327 FNNKNGKQAYAVADALNKGSDGSGSPNPVSPPPGSSGQIRGVASNCIDVFNKNT 386
QY 165 CDSG-----KQCKALYDPSIRPKQKQOCITSGDSVSTVITNVGCGASGS 215
Db 387 ADGTQVYLDCHSGSNQ-CMTYSSGSPRFGN-KCLDGGSSNAGVQIYSCNGR-N 442
QY 216 GSWFTNKGAILNKLKGLAND-VQANPRLRIIYIPATKPNQW 260
Db 443 QKMLRADDTIVQSGCLDVGSGGTNGTRLOIYSCNGANQKX 498

RESULT 15
US-08-468-812-5
Sequence 5, Application US/08468812
US-08-468-812-5
US-08-468-812-5

GENERAL INFORMATION:

APPLICANT: Vahmanper, Jari
APPLICANT: M. Uvi, Aija
APPLICANT: Ragerstr m, Richard
APPLICANT: Lantto, Raimo
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
APPLICANT: Kristo, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
SOFTWARE: IBM PC compatible
OPERATING SYSTEM: DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/468, 812

APPLICATION NUMBER: US/08/468, 812

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA: US 08/332,412

APPLICATION NUMBER: US 08/332,412

FILING DATE: 31-OCT-1994

PRIOR APPLICATION DATA: US 08/282,001

APPLICATION NUMBER: US 08/282,001

FILING DATE: 29-JUL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Bugalsky, Larry B.

REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 1050, 0340002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2640

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 480 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

POSITION IN GENOME:

CHROMOSOME/SEGMENT: AM50

Search completed: December 11, 2003, 14:11:33
Job time : 10.1403 secs

Query Match 6.6%; Score 122.5; DB 2; Length 480;
Best Local Similarity 32.4%; Pred. No. 0.00026;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;
Db 22 VDVRRDDPDHGNQOLMPKSNNDPNQWLTIRKQGTIRSNQS-CLTGYGYTGYVWF 80
QY 379 IDVPKNTADGTQVYLDCHSGS-NQMTYSSGSPRFGN-KCLDGGSSNAGVQIY 436
Db 81 CNTNRKRTIQTQINDGTITPNSULVLAASSGKRTITWQ 122
QY 437 CWGANQK-WELRADDTIVQSGCLDVGSGGTNGTRLO 476

Thu Dec 11 16:10:06 2003

us-09-601-667c-8.rpx

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 8.20622 Seconds
(Without alignments)
3093.817 Million cell updates/sec

Title: US-09-601-667C-8

Perfect score: 1414
Sequence: 1 DVTGSAEPTVTRVGRSGM.....RRITVATKRPQWMLPVF 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: PIR 76:*
2: Df1:*
3: PIR2:*
4: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1379	97.5	264	2	PD0019	mistletoe lectin I
2	1368.5	96.8	265	2	JM0090	lectin-I B chain -
3	896.5	63.4	576	1	RLCSD	ricin D precursor
4	863	61.0	263	2	S06330	ricin E - castor b
5	764.5	54.1	564	1	RLCSAG	agglutinin precurs
6	758	53.6	528	1	TLZSA	abrin-a precursor
7	744	52.6	527	2	S32430	abrin-b precursor
8	744	52.6	528	2	S32430	abrin-d precursor
9	744	52.5	528	2	S32430	abrin-g precursor
10	517	36.6	570	2	S62637	chitinase 1B39
11	129.5	9.2	377	2	JC7535	endo-1,4-beta-xyl
12	122.5	8.7	477	1	J50589	xylanase A - strep
13	119.5	8.5	383	2	T34603	probable hydrolase
14	113	8.0	464	2	T35943	glucan endo-1,3-be
15	108	7.6	548	2	A39094	arabinofuranosid
16	107.5	7.6	475	2	T35697	protease RPI - R
17	105	7.4	525	2	A45053	probable lipoprote
18	103.5	7.3	451	2	T34988	hypothetical prote
19	103.5	7.3	1067	2	T28663	hypothetical prote
20	103.5	7.3	891	2	T03244	hypothetical prote
21	94.5	6.7	591	2	B82414	probable adhesin h
22	93.5	6.6	476	2	B82414	actinobayn precu
23	93.5	6.6	1910	2	AF0394	WD-40 repeat prote
24	93	6.6	160	2	JC7622	polymorphic memba
25	91.5	6.5	1526	2	AC2239	polymorphic memba
26	90	6.4	1723	2	H86557	polymorphic memba
27	90	6.4	1723	2	E72067	polymorphic memba
28	90	6.4	1732	2	C81601	polymorphic memba
29	89.5	6.3	471	2	A41478	cytolysin vrbA pre

30	89.5	6.3	1708	2	AE1866	WD-40 repeat prote
31	88.5	6.3	722	2	H96986	endo-1,4-beta gluc
32	88.5	6.3	1008	2	T32986	hypothetical prote
33	88	6.2	295	2	H83452	probable short-cha
34	88	6.2	386	2	AE1996	hypothetical prote
35	87.5	6.2	326	2	AE1996	hypothetical prote
36	87.5	6.2	345	2	AE1996	hypothetical prote
37	87.5	6.2	345	2	AE1996	hypothetical prote
38	87.5	6.2	345	2	AE1996	hypothetical prote
39	87.5	6.2	345	2	AE1996	hypothetical prote
40	87	6.2	895	1	IXLCP	fimbriae-associate
41	86.5	6.1	1693	2	S76086	beta transducin-1i
42	86	6.1	875	2	I40862	icra toxin compone
43	86	6.1	943	2	S59317	D12 repeat - yea
44	86	6.1	1683	2	AE2071	WD-40 repeat prote
45	85.5	6.0	231	2	E20810	flagellar biosynth

ALIGNMENTS

```
RESULT 1
PD0019
mistletoe lectin I B chain - Viscum album (fragment)
C/Species: Viscum album
C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #ext_change 07-May-1999
C/Accession: PD0019
R/Eschscholm, S.; Kauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelker, W.
Biochem. Biophys. Res. Commun. 247, 367-372, 1998
A/Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum alb
A/Reference number: PD0019; MIMD:98308123; PMID:9642133
A/Accession: PD0019; MIMD:98308123; PMID:9642133
A/Molecule type: protein
A/Residues: 1-264 <BSC>
A/Superfamily: ricin; RNA N-glycosidase homology

Query Match          97.5% Score 1379; DB 2; Length 264;
Best local Similarity 97.7% / Predict. No. 1.3e-110;
Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVTGSAEPTVTRVGRSGMVDVDDPDGNOIOLMPSKSNPDNOLTKDNTIRS 60
DB 1 DVTGSAEPTVTRVGRSGMVDVDDPDGNOIOLMPSKSNPDNOLTKDNTIRS 60
QY 61 NGSCATVYGTAGVYVMPIDPQAVARERATVQINDGTINIPSSNIVLAASGKRTLT 120
DB 61 NGSCATVYGTAGVYVMPIDPQAVARERATVQINDGTINIPSSNIVLAASGKRTLT 120
QY 121 VQTLDTTGGWLAGNDTTFEFTVIGFRDLQMSNGSVVETCDSSQGNQKMAIYCD 180
DB 121 VQTLDTTGGWLAGNDTTFEFTVIGFRDLQMSNGSVVETCDSSQGNQKMAIYCD 180
QY 181 GSIRPNQDQCLTVGRDSVSTVINVSQASGSGRWFTNEVAILMKSGLMDVQA 240
DB 181 GSIRPNQDQCLTVGRDSVSTVINVSQASGSGRWFTNEVAILMKSGLMDVQA 240
QY 241 NPKLRRIITVATKRPQWMLPVF 264
DB 241 NPKLRRIITVATKRPQWMLPVF 264

RESULT 2
JW0090
lectin-I B chain - European mistletoe
M/Alternate names: NLI-I (European mistletoe)
C/Species: Viscum album
C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #ext_change 19-May-2000
C/Accession: JW0090
R/Giesler, M.H.; Stoeva, S.; Voelker, W.
Biochem. Biophys. Res. Commun. 246, 596-601, 1998
A/Title: Complete amino acid sequence of the B chain of mistletoe lectin I.
A/Reference number: JW0090; MIMD:98289575; PMID:9618256
A/Accession: JW0090
```

A/Molecule type: protein	
A/Residues: 1-265 <SOLO>	
C/Superfamily: ricin; xRNA N-glycosidase homology	
C/Keywords: Glycoprotein	
F/I/I_35_136/Binding site: carboxylate (asn) (covalent) #status experimental	
Query Match	96.8%; Score 136.6; Db 2; Length 265;
Best Local Similarity	97.4%; Pred. No. 1e-109;
Matches 258; Conservative 2; Mismatches 4; Indels 1; Gaps 1	
QY	1 DVTYSASFPFTRIVARSQNRVAVDDDFHDNDIQILPMSKSNDDPQWLTIKIDNITRS 60
Db	1 DVTYSASSEPTALIVARNQKMDVADDPHQNDIQILPMSKSNDDPQWLTIKIDNITRS 60
QY	61 NSGCTCYTRATKPKYKQNFECQNTNRTATQIINDGNTIINPESHVLAASGIKQITLT 120
Db	61 NSGCTCYTRATKPKYKQNFECQNTNRTATQIINDGNTIINPESHVLAASGIKQITLT 120
QY	121 VQGLDYLTLAQGLNLGNLDPAPEVITYGFRLDCHSNQSGVWVETDSSQNGKMLAYCD 180
Db	121 VQGLDYLTLAQGLNLGNLDPAPEVITYGFRLDCHSNQSGVWVETDSSQNGKMLAYCD 180
QY	181 GSIRKQNDQCLTAEQDSVSTYINIVYCSGASGSRWTFMEYALINIKSLDANVQA 240
Db	181 GSIRKQNDQCLTAEQDSVSTYINIVYCSGASGSRWTFMEYALINIKSLDANVQA 240
QY	241 NPELRRIITYPATCKSNQNW-LEPY 264
Db	241 NPELRRIITYPATCKSNQNW-LEPY 264
QY	241 NPELRRIITYPATCKSNQNW-LEPY 265
Db	241 NPELRRIITYPATCKSNQNW-LEPY 265

RESULT 3

riclin D precursor - castor bean
 M:Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C:Species: Ricinus communis (castor bean)
 C:Accession: J01393 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C:Release: 2404.1, S20513, A24614, A03372, A24010, A03374, S10501
 R:Publication: 118019, 118020, 118021, 118022, 118023, 118024, 118025, 118026, 118027, 118028, 118029, 118030, 118031, 118032, 118033, 118034, 118035, 118036, 118037, 118038, 118039, 118040, 118041, 118042, 118043, 118044, 118045, 118046, 118047, 118048, 118049, 118050, 118051, 118052, 118053, 118054, 118055, 118056, 118057, 118058, 118059, 118060, 118061, 118062, 118063, 118064, 118065, 118066, 118067, 118068, 118069, 118070, 118071, 118072, 118073, 118074, 118075, 118076, 118077, 118078, 118079, 118080, 118081, 118082, 118083, 118084, 118085, 118086, 118087, 118088, 118089, 118090, 118091, 118092, 118093, 118094, 118095, 118096, 118097, 118098, 118099, 118100, 118101, 118102, 118103, 118104, 118105, 118106, 118107, 118108, 118109, 118110, 118111, 118112, 118113, 118114, 118115, 118116, 118117, 118118, 118119, 118120, 118121, 118122, 118123, 118124, 118125, 118126, 118127, 118128, 118129, 118130, 118131, 118132, 118133, 118134, 118135, 118136, 118137, 118138, 118139, 118140, 118141, 118142, 118143, 118144, 118145, 118146, 118147, 118148, 118149, 118150, 118151, 118152, 118153, 118154, 118155, 118156, 118157, 118158, 118159, 118160, 118161, 118162, 118163, 118164, 118165, 118166, 118167, 118168, 118169, 118170, 118171, 118172, 118173, 118174, 118175, 118176, 118177, 118178, 118179, 118180, 118181, 118182, 118183, 118184, 118185, 118186, 118187, 118188, 118189, 118190, 118191, 118192, 118193, 118194, 118195, 118196, 118197, 118198, 118199, 118200, 118201, 118202, 118203, 118204, 118205, 118206, 118207, 118208, 118209, 118210, 118211, 118212, 118213, 118214, 118215, 118216, 118217, 118218, 118219, 118220, 118221, 118222, 118223, 118224, 118225, 118226, 118227, 118228, 118229, 118230, 118231, 118232, 118233, 118234, 118235, 118236, 118237, 118238, 118239, 118240, 118241, 118242, 118243, 118244, 118245, 118246, 118247, 118248, 118249, 118250, 118251, 118252, 118253, 118254, 118255, 118256, 118257, 118258, 118259, 118260, 118261, 118262, 118263, 118264, 118265, 118266, 118267, 118268, 118269, 118270, 118271, 118272, 118273, 118274, 118275, 118276, 118277, 118278, 118279, 118280, 118281, 118282, 118283, 118284, 118285, 118286, 118287, 118288, 118289, 118290, 118291, 118292, 118293, 118294, 118295, 118296, 118297, 118298, 118299, 118300, 118301, 118302, 118303, 118304, 118305, 118306, 118307, 118308, 118309, 118310, 118311, 118312, 118313, 118314, 118315, 118316, 118317, 118318, 118319, 118320, 118321, 118322, 118323, 118324, 118325, 118326, 118327, 118328, 118329, 118330, 118331, 118332, 118333, 118334, 118335, 118336, 118337, 118338, 118339, 118340, 118341, 118342, 118343, 118344, 118345, 118346, 118347, 118348, 118349, 118350, 118351, 118352, 118353, 118354, 118355, 118356, 118357, 118358, 118359, 118360, 118361, 118362, 118363, 118364, 118365, 118366, 118367, 118368, 118369, 118370, 118371, 118372, 118373, 118374, 118375, 118376, 118377, 118378, 118379, 118380, 118381, 118382, 118383, 118384, 118385, 118386, 118387, 118388, 118389, 118390, 118391, 118392, 118393, 118394, 118395, 118396, 118397, 118398, 118399, 118400, 118401, 118402, 118403, 118404, 118405, 118406, 118407, 118408, 118409, 118410, 118411, 118412, 118413, 118414, 118415, 118416, 118417, 118418, 118419, 118420, 118421, 118422, 118423, 118424, 118425, 118426, 118427, 118428, 118429, 118430, 118431, 118432, 118433, 118434, 118435, 118436, 118437, 118438, 118439, 118440, 118441, 118442, 118443, 118444, 118445, 118446, 118447, 118448, 118449, 118450, 118451, 118452, 118453, 118454, 118455, 118456, 118457, 118458, 118459, 118460, 118461, 118462, 118463, 118464, 118465, 118466, 118467, 118468, 118469, 118470, 118471, 118472, 118473, 118474, 118475, 118476, 118477, 118478, 118479, 118480, 118481, 118482, 118483, 118484, 118485, 118486, 118487, 118488, 118489, 118490, 118491, 118492, 118493, 118494, 118495, 118496, 118497, 118498, 118499, 118500, 118501, 118502, 118503, 118504, 118505, 118506, 118507, 118508, 118509, 118510

[illegible]

ricin E - castor bean (fragment)
 506330
 N/Contains: chain B; rRNA N-glycosidase (EC 3.2.2.22) (chain A)
 C/Species: Ricinus communis (castor bean)
 C/Accession: J1-Mar-1990 #sequence_revision 31-Mar-1990 #extl_change 20-Aug-1999
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #extl_change 16-Jul-1999
 R/Author: B.P. Murray, J.E. Halling, A.C. Halling, K.C. Takarame, N. Long, G.L. Plant Mol. Biol. 9, 287-295, 1997
 A/RTitle: The complete amino acid sequence of the B-chain of ricin E isolated from small
 A/Reference number: 506330
 A/Accession number: 506330
 A/Status: not compared with conceptual translation
 A/Molecule type: rRNA
 A/Residues: 1-263 <LMD>
 R/Author: B.P. Murray, J.E. Halling, A.C. Halling, K.C. Takarame, N. Long, G.L. Plant Mol. Biol. 9, 287-295, 1997
 A/RTitle: The complete amino acid sequence of the B-chain of ricin E isolated from small
 A/Reference number: JCS381, PMID 87101186; PMID:3801493
 A/Accession: JCS381
 A/Molecule type: Protein
 A/Residues: 1-69, 'PS', 'T', '209', 'A', '211-241, 243-250', 'V', '252-263 <ABA>
 C/Superfamily: ricin; rRNA N-glycosidase homology
 A/Experimental source: seed
 F/1-69, 69-100, 103-141, 148-183, 185-252, 255-263, 265-269, 270-272, 273-274, 275-276, 277-278, 279-280, 281-282, 283-284, 285-286, 287-288, 289-290, 291-292, 293-294, 295-296, 297-298, 299-300, 301-302, 303-304, 305-306, 307-308, 309-310, 311-312, 313-314, 315-316, 317-318, 319-320, 321-322, 323-324, 325-326, 327-328, 329-330, 331-332, 333-334, 335-336, 337-338, 339-340, 341-342, 343-344, 345-346, 347-348, 349-350, 351-352, 353-354, 355-356, 357-358, 359-360, 361-362, 363-364, 365-366, 367-368, 369-370, 371-372, 373-374, 375-376, 377-378, 379-380, 381-382, 383-384, 385-386, 387-388, 389-390, 391-392, 393-394, 395-396, 397-398, 399-400, 401-402, 403-404, 405-406, 407-408, 409-410, 411-412, 413-414, 415-416, 417-418, 419-420, 421-422, 423-424, 425-426, 427-428, 429-430, 431-432, 433-434, 435-436, 437-438, 439-440, 441-442, 443-444, 445-446, 447-448, 449-450, 451-452, 453-454, 455-456, 457-458, 459-460, 461-462, 463-464, 465-466, 467-468, 469-470, 471-472, 473-474, 475-476, 477-478, 479-480, 481-482, 483-484, 485-486, 487-488, 489-490, 491-492, 493-494, 495-496, 497-498, 499-500, 501-502, 503-504, 505-506, 507-508, 509-510, 511-512, 513-514, 515-516, 517-518, 519-520, 521-522, 523-524, 525-526, 527-528, 529-530, 531-532, 533-534, 535-536, 537-538, 539-540, 541-542, 543-544, 545-546, 547-548, 549-550, 551-552, 553-554, 555-556, 557-558, 559-560, 561-562, 563-564, 565-566, 567-568, 569-570, 571-572, 573-574, 575-576, 577-578, 579-580, 581-582, 583-584, 585-586, 587-588, 589-590, 591-592, 593-594, 595-596, 597-598, 599-600, 601-602, 603-604, 605-606, 607-608, 609-610, 611-612, 613-614, 615-616, 617-618, 619-620, 621-622, 623-624, 625-626, 627-628, 629-630, 631-632, 633-634, 635-636, 637-638, 639-640, 641-642, 643-644, 645-646, 647-648, 649-650, 651-652, 653-654, 655-656, 657-658, 659-660, 661-662, 663-664, 665-666, 667-668, 669-670, 671-672, 673-674, 675-676, 677-678, 679-680, 681-682, 683-684, 685-686, 687-688, 689-690, 691-692, 693-694, 695-696, 697-698, 699-700, 701-702, 703-704, 705-706, 707-708, 709-710, 711-712, 713-714, 715-716, 717-718, 719-720, 721-722, 723-724, 725-726, 727-728, 729-730, 731-732, 733-734, 735-736, 737-738, 739-740, 741-742, 743-744, 745-746, 747-748, 749-750, 751-752, 753-754, 755-756, 757-758, 759-760, 761-762, 763-764, 765-766, 767-768, 769-770, 771-772, 773-774, 775-776, 777-778, 779-780, 781-782, 783-784, 785-786, 787-788, 789-790, 791-792, 793-794, 795-796, 797-798, 799-800, 801-802, 803-804, 805-806, 807-808, 809-810, 811-812, 813-814, 815-816, 817-818, 819-820, 821-822, 823-824, 825-826, 827-828, 829-830, 831-832, 833-834, 835-836, 837-838, 839-840, 841-842, 843-844, 845-846, 847-848, 849-850, 851-852, 853-854, 855-856, 857-858, 859-860, 861-862, 863-864, 865-866, 867-868, 869-870, 871-872, 873-874, 875-876, 877-878, 879-880, 881-882, 883-884, 885-886, 887-888, 889-890, 891-892, 893-894, 895-896, 897-898, 899-900, 901-902, 903-904, 905-906, 907-908, 909-910, 911-912, 913-914, 915-916, 917-918, 919-920, 921-922, 923-924, 925-926, 927-928, 929-930, 931-932, 933-934, 935-936, 937-938, 939-940, 941-942, 943-944, 945-946, 947-948, 949-950, 951-952, 953-954, 955-956, 957-958, 959-960, 961-962, 963-964, 965-966, 967-968, 969-970, 971-972, 973-974, 975-976, 977-978, 979-980, 981-982, 983-984, 985-986, 987-988, 989-990, 991-992, 993-994, 995-996, 997-998, 999-1000, 1001-1002, 1003-1004, 1005-1006, 1007-1008, 1009-1010, 1011-1012, 1013-1014, 1015-1016, 1017-1018, 1019-1020, 1021-1022, 1023-1024, 1025-1026, 1027-1028, 1029-1030, 1031-1032, 10

A:Reference number: A24210
A:Acession: A24210

A:Molecule type: protein
A:Residues: 303-326; F, .327-.330, T, .332-.361, D, .363-373, G, .375-403, V, .405-551, Y, .55;
C:Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
D:Support family: ricinB_RNA_N-glycosylase homology
E:keywords: duplicate(s); glycoprotein; #status predicted; <SIG> hydroxylase; lectin; RNA binding; se
F:329-380; domain: signal sequence; #status predicted; <SIG> N-glycanase; hydrolase; catalytic site
F:325-380; domain: rRNA_N-glycosylase homology; cno<H>> <ACH>
F:305-584; domain: rRNA_N-glycosylase homology; cno<H>> <ACH>
F:313-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeat
F:34,259/Binding site: carboxydrate (asn) (covalent) #status predicted
F:104,147,211,232/Binding site: substrate (Tyr, Trp, Glu, Asn) #status predicted
F:200,203/Active site: Glu, Arg #status predicted
F:282-306,302-341,365-382,445-466,492-509/Disulfide bonds: #status predicted
F:324,337,349/Binding site: R-acetylargininecarbamate (asp, Asp, Asn) #status predicted
F:357/Binding site: carbonylarginine (asn) (covalent) #status experimental
F:336,357/Binding site: N-acetylgalactosamine (asp, Asn) #status predicted

Query Match Best Local Similarity 54.1%; Score 764.5; DB 1; Length 564;
Matches 143; Conservative 43; Mismatches 73; Indels 1; Gaps 1;

DY CSASEPTATVRSQGVTRVDKDDFDNDNQLOMPSSNNPDNQLMTIKEDYTIRNSGQC 64
Db CMDEPRPVALVSGMGLCVDTESFPDPANCLQMCKSMSTMNQMLTLRSDSTRNSGC 365
OY LTTGGTGAGTVGMIDPCDNRAETITINDGTINPSNTLTAASGCTKTGTTCYL 124
Db LTTSKSPPROOVYNISSTIVCATGWGDNRRTIIPSSGLVAATSNGSQTLLVCQN 425
OY DLTLGGTMAGNDVPSEVTLYIGFRRLCMESNGSVWSTCDSSQONQMKALVGDSISR 184
Db ITAVSQGPLTNTPGFVIITYLGVLGNCLANSNGWLDC-TSEAQQMALVADSIIR 484
OY ILSPKNOOCITVRGSVSFTINTSCSGASSQGAPTFHTXIALNLTKSLAMPDAQNEL 244
Db PQQRMDICLTLDANKETGYALLLCOPRSSQPWFCEODGITLNLELVDRSRSEL 544
OY RLRIITYPATGEKPOMILPEPV 264
Db KILLTHVFPHGNLMTEPLF 564

RESULT 6
Abirata precursor - Indian licorice (ferment)
N:Contains: rRNA_N-glycosylase (EC 3.2.2.22)
C:Species: Abura precatarius (Indian Licorice)
C>Date: 31-Dec-1993 #sequence revision 01-Aug-1997 #ext Change 16-Jul-1999
C:Acession: S34429; J70202; X9761; LCJ389; S44472; S24133; S74110; S74111
E:hung, C.H.; Lee, M.C.; Lee, T.C.; Tan, T.Y.
F: Mol. Biol. 229, 263-267, 1993
A>Title: Primary structure of three distinct isoforms determined by cdna sequencing. (
A:Reference number: S37429; NCBI:U9131798; PMID:8421313
A:Acession: U9131798
A:Molecule type: mRNA acid sequence not shown
A>Status nucleic
A:Residues: 78; 2-528 <HM>
A:Molecule type: mRNA
A:Cross-references: GB:I9894; NID:g166294; PIN:AA32624.1; PID:g166295
A>Note: The coding region for the gene shown is preceded by an ATG codon
A>Note: residues 1-8 were derived from the synthesized primer
F:Punaru, G.; Taguchi, Y.; Kamemoto, M.; Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988
A>Title: The complete amino acid sequence of the A-chain of abirin-a, a toxic protein fr
A:Acession: J70202

A:Molecule type: protein
A:Residues: 1-201,203-251 <FM>
A>Note: the amino-terminal residue forms pyrroldione carboxylic acid; they have
E:Iverson, G.; Mahlessen, A.; Sundan, A.
Bio. Chem. 266, 6848-6852, 1991

A:Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A:Reference number: A39761; PMID:91201329; PMID:2016300
A:Accession: A39761
A:Status: nucleic acid sequence not shown
A:Species: *Canis lupus familiaris*
A:Residues: 177, 2-251 <EVS>
A:Cross-references: GB:X54872
A:Note: residues 1-8 were derived from the synthesized primer
R:Kimura, M.; Sumizawa, T.; Panatier, G.
R:Bioest. Biotechnol. Biochem. 57, 166-169, 1993
A:Title: The complete amino acid sequence of the B-chains of abrin-a and abrin-b, toxic
A:Reference number: J01398; PMID:53165023; PMID:7763422
A:Accession: J01398
A:Status: protein
A:Molecule type: protein
A:Residues: 261-347, 'V', 349-351, 'V', 353-357, 'L', 359-528 <XIM>
A:Experimental source: seed
R:Evensen, G.; Mathiesen, A.; Sundan, A.
A:Description: Direct molecular cloning of two distinct abrin A-chains.
A:Reference number: S14471
A:Accession: S14472
A:Status: protein
A:Molecule type: DNA
A:Residues: 'ME', 2-251 <EVZ>
A:Cross-references: EMBL:X54873; NID:g1609; PIDD:CA38655.1; PID:g16091
R:Chen, Y.L.; Chow, L.P.; Tengsta, A.; Lin, Y.Y.
FEBS Lett. 309, 115-118, 1992
A:Title: The complete primary structure of abrin-a B chain.
A:Reference number: S24133; PMID:9237356; PMID:1505674
A:Accession: S24133
A:Status: protein
A:Molecule type: protein
A:Residues: 262-297, 'Y', 299-425, 'V', 428-466, 'P', 466-482, 'V', 484-528 <CBE>
R:Lin, S.H.; Chow, L.P.; Chen, Y.C.; Lin, Y.C.; Chen, Y.K.; Lin, Y.Y.
Eur. J. Biochem. 240, 564-569, 1996
A:Title: Probing the domain structure of abrin-a by tryptic digestion.
A:Reference number: S74110; PMID:97008945; PMID:8856055
A:Accession: S74110
A:Status: protein
A:Molecule type: protein
A:Residues: 104-104, 472 <LIN>
A:Experimental source: seed
A:Molecule type: protein
A:Accession: S74111
A:Status: protein
A:Residues: 262-276, 'X', 278-280, 329-348, 369-388, 399-418 <LIN>
A:Experimental source: seed
A:Comment: Abtin-a is more toxic than ricin. The toxin consists of an A chain, which inhibits
cloning receptors on the cell surface. The B chains are linked by a single disulfide
A:Superfamily: ricin; rRNA N-glycosidase homology
P:1-551/Product: abrin; glycosyltransferase; hydrolase; lectin; pyroglyutamic acid
F:7-246/Domains: rRNA N-glycosidase homology <RNG> lectin <LCT>
F:7-246/Domains: rRNA N-glycosidase homology <RNG> lectin <LCT>
F:283-325, 326-366, 369-407, 414-447, 453-492, 495-528/Region: 40-residue repeats
F:1/Modified sites: pyroglutamic carboxylic acid (gln) #status experimental
F:14, 113, 159, 196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:164, 157/Active sites: Gln, Arg #status predicted
F:164, 157/Disulfide bonds: 146-430, 166-473/disulfide bonds: #status predicted
F:288, 312/Binding site: carbohydrate (Asn) covalent #status predicted
F:361-411/Binding site: carbohydrate (Asn) covalent #status predicted
F:500, 551/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

[illegible]

RESULT 8
A:Cross-references: Indian licorice
A:Residues: 1-562 <IND>
A:Reference number: S16022
A:Accession: S16022
A:Title: Preprobrutin: genomic cloning, characterization and the expression of the A-chain
A:Reference number: S16022; PMID:91266957; PMID:2050149
A:Status: Preliminary
A:Residues: 1-562 <IND>
A:Residues: 1-562 <IND>
A:Comment: A chain consists of an A chain which inhibits protein synthesis by inactivating
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglycamic acid
F/35-285/Product: abrin-c chain A #status predicted <RNG>
F/41-280/Domain: RNA N-glycosidase homology <RNG>
F/295-562/Product: abrin-c chain B #status predicted <RNG>
F/311-359/380-400, 403-441, 448-483, 487-526, 529-562/Region: 40-residue repeats
F/306/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F/198-201/Active site: Arg #status predicted (Asn) (covalent) #status predicted
F/234-287, 395-435, 436/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/281-303, 320-339, 363-380, 451-464, 480-507/Disulfide bonds: 2 #status predicted
F/322, 346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/534, 555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
Query Match 52.6%; Score 744; DB 2; Length 562;
Best Local Similarity 53.6%; Pred. No. 7, 8e-56;
Matches 140; Conservative 42; Mismatches 77; Indels 2; Gaps 2;
QY 5 CSAS-EPTVAIVGSGRWVDYDDDFDHQIQOLMPKSNNDPNQWLTIRKNTIRNSGS 63
DB 303 CSKRREPTVIRIGRDQKQCVDDYDDDFDHQIRKNTIRKNCORLENOQWLTIRKNSGK 362
QY 64 CLTVGYTAGVYVTFDQNTAVREATITNGINDGTTINPNSVTLAASGIGKTLTYGT 123
DB 363 CLTTEGVAPGVYVITDCTSAVAETVWEINDGTTINPNSVTLAASGIGKTLTYGT 422
QY 124 LDYTLQGMVLAGNDTAPREVTIYGFDDLOHESNQSVWETGDSQKQKMAVYGGSI 183
DB 423 NSEIVMRQKRTGNTNTPPTVTSIGYSDLCQKQKSNVWALDDNNKKQ-QVALVTGSI 481
QY 164 RKQNDQCLTVGRDSVTVINIVCSGASGSGRWVTFEYATILNKSGIADVYQANPK 243
DB 482 RYQNTNNTCLTSKDKQSGPTVWASQKSNVWALDDNNKKQ-QVALVTGSI 541
QY 244 LRRIITYPATGKQKQWLPVF 264
DB 542 LREIILHPHKGKQKQWLPVF 562

RESULT 9
A:Cross-references: Indian licorice (fragment)
A:Residues: 1-562 <IND>
A:Reference number: S16022
A:Accession: S16022
A:Title: Preprobrutin: genomic cloning, characterization and the expression of the A-chain
A:Reference number: S16022; PMID:91266957; PMID:2050149
A:Status: Preliminary
A:Residues: 1-562 <IND>
A:Residues: 1-562 <IND>
A:Comment: A chain consists of an A chain which inhibits protein synthesis by inactivating
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglycamic acid
F/35-285/Product: abrin-c chain A #status predicted <RNG>
F/41-280/Domain: RNA N-glycosidase homology <RNG>
F/295-562/Product: abrin-c chain B #status predicted <RNG>
F/311-359/380-400, 403-441, 448-483, 487-526, 529-562/Region: 40-residue repeats
F/306/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F/198-201/Active site: Arg #status predicted (Asn) (covalent) #status predicted
F/234-287, 395-435, 436/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/281-303, 320-339, 363-380, 451-464, 480-507/Disulfide bonds: 2 #status predicted
F/322, 346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/534, 555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
Query Match 52.6%; Score 744; DB 2; Length 562;
Best Local Similarity 53.6%; Pred. No. 7, 8e-56;
Matches 140; Conservative 42; Mismatches 77; Indels 2; Gaps 2;
QY 5 CSAS-EPTVAIVGSGRWVDYDDDFDHQIQOLMPKSNNDPNQWLTIRKNTIRNSGS 63
DB 303 CSKRREPTVIRIGRDQKQCVDDYDDDFDHQIRKNTIRKNCORLENOQWLTIRKNSGK 362
QY 64 CLTVGYTAGVYVTFDQNTAVREATITNGINDGTTINPNSVTLAASGIGKTLTYGT 123
DB 363 CLTTEGVAPGVYVITDCTSAVAETVWEINDGTTINPNSVTLAASGIGKTLTYGT 422
QY 124 LDYTLQGMVLAGNDTAPREVTIYGFDDLOHESNQSVWETGDSQKQKMAVYGGSI 183
DB 423 NSEIVMRQKRTGNTNTPPTVTSIGYSDLCQKQKSNVWALDDNNKKQ-QVALVTGSI 481
QY 164 RKQNDQCLTVGRDSVTVINIVCSGASGSGRWVTFEYATILNKSGIADVYQANPK 243
DB 482 RYQNTNNTCLTSKDKQSGPTVWASQKSNVWALDDNNKKQ-QVALVTGSI 541
QY 244 LRRIITYPATGKQKQWLPVF 264
DB 542 LREIILHPHKGKQKQWLPVF 562

RESULT 10
A:Cross-references: European elder
A:Residues: 1-570 <VAN>
A:Reference number: S62627
A:Accession: S62627
A:Title: The Neuc(a)lpha-2-(6)-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)
A:Reference number: S62619; PMID:96202262; PMID:8631119
A:Status: Preliminary
A:Residues: 1-570 <VAN>
A:Residues: 1-570 <VAN>
A:Comment: A chain consists of an A chain, which inhibits protein synthesis by inactivating
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglycamic acid
F/35-285/Product: abrin-c chain A #status predicted <RNG>
F/41-280/Domain: RNA N-glycosidase homology <RNG>
F/295-562/Product: abrin-c chain B #status predicted <RNG>
F/311-359/380-400, 403-441, 448-483, 487-526, 529-562/Region: 40-residue repeats
F/306/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F/198-201/Active site: Arg #status predicted (Asn) (covalent) #status predicted
F/234-287, 395-435, 436/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/281-303, 320-339, 363-380, 451-464, 480-507/Disulfide bonds: 2 #status predicted
F/322, 346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/534, 555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
Query Match 52.5%; Score 743; DB 2; Length 528;
Best Local Similarity 53.6%; Pred. No. 8, 7e-56;
Matches 140; Conservative 43; Mismatches 76; Indels 2; Gaps 2;
QY 5 CSAS-EPTVAIVGSGRWVDYDDDFDHQIQOLMPKSNNDPNQWLTIRKNTIRNSGS 63
DB 269 CSKRREPTVIRIGRDQKQCVDDYDDDFDHQIRKNTIRKNCORLENOQWLTIRKNSGK 328
QY 64 CLTVGYTAGVYVTFDQNTAVREATITNGINDGTTINPNSVTLAASGIGKTLTYGT 123
DB 329 CLTTEGVAPGVYVITDCTSAVAETVWEINDGTTINPNSVTLAASGIGKTLTYGT 386
QY 124 LDYTLQGMVLAGNDTAPREVTIYGFDDLOHESNQSVWETGDSQKQKMAVYGGSI 183
DB 389 NSEIVMRQKRTGNTNTPPTVTSIGYSDLCQKQKSNVWALDDNNKKQ-QVALVTGSI 447
QY 164 RKQNDQCLTVGRDSVTVINIVCSGASGSGRWVTFEYATILNKSGIADVYQANPK 243
DB 448 RYQNTNNTCLTSKDKQSGPTVWASQKSNVWALDDNNKKQ-QVALVTGSI 507
QY 244 LRRIITYPATGKQKQWLPVF 264
DB 508 LKQIILHPHKGKQKQWLPVF 528

RESULT 11
A:Cross-references: European elder
A:Residues: 1-570 <VAN>
A:Reference number: S62627
A:Accession: S62627
A:Title: The Neuc(a)lpha-2-(6)-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)
A:Reference number: S62619; PMID:96202262; PMID:8631119
A:Status: Preliminary
A:Residues: 1-570 <VAN>
A:Residues: 1-570 <VAN>
A:Comment: A chain consists of an A chain, which inhibits protein synthesis by inactivating
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglycamic acid
F/35-285/Product: abrin-c chain A #status predicted <RNG>
F/41-280/Domain: RNA N-glycosidase homology <RNG>
F/295-562/Product: abrin-c chain B #status predicted <RNG>
F/311-359/380-400, 403-441, 448-483, 487-526, 529-562/Region: 40-residue repeats
F/306/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F/198-201/Active site: Arg #status predicted (Asn) (covalent) #status predicted
F/234-287, 395-435, 436/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/281-303, 320-339, 363-380, 451-464, 480-507/Disulfide bonds: 2 #status predicted
F/322, 346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/534, 555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
Query Match 52.5%; Score 743; DB 2; Length 528;
Best Local Similarity 53.6%; Pred. No. 8, 7e-56;
Matches 140; Conservative 43; Mismatches 76; Indels 2; Gaps 2;
QY 5 CSAS-EPTVAIVGSGRWVDYDDDFDHQIQOLMPKSNNDPNQWLTIRKNTIRNSGS 63
DB 269 CSKRREPTVIRIGRDQKQCVDDYDDDFDHQIRKNTIRKNCORLENOQWLTIRKNSGK 328
QY 64 CLTVGYTAGVYVTFDQNTAVREATITNGINDGTTINPNSVTLAASGIGKTLTYGT 123
DB 329 CLTTEGVAPGVYVITDCTSAVAETVWEINDGTTINPNSVTLAASGIGKTLTYGT 386
QY 124 LDYTLQGMVLAGNDTAPREVTIYGFDDLOHESNQSVWETGDSQKQKMAVYGGSI 183
DB 389 NSEIVMRQKRTGNTNTPPTVTSIGYSDLCQKQKSNVWALDDNNKKQ-QVALVTGSI 447
QY 164 RKQNDQCLTVGRDSVTVINIVCSGASGSGRWVTFEYATILNKSGIADVYQANPK 243
DB 448 RYQNTNNTCLTSKDKQSGPTVWASQKSNVWALDDNNKKQ-QVALVTGSI 507
QY 244 LRRIITYPATGKQKQWLPVF 264
DB 508 LKQIILHPHKGKQKQWLPVF 528

	Matches	115,	Conservative	32,	Mismatches	100,	Indels	12,	Gaps	6,
Qy	5	CSASEPTVIVGSGARVDEVD	PFHDCNOLOLMSKNNPDL	LTXTXNDITRNSVSC	64					
Db	316	CSVEVETRIISGMDGLCADVRG	YHIDNPVOLF--	CSNECNDLWTFPRDITGIRMLGIC	373					
Qy	65	LITVGGVAGVYVMI	PDCTVNEKRTITMOJMDNTI	INFSNLI	VAASGIGKFTLVQTL	124				
Dy	374	L--T--TASSMVIYDNC	IVPEKATVWYSIDITITP	SHGLVLTVA	POAABGSLSTENR	428				
Qy	125	YLTGGGHTACGNTPA	PSATYIYGRDL	CHSEN--	QSGVETFCSSGQSGKNAI	YDGS	162			
Dy	429	HAARQGWTVG--DYEL	LVETLITVYKQK	CLASBNSQWFTN	ELCTALRQD--	EMHLYDGT	466			
Qy	183	IIPKPNODCLTVGRDS	SVTVINIVSG	CSAASQGWFTN	ELTZALMLSG	LDVNDPAAQ	242			
Dy	487	IKVNSNRSILCTSE	DEHSDLDLIVLKCRG--	SAGQWTFVFN	NGTISVPAKL	LDVNDPQDV	545			
Qy	243	KLRRLIIVPATGK	ENQML	261						
Dy	546	SLRKIIIVKPTG	ENQMI	564						

RESULT 11

UC7535
Chitinase [BC 3.2.1.14] 35 - Streptomyces thermoviolaceus
C:Species: Streptomyces thermoviolaceus
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #ext_change 30-Jun-2001
C:Accession: UC7535
R:Fujisawa, H.; Okamoto, T.; Harano, N.; Miyamoto, K.; Watanabe, T.; Mitsutomi, M.; Inamori, A.; Hiroseki, Y.
Biosci., Biotechnol., Biochem., 64, 2445-2453, 2000
A>Title: Family 19 chitinases from Streptomyces thermoviolaceus OPC-520: Molecular cloning,
A:Reference number: UC7535; PMID:21036907; PMID:11199414
A:Accession: UC7535
A:Molecule type: DNA
A:Residues: 1-377 <TSU>
A:Cross-references: DDBJ:A016842
C:Experimental source: strain OPC-520
C:Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin degradation by Streptomyces thermoviolaceus.
C:Enthetic:
L:Lysochitinase-binding domain that is important in the efficient hydrolysis of insoluble d
A:Gene: chi35
A:Keywords: glycosylase; hydrolase

[illegible]

RESULT 12
J50589
end-1,4-beta-xylosylase (EC 3.2.1.8) A precursor - Streptomyces lividans
N:Alternate names: xylosylase A

C.Species: Streptomyces lividans
C.Date: 10-Mar-1994 #sequence_rev:revision 22-Nov-1996 #ext_change 26-Feb-1999
A.Accession: J050589; P80238
R.Shareck, F.; Roy, C.; Yasuchi, M.; Morosoli, R.; Kluepfel, D.
Gene 107, 75-92, 1991
A.Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A.Accession: J050589; M018747439; PMID:1743521
A.Molecule type: DNA
A.Residues: 1-477 <SHA>
A.Cross-references: GB:M64551
A.Molecule type: Protein
A.Name: XylA
C.Genetics: 42-92 <SMZ>
A.Gene: xlnA
C.Function:
A.Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A.Pathway: xylan degradation
C.Superfamily: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-xylanase B; Keywords: extracellular protein, glycosylase, hydrolase, polysaccharide degradation
F:1-2-477/Product: endo-1,4-beta-xylanase A [status experimental <MT>
F:1-2-4-341/Domains: Streptomyces endo-1,4-beta-xylanase A homology <SXY>
F:169,207/Active site: Glu #status predicted

Query Match	9.7%	Score 123.5	DB 1	Length 477
Best Local Similarity	92.9%	Pctd No 0	01	
Matches 40	Conservative 19	Mismatches 62	Indels 13	Gaps 6
Qy	7	AESP-----	TYRAYSQSMVAVRDQDFHDKNQIQQLAMSSKNNDNDLMTYRKANTIRSN	61
Db	346	SSSPADGQIKRG-SG	SRCLDVPDASTDSTQLQIMCSCSG--NOQAATDAGRLRY	402
Qy	62	G-SCLITATGYATGYT	PFQNTAREATQQLINDGIIINPSLWLA--SSGIKQT	118
Db	403	GCLDITATGSSKTIQ	YQICGNGNKK--WMASSSVYQGSCLDIAWNTFANITL	460
Qy	119	LVTQTLDTYLQSQN	132	
Db	461	IDLATYCSNSNGNR	474	

```

RESULT 13
T34603
Xylanase A - Streptomyces coelicolor (fragment)
C.Species: Streptomyces coelicolor
C.Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 28-Jul-2000
C.Accession: T34603
R.Murphy, L. J. Harris, D. J. Parkhill, J. J. Barrell, B. G. Bagdikian, M. A.
submitted to the EMBL Data Library, January 1998
A.Reference number: Z21548
A.Accession: T34603
A.Structure: preliminary; translated from GB/EMBL/DBJ
T34603
A.Position: 17383 <MB>
A.Cross-references: EMBL:AL021529; PINO:CAAL468.1; GSDB:G000070; SCEEBA:SC10A5.36C
A.Experimental source: strain A3(2)
C.Genetics:
A.Gene: xlnA; SCEEBA:SC10A5.36C
C.Superfamily: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-xylan
11-247; Domain: Streptomyces endo-1,4-beta-xylanase A homology <SV>

```

	Query Match	8.5%	Score 119.51	B2	length 383
	Best local	Similarity 29.9%	Pred. No. 0.0124		
	Matches	40	Conservative	18	Mismatches 63
					Indels 13
Qy	7 ASP-----TRIVGSGMGRVYEDFDHNGIQGLWASGKNDDEPLKTRIGRTREN	61			
Dh	252 SEEPAPDQGLQKCG--GSRCLDVPASTSDGGLQLQMLCHSGG--NQGVAARDGELFLV	308			
Oy	62 G-SCTTGTGTDVYMYEIPONTNREATITQINDGCTINFSNULIA--SGAIKTT	118			

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protease - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 4.53677 Seconds

(without alignments)

2736.539 Million cell updates/sec

Title: US-09-601-667C-8

Perfect score: 1414

Sequence: 1 DDTGCSASEPTVRIYVNSGM.....RRIIYPAKGNQWLPVF 264

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1379	97.5	264	1 MIB_VITNL
2	896.5	63.4	596	1 RICI_RICCO
3	764.5	54.1	564	1 AGGL_RICCO
4	758	53.6	528	1 ABRA_ARPP
5	744	52.6	527	1 ABRC_ARPP
6	744	52.6	562	1 ABRC_ARPP
7	516.5	36.5	563	1 NIGB_SAMNI
8	122.5	8.7	477	1 XYNA_STRLI
9	108	7.6	348	1 E11B_ARPP
10	107.9	7.6	348	1 E11B_ARPP
11	107.9	7.6	348	1 E11B_ARPP
12	105	7.4	525	1 SPI_ESTR
13	104.5	7.4	475	1 ABRA_STRLI
14	91.5	6.5	1526	1 Y146_AANSP
15	90	6.4	1723	1 PM40_CHLPM
16	87.5	6.2	545	1 AGAL_ASPNP
17	87.5	6.2	827	1 Y223_METVA
18	87.5	6.2	1258	1 YS00_AANSP
19	87	6.2	880	1 CADP_XANLA
20	86.5	6.1	1693	1 Y163_YANV3
21	86	6.1	1943	1 D1E2_YANST
22	85	6.1	1483	1 Y124_AANSP
23	85	6.0	1054	1 RPOC_XERPA
24	85	6.0	1054	1 RPOC_XERPA
25	84.5	6.0	231	1 F1CD_PICOLI
26	84.5	6.0	288	1 Y146_AANSP
27	84.5	6.0	1577	1 HLYA_PICOM
28	84.5	6.0	1577	1 HLYA_PICOM
29	84	5.9	1265	1 RPOD_CVAPN
30	84	5.9	4074	1 PKMD_HUMAN
31	82.5	5.8	471	1 V14A_VIBUV
32	82.5	5.8	510	1 Y14D_SCHPO
33	82	5.8	510	1 Y14D_SCHPO
				064226 mycobacteri

ALIGNMENTS

Result ID	Query	DB ID	Description	Score	Query Length	DB ID	Description
1	MIB_VITNL	264	1 MIB_VITNL	1379	97.5	264	1 MIB_VITNL
2	RICI_RICCO	596	1 RICI_RICCO	896.5	63.4	596	1 RICI_RICCO
3	AGGL_RICCO	564	1 AGGL_RICCO	764.5	54.1	564	1 AGGL_RICCO
4	ABRA_ARPP	528	1 ABRA_ARPP	758	53.6	528	1 ABRA_ARPP
5	ABRC_ARPP	527	1 ABRC_ARPP	744	52.6	527	1 ABRC_ARPP
6	ABRC_ARPP	562	1 ABRC_ARPP	744	52.6	562	1 ABRC_ARPP
7	NIGB_SAMNI	563	1 NIGB_SAMNI	516.5	36.5	563	1 NIGB_SAMNI
8	XYNA_STRLI	477	1 XYNA_STRLI	122.5	8.7	477	1 XYNA_STRLI
9	E11B_ARPP	348	1 E11B_ARPP	108	7.6	348	1 E11B_ARPP
10	E11B_ARPP	348	1 E11B_ARPP	107.9	7.6	348	1 E11B_ARPP
11	E11B_ARPP	348	1 E11B_ARPP	107.9	7.6	348	1 E11B_ARPP
12	SPI_ESTR	525	1 SPI_ESTR	105	7.4	525	1 SPI_ESTR
13	ABRA_STRLI	475	1 ABRA_STRLI	104.5	7.4	475	1 ABRA_STRLI
14	Y146_AANSP	1526	1 Y146_AANSP	91.5	6.5	1526	1 Y146_AANSP
15	PM40_CHLPM	1723	1 PM40_CHLPM	90	6.4	1723	1 PM40_CHLPM
16	AGAL_ASPNP	545	1 AGAL_ASPNP	87.5	6.2	545	1 AGAL_ASPNP
17	Y223_METVA	827	1 Y223_METVA	87.5	6.2	827	1 Y223_METVA
18	YS00_AANSP	1258	1 YS00_AANSP	87.5	6.2	1258	1 YS00_AANSP
19	CADP_XANLA	880	1 CADP_XANLA	87	6.2	880	1 CADP_XANLA
20	Y163_YANV3	1693	1 Y163_YANV3	86.5	6.1	1693	1 Y163_YANV3
21	D1E2_YANST	1943	1 D1E2_YANST	86	6.1	1943	1 D1E2_YANST
22	Y124_AANSP	1483	1 Y124_AANSP	85	6.1	1483	1 Y124_AANSP
23	RPOC_XERPA	1054	1 RPOC_XERPA	85	6.0	1054	1 RPOC_XERPA
24	RPOC_XERPA	1054	1 RPOC_XERPA	85	6.0	1054	1 RPOC_XERPA
25	F1CD_PICOLI	231	1 F1CD_PICOLI	84.5	6.0	231	1 F1CD_PICOLI
26	Y146_AANSP	288	1 Y146_AANSP	84.5	6.0	288	1 Y146_AANSP
27	HLYA_PICOM	1577	1 HLYA_PICOM	84.5	6.0	1577	1 HLYA_PICOM
28	HLYA_PICOM	1577	1 HLYA_PICOM	84.5	6.0	1577	1 HLYA_PICOM
29	RPOD_CVAPN	1265	1 RPOD_CVAPN	84	5.9	1265	1 RPOD_CVAPN
30	PKMD_HUMAN	4074	1 PKMD_HUMAN	84	5.9	4074	1 PKMD_HUMAN
31	V14A_VIBUV	471	1 V14A_VIBUV	82.5	5.8	471	1 V14A_VIBUV
32	Y14D_SCHPO	510	1 Y14D_SCHPO	82.5	5.8	510	1 Y14D_SCHPO
33	Y14D_SCHPO	510	1 Y14D_SCHPO	82	5.8	510	1 Y14D_SCHPO
	064226 mycobacteri	617	1 064226 mycobacteri	82	5.8	617	1 064226 mycobacteri

FT VARIANT 231 231 N -> S OR T.
FT VARIANT 231 233 NGL -> KGP.
FT VARIANT 232 235 GLAM -> SLAV.
SQ SEQUENCE 264 AA; 28981 MW; 7D0DC26CFCF5A4 CRC64;
Query Match 97.5%; Score 1379; DB 1; Length 264;
Best Local Similarity 97.7%; Pred. No. 3,6e-112;
Matches 259; Conservative 2; Misses 4; Indels 0; Gaps 0;
QY 1 DPTCCASPTVRIYVRSQARVDPDDPHQNOQLMPKSNDDPVLMTIKENTIS 60
DB 1 DPTCCASPTVRIYVRSQARVDPDDPHQNOQLMPKSNDDPVLMTIKENTIS 60
QY 61 NSGCLTVYGYTGYVYVWIPDCTAVRENTIMQIMNGIINFRSNVLAASGIGKTTLT 120
DB 61 NSGCLTVYGYTGYVYVWIPDCTAVRENTIMQIMNGIINFRSNVLAASGIGKTTLT 120
QY 121 VOTLDITLQGNLAQNTAPREVTITVFDDICENSGSYWETCGSSQKQGNALXED 180
DB 121 VOTLDITLQGNLAQNTAPREVTITVFDDICENSGSYWETCGSSQKQGNALXED 180
QY 181 GSIRKONODCLTVGEPSTVNTIVSGASGSGWPTFEVAILNLSGLADVNAK 240
DB 181 GSIRKONODCLTVGEPSTVNTIVSGASGSGWPTFEVAILNLSGLADVNAK 240
QY 241 NPKLRRIIYVATGKKNQWLPVP 264
DB 241 NPKLRRIIYVATGKKNQWLPVP 264
RESU" 2
ID RICI RICO STANDARD; PRT; 576 AA.
AC P02879; P02880;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ricin precursor (Contains: Ricin A chain (cRNA N-glycosidase)
DE (EC 3.2.2.22) / Ricin B chain)
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosidae; I; Malpighiales; Euphorbiales; Ricinus.
OC NCBI TaxID=3989;
RN 111 TextID=3989;
RP SEQUENCE FROM N.A.
RX MEDLINE=85179479; PubMed=3839723;
RA Halling K.C.; Halling A.C.; Murray E.E.; Ladin B.F.; Houston L.L.;
RA Weaver R.F.;
RT "Genomic cloning and characterization of a ricin gene from Ricinus
RT communis."
RL Nucleic Acids Res. 13:8019-8033(1985).
RN 121
RP SEQUENCE FROM N.A.
RX MEDLINE=92433016; PubMed=171405;
RA Trepanier J.; Robert J.M.;
RT "The lectin gene family of Ricinus communis: cloning of a functional
RT ricin gene and three lectin pseudogenes."
RL Plant Mol. Biol. 18:515-525(1992).
RN 131
RP SEQUENCE OF 12-576 FROM N.A.
RX MEDLINE=85179479; PubMed=3839723;
RA Lamb A.; Roberts L.M.; Lord J.M.;
RT "Nucleotide sequence of cloned cDNA coding for preproricin."
RL Eur. J. Biochem. 148:265-270(1985).
RN 141
RP SEQUENCE OF 36-302
RX Yoshitake S.; Funatsu G.; Funatsu M.;
RT "Isolation and sequences of peptide peptides, and the complete
RT sequence of the chain of ricin-D."
RL Agric. Biol. Chem. 42:1267-1274(1978).
RN 151
RP SEQUENCE OF 315-576.
RA Funatsu G.; Kimura M.; Funatsu M.;
RT "Primary structure of Ala chain of ricin D."
RL Agric. Biol. Chem. 43:2221-2224(1979).
RN 161
RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
RX MEDLINE=90344223; PubMed=1368517;
RA Kimura Y.; Kusuku H.; Tada M.; Takagi S.; Funatsu G.;
RT "Structural analyses of sugar chains from ricin A-chain variant."
RL Agric. Biol. Chem. 54:157-162(1990).
RN 171
RP REVIEW.
RX MEDLINE=21480122; PubMed=1159654;
RA Olness S.; Kozlov J.V.;
RT "Ricin."
RL Toxicon 39:1723-1728(2001).
RN 181
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=87165983; PubMed=3558397;
RA Kohnfort M.; Villalobos J.E.; Monzinger A.P.; Ernst S.R.; Katzin B.;
RT "The three-dimensional structure of ricin A-chain at 2.8 A."
RL J. Biol. Chem. 262:5398-5403(1987).
RN 191
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=93352004; PubMed=1681881;
RA Katzin B.J.; Collins B.J.; Robertus J.D.;
RT "Structure of ricin A-chain at 2.5 A."
RL Proteins 10:251-259(1991).
RN 201
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
RX MEDLINE=91352005; PubMed=1681882;
RA Robertus J.D.;
RT "Structure of ricin B-chain at 2.5-A resolution."
RL Proteins 10:260-269(1991).
RN 211
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=95082010; PubMed=7990130;
RA Weston S.A.; Tucker A.D.; Thatcher D.R.; Derbyshire D.J.;
RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution."
RL J. Mol. Biol. 244:410-422(1994).
RN 221
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF MUTANT HIS-215.
RX MEDLINE=96374222; PubMed=8706513;
RA Dwyer J.D.; Smith M.C.; Robertus J.D.; Monzinger A.P.; Pascal J.M.;
RT "Structure and activity of an active site substitution of ricin A
RT chain."
RL Biochemistry 35:11098-11103(1996).
RN 231
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=97240820; PubMed=906280;
RA Yan X.; Hollis T.; Syvith M.; Day P.; Monzinger A.F.; Milne G.W.;
RT "Structure-based identification of a ricin inhibitor."
RL J. Mol. Biol. 266:1043-1049(1997).
RN 241
RP MUTAGENESIS.
RX MEDLINE=93165632; PubMed=1287657;
RA Kin Y.; Robertus J.D.;
RT "Analysis of several key active site residues of ricin A chain by
RT mutagenesis and X-ray crystallography."
RL Protein Eng. 5:775-779(1992).
RN 251
RP -1- FUNCTION: Ricin is highly toxic to animal cells and to a less
RP extent to plant cells. The A chain is responsible for inhibiting
RP protein synthesis through the catalytic inactivation of 60S
RP ribosomal subunits. It acts as a glycosylase that removes a
RP 280 kDa protein from the cell surface. The B chain is responsible for
RP binding to the cell surface. The modified ribosomes are unable to support protein
RP synthesis. The A chain can inactivate a few thousand ribosomes
RP per minute, thus inactivating them faster than the cell can make
RP new ones. A single A-chain molecule can therefore kill an animal

CC cell. The B chain binds to cell receptors and facilitates the
CC entry into the cell of the A chain; B chains are also responsible
CC for cell agglutination (lectin activity). It binds to beta-D-
CC galactopyranoside moieties.
CC
CC CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC
CC -1- SUBUNIT: Disulfide-linked dimer of A and B chains.
CC
CC -1- DOMAIN: The B chain is composed of two domains, each domain
CC consists of 3 homologous subdomains (alpha, beta, gamma).
CC -1- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE
CC MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 221.
CC
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.
CC
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC
CC -1- CAUTION: REF. 4 AND REF. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
CC WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
CC
CC DATABASE: NAME=Protein Spotlight;
CC
CC NOTE=Issue 31 of February 2003;
CC
CC WWW=http://www.expasy.org/spotlight/articles/spclt031.html".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: X03179; CA26939.1; -;
CC EMBL: X52908; CA37095.1; -;
CC EMBL: X02388; CA26230.1; -;
CC EMBL: A12892; CA01058.1; -;
CC PIR: A24041; RLCSD.
CC
CC PDB: 2A41; 3I-DUN-94.
CC
CC PDB: 1AB9; 3I-DUN-94.
CC
CC PDB: 1FNP; 3I-OCT-93.
CC
CC PDB: 1IFP; 14-DUN-98.
CC
CC PDB: 1IFU; 14-DUN-98.
CC
CC PDB: 1R7C; 3I-OCT-93.
CC
CC PDB: 1OBS; 16-DUN-97.
CC
CC PDB: 1OBT; 16-DUN-97.
CC
CC PDB: 1BR5; 02-SRP-98.
CC
CC PDB: 1BR6; 02-SRP-98.
CC
CC PDB: 1113; 16-DUN-02.
CC
CC PDB: 1114; 16-DUN-02.
CC
CC PDB: 1115; 16-DUN-02.
CC
CC GlycoSuiteDB: P02879; -;
CC
CC InterPro: IPR000772; Ricin_B_lectin.
CC
CC InterPro: IPR001574; RIP.
CC
CC Pfam: PF00652; Ricin_B_lectin; 6.
CC
CC Pfam: PF00161; RIP; 1.
CC
CC PRINTS: PR00396; SHIGARICIN.
CC
CC SMART: SM00458; RICIN; 2

FT DISULFID 377 394
FT DISULFID 465 478
FT DISULFID 504 521
FT CARBOHYD 45 45
FT CARBOHYD 271 271
FT CARBOHYD 409 409
FT CARBOHYD 449 449
FT CONFLICT 76 76
FT CONFLICT 551 551
FT STRAND 43 47
FT TURN 49 50
N-LINKED (GLCNAc...).
/FTID-CAR_000080.
N-LINKED (GLCNAc...) (IN MINOR FORM).
/FTID-CAR_000081.
N-LINKED (GLCNAc...).
N-LINKED (GLCNAc...).
E -> D (IN REF. 3).
A -> R (IN REF. 3).
Query Match 63.4%; Score 896.5; DB 1; Length 576;
Best Local Similarity 63.5%; Pred. No. 4,8e-70;
Matches 185; Conservative 33; Mismatches 61; Indels 1; Gaps 1;
5 CSASEPTVRIYSGSRVDYRDDPHDNOIOLAPSKSNDDPNQMTIKEDNTRNSGSC 64
318 CMPEPIYRVARNGLOVDYDGRFNNHAIQMPCKNTDAQMLTKEDNTRNSGSC 377
65 LITVGTAGVYVIFDONTAVRENTIWIWDGIIINPSMLVLAASGKIGTLLTYQTL 124
378 LITVGSQGVYVWIDNTAATRAIRNGIWDGIIINPSSTVLAATSQSTLLTYQTN 437
125 DYTGGWLAGNDTAPREVTIYGFRLDQMESQSVAVETCSSQNGGMAVYGGSGIR 184
438 IYVSGGLPTWNTQPEVTIIVGLGLQANSQVWIEDC-SSEKMQQMALYADGSIR 496
188 EKNDQGLTVGRDSYVIMVIVISGSGSRQRTFNNVYLAINKSLMVDYQANPEFL 244
497 PQQRNGLTSDSNIRETVYKILSGPSSGGRWKFNDGIIINLYSGVLVYRASPDL 556
245 RRIITPATKGNQMLPVF 264
557 KQIIIVFPGEDNQIMLVF 576
RESULT 3
AGGL_RICCO STANDARD; PRT; 564 AA.
AC P06750;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Agglutinin precursor (RCA) [Contains: Agglutinin A chain (RNA N-
DE glycosidase) (EC 3.2.2.22); Agglutinin B chain).
OS Ricinus communis (castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids I; Malpighiales; Euphorbiaceae; Ricinus.
NCBI_TaxID=3988;
EN [1]

Thu Dec 11 16:10:06 2003

us-09-601-667c-8.rtf

Page 4

[illegible]

```

Dy 1456 IYASGCGMFPNNRQCFVTTTIVLQMGICQIQAOSKRWLEDC-ITSEKQCCOMALYADDSIR 494
Oy 1455 PRANDQCLTVGRDSYFVNIIVYSSGASGSGRWVTEVAALINLKSGLMDVYQAQNPCL 244
Db 1455 FQANDQCLTVGRDSYFVNIIVYSSGASGSGRWVTEVAALINLKSGLMDVYQAQNPCL 544
Cy 245 RRIIVPARGKQMDLVEF 264
Db 545 KQIVHPFQNLQIMLELF 564

SEQUIT 4
AREA,ABRP
ID AREA,ABRP STANDED, PRT, 528 AA.
PII10: PRS89;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Abin-a.2.222; Abin-a.2 chain (tRNA N-glycosidase)
DB Abin-a.2.222; Abin-a.2 chain (Crab's eye)
OC Bursariophyta; Viridiplantae; streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucodids 1; Fabales; Fabaceae; Papilionoideae; Abrusae; Abrus;
NCBI_TaxID=3816;
RN (1)
RN SEQUENCE FROM N.A. PubMed:4842111;
RN MEDLINE=91201123; Pubmed:4842111;
RN "Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
RN "Primary structure of three distinct isobitins determined by cDNA
RN sequencing. Conservation and significance.";
RN J. Mol. Biol. 229:263-267 (1993).
RN (2)
RN SEQUENCE OF 1-251.
RN TISSUE=seed.
RN "Gratch Y., Kamenosov M., Yanka M.;
RN "The complete amino acid sequence of the a-chain of abrin-a, a toxic
RN protein from the seeds of Abrus precatorius";
RN Agric. Biol. Chem. 52:1095-1097 (1988).
RN (3)
RN SEQUENCE OF 1-251 FROM N.A.
RN TISSUE=leaf.
RN MEDLINE=91201123; Pubmed:2016300;
RN "Gratch Y., Gratch L.-P., Tsengia A.;
RN "Direct molecular cloning and expression of two distinct abrin
RN A-chains";
RN J. Biol. Chem. 266:16848-6852 (1991).
RN (4)
RN SEQUENCE OF 262-528.
RN MEDLINE=9231165; Pubmed:1505674;
RN Chen Y.-D., Chen L.-P., Tsengia A.;
RN "Primary structure of abrin-a B chain.";
RN FEBS Lett. 309:115-116 (1992).
RN (5)
RN X-RAY CRYSTALLOGRAPHY (2.14 ANGSTOMS).
RN MEDLINE=95331183; Pubmed:7608980;
RN Tahirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-D., Lin J.-Y.;
RN "Crystal structure of abrin-a at 2.14 A.";
RN J. Mol. Biol. 250:35-46 (1995).
RN "Amino acid sequence of abrin-a B chain.
RN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
RN SUBUNIT BY REMOVING ABRININ FROM POSITION 4,124 OF 28 S RRNA.
RN ABRIN-A IS MORE TOXIC THAN RICIN.
RN -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
RN FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
RN PERMEATES ENDOCYTOSIS.
RN -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
RN Specific denaturation of the 28S rRNA.
RN -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
RN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
RN -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
RN INACTIVATING PROTEIN FAMILY, TYPE 2 RIB SUBFAMILY.

```

```

Dy 1456 IYASGCGMFFNNRQCFVTTTIVLQMGICQIQAOSKRWLEDC-ITSEKQCCOMALYADDSIR 494
Oy 1455 PRANDQCLTVGRDSYFVNIIVYSSGASGSGRWVTEVAALINLKSGLMDVYQAQNPCL 244
Db 1455 FQANDQCLTVGRDNGVAVLIVYSSGASGSGRWVTEVAALINLKSGLMDVYRDSFSL 544
Cy 245 RRIIVPARGKQMDLVEF 264
Db 545 KQIVHPFQNLQINQIMLELF 564

SEQUIT 4
AREA,ABRP
ID AREA,ABRP STANORD, PRT, 528 AA.
PII10: P2889;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Abin-a.2.222; Abin-a.2 chain (fRNA N-glycosidase)
DB Abin-a.2.222; Abin-a.2 chain (Crab's eye).
OC Bursariophyta; Viridiplantae; streptophytes; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucoidae I; Fabales; Fabaceae; Papilionoideae; Abrusae; Abrus;
NCBI_TaxID=3816;
RN (1)
RN SEQUENCE FROM N.A. PubMed:4842131;
RN PubMed:4842131;
RN PubMed:4842131;
RT "Primary structure of three distinct isobiotins determined by cDNA sequencing. Conservation and significance.";
RT J. Mol. Biol. 229:263-267 (1993).
RN (2)
RN SEQUENCE OF 1-251.
RN TISSUE=seed.
RN "Abin-a.2 chain amino acid sequence of the a-chain of abin-a, a toxic protein from the seeds of Abrus precatorius";
RN Agrif. Biol. Chem. 52:1095-1097 (1988).
RN (3)
RN SEQUENCE OF 1-251 FROM N.A.
RN TISSUE=leaf.
RN MEDLINE=9231165; PubMed:2016300;
RN PubMed:9231165; PubMed:2016300;
RN "Direct molecular cloning and expression of two distinct abtin A-chains.";
RN J. Biol. Chem. 266:16848-6852 (1991).
RN (4)
RN SEQUENCE OF 262-528.
RN MEDLINE=9231165; PubMed:1505674;
RN PubMed:9231165; PubMed:1505674;
RN Chen Y.-D., Chen L.-P., Tseng A.-C., Lin J.-Y.;
RN "Primary structure of abin-a.2 chain A";
RN FEBS Lett. 309:115-118 (1992).
RN (5)
RN X-RAY CRYSTALLOGRAPHY (2.14 ANGSTOMS).
RN MEDLINE=9533188; PubMed:7608980;
RN PubMed:9533188; PubMed:7608980;
RN Tahirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-D., Lin J.-Y.;
RN "Crystal structure of abin-a.2 at 2.14 A.";
RN J. Mol. Biol. 250:35-46 (1995).
RN "Primary structure of abin-a.2 chain A";
RN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNIT BY REMOVING ABRININ FROM POSITION 4,124 OF 28 S RRNA.
RN ABRIN-A IS MORE TOXIC THAN RICIN.
RN -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PERMEASIS ENOCYTOSTS.
RN -1- SPECIFIC DEMONSTRATION OF THE 28S rRNA.
RN -1- STEADY-STATE KINETIC ANALYSIS OF THE N-glycosidic bond at one
RN -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA)
RN -1- SIMILARITY: IN THE N-TERMINAL TYPE 2 RID SUBFAMILY.
RN INACTIVATING PROTEIN FAMILY. TYPE 2 RID SUBFAMILY.

```

CC	-1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC	This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - CC
CC	the European Bioinformatics Institute. There are no restrictions on its use by CC
CC	anybody and this statement is not removed, changed by, and for commercial CC
CC	purposes and email no license@sb.scrib.ch) (see http://www.isb-sb.ch/announcements or send an email to
CC	EMBL; M9344; AAA3264.1; ALT INIT.
CC	EMBL; X54872; -; NOT ANNOTATED_CDS.
CC	PIR; S32429; TZLSA.
CC	DR PDB; 1ABR; 07-FEB-95.
CC	DR InterPro; IPR000772; Ricin_B_Lectin.
CC	DR InterPro; IPR001574; Ricin_B_Lectin; 6.
CC	DR Pfam; PF00652; Ricin_B_Lectin; 6.
CC	DR Pfam; PF00651; Ricin_B_Lectin; 6.
CC	DR PRINTS; PR00396; SHIGACICIN.
CC	DR SMART; SM00468; RICIN; 2.
CC	DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
CC	DR PROSITE; PS00275; SHIG_RICIN; 1.
CC	KM Plant defense: Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;
CC	XV Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.
CC	PT CHAIN 1 251
CC	PT PEPTIDE 252 261
CC	PT CHAIN 252 528
CC	PT CHAIN 252 528
CC	PT DOMAIN 403 520
CC	PT REPEAT 283 325
CC	PT REPEAT 326 365
CC	PT REPEAT 369 401
CC	PT REPEAT 414 449
CC	PT REPEAT 453 492
CC	PT REPEAT 495 528
CC	PT ACT_SITE 164 164
CC	PT DISULFID 247 269
CC	PT DISULFID 284 306
CC	PT DISULFID 329 345
CC	PT DISULFID 417 430
CC	PT DISULFID 456 473
CC	PT MOD_RES 1 1
CC	PT CARBOHYD 361 361
CC	PT CARBOHYD 401 401
CC	PT CONFLICT 202 202
CC	PT CONFLICT 288 298
CC	PT CONFLICT 427 427
CC	PT CONFLICT 467 467
CC	PT CONFLICT 487 487
CC	PT STRAND 5 5
CC	PT TURN 10 11
CC	PT HELIX 14 28
CC	PT STRAND 32 33
CC	PT TURN 34 35
CC	PT STRAND 36 38
CC	PT TURN 42 43
CC	PT HELIX 47 49
CC	PT STRAND 61 67
CC	PT TURN 70 72
CC	PT STRAND 75 79
CC	PT STRAND 83 86
CC	PT TURN 88 89
CC	PT TURN 92 93
CC	PT HELIX 94 97
CC	PT TURN 100 101
CC	PT STRAND 103 106
CC	PT TURN 113 115
CC	PT HELIX 116 119
CC	PT TURN 124 126
CC	PT STRAND 129 129
CC	PT HELIX 131 142
CC	PT TURN 143 144

Query Match	Best Local	Similarity	Score	DB 1	Length
5	CSAS-EFTYRIVRSGRKVDYDDDFDHCNIOIOWESKNNPNDIWKDKNTIRKNGS	64.8%	750	DB 1	528
Matches	142	Conservative	42	Mismatches	75
				Indels	2
				Gaps	2

DB 269 CSSEYPTVIRIGRGMCVVDYDGNHNGNRIIMKCKLEEMQWTLKSDKTRSNK 328
QY 64 CLTGYAGYVWIMFDCNTAVRENTIWIQWNGTIIINPNSNLYLAASGIGKOTLTAVOT 123
DB 329 CLTGYAGYVWIMFDCNTAVRENTIWIQWNGTIIINPNSNLYLAASGIGKOTLTAVOT 388
QY 124 LPTLQGMALNDPAPREVTIYGRDLCMESQSVVETCSQSQNGKALYGGSI 183
DB 389 NEYLMQGMRTGNNSPVTISISGSDLMQSGSNVWADSDNKQ QNALYDGGI 447
QY 184 RPKNOQDCLTVGRDSVSTVIVYSCSGASGSGQWTFNEVAILNKSGCLAMVQANX 243
DB 448 RSVQNNKCLTSKDKHQSITLLMGCSNMAASQWVFVNDGSIYLDYDMDVGRSDS 507
QY 244 LRRIITPATGKPNQWMLPVF 264
DB 508 LKQIILPPTKRNQWMLPVF 528

RESULT 5

ABRB_ABRP

ID ABRB_ABRP STANDARD: PRT: 527 AA.

AC 006077: P81374;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Abria-b precursor [Contains: Abria-b A chain (RNA N-glycosidase)
DE (EC 3.2.2.22); Abria-b B chain)
OS Abria-b precursor (Indian Alciacea) (Crab's eye)
OS Abria-b precursor (Indian Alciacea) (Crab's eye)
OC Spermatophyta: Magnoliopsida: Ericaceae: Calluna
OC Eurosidia I: Fabales/ Fabaceae, Papilionoideae, Abreae, Abriae;
OX NCBI_TaxID=3816;
RN [1] _TaxID=3816;
RP SEQUENCE FROM N.A.
RX MEDLINE=9332798; PubMed=842333;
RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
RT "Primary structure of three distinct isobritins determined by cDNA
RT sequencing. Conservation and significance.";
RN [2] Mol. Biol. 229:263-267 (1993).
RP SEQUENCE OF 260-527.
RC TISSUE=Seed;
RX MEDLINE=9316903; PubMed=7763422;
RA Kimura M., Sumitawa T., Funatsu G.;
RT "The complete amino acid sequences of the B-chains of Abria-a and
RT Abria-b, toxic proteins from the seeds of Abria precatorius";
RL Biosci. Biotechnol. Biochem. 57:166-169 (1993).
CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
CC -1- SIMILARITY: CONTAINS 2 RICHIN-B-TYPE LECTIN DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 RICHIN-B-TYPE LECTIN DOMAINS.
CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
CC -1- SIMILARITY: CONTAINS 2 RICHIN-B-TYPE LECTIN DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 RICHIN-B-TYPE LECTIN DOMAINS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION BELONGS TO THE RIBOSOME-
CC BINDING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 2 RICHIN-B-TYPE LECTIN DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 RICHIN-B-TYPE LECTIN DOMAINS.
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: M98345; AAA3625.1) -
DR F01: S12430; S32430.
DR HSP: P1140; 1AER.
DR Interpro: IPR000772; RICHIN_B_lectin.
DR Interpro: IPR001574; RIP.
DR Pfam: PF00652; RICHIN_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00356; SHIGARICIN.
DR SMART: S00458; RICHIN_2; LECTIN; 2.
DR PROSITE: PS00227; SHIGARICIN; 1.
KW Plant defense; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lactin; Pyridoxine carboxylic acid.
FT CHAIN 1 260
FT PEPTIDE 251 260
FT CHAIN 1 260
FT ACT SITE 163 163
FT DOMAIN 272 399
FT DOMAIN 402 526
FT REPEAT 282 324
FT REPEAT 325 365
FT REPEAT 366 400
FT REPEAT 401 448
FT REPEAT 452 491
FT ACT SITE 163 163
FT DISULFID 246 268
FT DISULFID 285 304
FT DISULFID 328 345
FT DISULFID 416 429
FT DISULFID 455 472
FT MOD_RES 1 1
FT CARBOHYD 110 110
FT CARBOHYD 360 360
FT CARBOHYD 400 400
FT CONFLICT 282 282
FT CONFLICT 291 291
FT CONFLICT 350 351
FT CONFLICT 378 378
FT CONFLICT 426 426
FT CONFLICT 428 428
FT CONFLICT 432 432
FT CONFLICT 434 434
FT CONFLICT 491 491
FT CONFLICT 493 493
FT CONFLICT 502 502
FT CONFLICT 509 509
FT CONFLICT 513 513
FT CONFLICT 516 516
FT SEQUENCE 527 AA; 59114 MW; 3253A94DCE949A CRC64;
Query Match 52.6%; Score 744; DB 1; Length 527;
Best Local Similarity 53.6%; Freq. No. 6; 7e-57;
Matches 140; Conservative 43; Mismatches 76; Indels 2; Gaps 2;
QY 5 CSSEYPTVIRIGRGMCVVDYDGNHNGNRIIMKCKLEEMQWTLKSDKTRSNK 63
DB 268 CSSEYPTVIRIGRGMCVVDYDGNHNGNRIIMKCKLEEMQWTLKSDKTRSNK 327
QY 64 CLTGYAGYVWIMFDCNTAVRENTIWIQWNGTIIINPNSNLYLAASGIGKOTLTAVOT 123
DB 329 CLTGYAGYVWIMFDCNTAVRENTIWIQWNGTIIINPNSNLYLAASGIGKOTLTAVOT 388
QY 124 LPTLQGMALNDPAPREVTIYGRDLCMESQSVVETCSQSQNGKALYGGSI 183
DB 389 NEYLMQGMRTGNNSPVTISISGSDLMQSGSNVWADSDNKQ QNALYDGGI 446
QY 184 RPKNOQDCLTVGRDSVSTVIVYSCSGASGSGQWTFNEVAILNKSGCLAMVQANX 243
DB 448 RSVQNNKCLTSKDKHQSITLLMGCSNMAASQWVFVNDGSIYLDYDMDVGRSDS 506
QY 244 LRRIITPATGKPNQWMLPVF 264

Thu Dec 11 16:10:06 2003

us-09-601-667c-8.rsp

Page 8

Cc		SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28S RNA. THE B CHAIN IS A CALGOSOL-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF THE N-GLYCOPROTEIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
Cc	-1-	CATALYTIC ACTIVITY: Endopolyd(A)ase of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
Cc	-1-	SUBSTRATE: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
Cc	-1-	SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 LEC SUPPLEMENT.
Cc	-1-	SIMILARITY: Contains 2 x c1ch B-type lectin domain(s).
Cc		This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL consortium - the European Bioinformatics Institute. There are no restrictions on how it can be used by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.ebi.ac.uk/submit/cv/announcements/) or send an email to license@ebi.ac.uk .
Cc		Swiss-Prot accession number: P00947.5.1.
Dc	PIR: S37382; S37382;	Ricin B_lectin.
Dc	Interpro: IPR007732;	Ricin B_lectin.
Dc	Interpro: IPR001574; RFP:	
Dc	DR Pfam: PF00652; Ricin B_lectin; 6.	
Dc	Pfam: PF00161; RIP; 1.	
Dc	PRINTS: PR00396; SHIGAMICIN.	
Dc	SMART: PS00458; RCTCN; 1.	
Dc	PROSITE: PS00275; SHIGA_RICIN; 1.	
Dc	PROSITE: PS00203; RICIN_B_LLECTIN; 2.	
Kw		N-glycanase, N-glycan synthetase inhibitor, Toxin, Repeat, Glycoprotein, Lectin, Signal.
FT	CHAIN	26 297
FT	FT CHAIN	1 25
FT	FT CHAIN	298 563
FT	FT DOMAIN	305 431
FT	FT DOMAIN	434 559
FT	REPEAT	316 359
FT	REPEAT	316 359
FT	REPEAT	400 437
FT	REPEAT	400 437
FT	REPEAT	445 482
FT	REPEAT	456 524
FT	REPEAT	527 554
FT	ACT_SITE	188 188
FT	DISULFD	274 302
FT	DISULFD	319 338
FT	DISULFD	319 338
FT	DISULFD	360 377
FT	DISULFD	489 505
FT	DISULFD	489 505
FT	CARBOND	221 221
FT	CARBOND	368 368
FT	CARBOND	376 376
FT	CARBOND	483 483
FT	CARBOND	537 537
FT	CONFLICT	39
SO	SEQUENCE	563 AA; 6200 PWM; F250CBK24621BF14 GRC64;
Query Match		36.5%; Score 516.5; DB 1; Length 563;
Best local similarity		Prod. No 3,48-137
Matches 108; Conservative 43; Mismatches 106; Indels 7; Gaps 5		
Qy	1	DVDTSSASPTFR-IYGSAGRVADPDHDFGNQCLMPKSNNDNPQLMTIKRNTIR 59
Dy		DSSTLTETTSFNRYVGEGDGLGVNRNGDYDTLPCTPACPGTGR-NQPMFSDDIR 355
Oy	60	SNSGSTGGTGATTAATVPCKTVLWNTIQTWLNTPINRSNPLAASSGISTTL 119
Dy		SVNGKCPANGNLNNNVIFVPCSTDAEMALKVEPIIDSSINPSGLWTAPPAARFIL 415
Qy	120	TVOITLDITLGGMLANQVAPREVLYVGEPLCAJSEN-QGSVWVCSSQKQCKAKL 177
Dy		LLENDVIASQGVTVNNKVFVAISVYGVMCGNSKNENNVMGCHECATSLD-QVAL 474

QY 178 YADDS:HEPCMOOGLVTGSDVSSTVINVCSSGSSGSKRMVFNELVILKXSLANDU 23
 Db 475 YEDRLINVSFTRLCVTHGNSKDLITLILCOGLAP-SQRMFFNSDGLVNPMSRNVDD 533
 QY 238 AADNPCEPITITVFRANGCEPKNWU 261
 Db 534 RASNVSLPEITITFPAISNPOOWV 557
 RESULT 8
 ID XYXA_STRELL STANDARD: FRT 477 AA.
 AC P28154.1; 996464;
 AC P28154.2; 82 (Rel. 23. Created)
 DT 31-MAR-2003 (Rel. 39. Last annotation update)
 DT 15-SEP-2003 (Rel. 42. Last annotation update)
 DE Endo-1,4-beta-xylinase A precursor (EC 3.2.1.8) (Xylanase A)
 DE (1,4-beta-D-xylin xylanohydrolase A).
 GN XINA.
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomyces; Streptomycesaceae; Streptomyces.
 DX NCBI_TextID:1916;
 DX SOURCE FROM N.A., AND SEQUENCE OF 42-92.
 RX STRAIN-66 / 1326.
 RX MEDLINE=92079439; PubMed=1145251;
 RA Sharkey F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
 RT "Sequences of three genes specifying Xylanases in Streptomyces
 lividans.";
 RL Gene 107:75-82(1991).
 RN [2].
 RP REVISIONS TO 20 AND 140-141.
 RA SHARKEY F.;
 RA SHARKEY F.;
 RN [3].
 RZ X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 42-340.
 RX MEDLINE=94342232; PubMed=8065653;
 RA Devereux U., Swenson L., Green R., Wei Y.Y., Morosoli R., Sharkey F.,
 R Kluepfel D., Devereux Z.S.;
 RT "Crystal structure, at 2.6-A resolution, of the Streptomyces lividans
 Xylanase A, a member of the F family of beta-1,4-D-glycosidases.";
 RL J. Biol. Chem. 269:12081-12084(1994).
 CC -1: CATALYTIC ACTIVITY: hydrolysis of beta-1,4-D-hemicellulose, the major
 CC component of plant cell walls. XINA and XINB seem to act
 CC sequentially on the substrate to yield xylobiose and xylose
 CC as carbon sources.
 CC -1: CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloisidic
 CC linkages in xylans.
 CC -1: PATHWAY: Xylan degradation.
 CC -1: SUBCELLULAR LOCATION: secreted.
 CC -1: SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
 CC HYDROLASES).
 CC -1: SIMILARITY: Contains 1 ricin B-type lectin domain.
 CC This Swiss-Prot entry is copyright ©. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL annotation
 CC group at the European Bioinformatics Institute. There are no restrictions on ways
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M64551; AAC6525.1; -.
 CC EMBL: J20893; J20893.6
 CC EMBL: J20893; J20893.6
 CC PDB: 1E0V; 25-MAY-01.
 CC PDB: 1E0V; 25-MAY-01.
 CC PDB: 1KUL; 19-JUN-02.
 CC PDB: 1KUL; 19-JUN-02.
 CC PDB: 1KMW; 19-JUN-02.
 CC PDB: 1MC3; 11-SEP-02.
 CC InterPro: IFS001000, Glyco_hydro.10.

```

DR SMART: SM00458: RCIN1: 1.
DR PROSITE: PS00231: RCIN1 B LECTIN: 1.
FW Hydrolase: Glycosidase; Signal; Potentiatic; Cell wall; Lectin.
FT SIGNAL 1 36
FT CHAIN 37 548 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE.
FT DOMAIN 422 548 RCIN1 B-TYPE LECTIN.
SQ SEQUENCE 548 AA: 581c5 NM: BD56538315750596 CMC64:

Query Match 7.6%; Score 108; DB 1: length 548;
Best Local Similarity 31.7%; Pred. No. 0.07;
Matches 39; Conservative 18; Mismatches 52; Indels 14; Gaps 6

18 SGRVYRDEDFHNGNQIQDLPKSKNNDDPNQVLTAKENTIRNSQCT--TVGYAPGY 75
DB 430 STLCIDVPAAPDPTTNOVCL--ATGSCNAAAOQDPTGTGATLQKCLDVAASGTADGTA 487

```

DB	488	WMYTCGATGATGKMT---	YDSATLALNPSGKCLDAGSAPFLDDQAVQVLTQCNQTEA	543
QY	130	QCGM	132	
DB	544	QRM	546	
RESULT 10				
ID	E13B	OEEXA		
AC	P22232		STANDARD;	PRT; 548 AA.
DT	01-AUG-1991	(Rel. 19, Created)		
DT	01-AUG-1991	(Rel. 19, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DT				

OS	Oerskovia xanthinolytica.
OC	Bacteria; Actinomycetales; Actinomycetaceae; Actinomycetales;
CC	Micrococciinae; Promicromonosporaceae; Cellulosistricium.
NCBI_TextID=1710;	
[1]	
AN	
RT	SEQUENCE FROM N.A., AND SEQUENCE OF 37-63.
RL	MEDLINE=1093212; Pubmed=1885933;
RA	Shen S.-H., Chretien P., Bastien L., Allary S.N.;
PT	Primary sequence of the glucanase gene from Oerskovia
FT	xanthinolytica. Expression and purification of the enzyme from
ET	Escherichia coli.
RT	J Biol Chem. 266:1056-1063[1991].
CC	-1 FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
CC	-1 IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS.
CC	-1 CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
CC	in 1,3-beta-D-glucans.
CC	-1 SUBCELLULAR LOCATION: Periplasmic.
CC	-1 SIMILARITY: BELONGS TO Family 64 Of GLYCOSYL HYDROLASES.
CC	-1 SIMILARITY: Contains 1 Ricin B-type lectin domain.
CC	
CC	This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC	between EMBL, EMBL Bioinformatics and the EMBL Information Services
CC	at the European Bioinformatics Institute. Its contents are made available in no way
CC	use by the European institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC	or send an email to license@sib-sib.ch).
CC	
DR	EMBL; M60826; AAA25520.1; -
DR	PIR; A39094; AA3094.
DR	HSPB; P02879; ZMAI.
DR	IncepCo; IPR000772; Ricin_B_lectin.
DR	SWISSPROT; P02879; Ricin_B_lectin.3.
DR	Tram; F00052; Ricin_B_lectin.1.
DR	PROSITE; PS0204; RICIN_B_LECTIN.1
KW	Hydrolase, Glycosylase, Signal, Periplasmic, Cell wall, Lectin.
FT	SIGNAL 1
FT	CHAIN 37
FT	CHARN 37
FT	DOMAIN 422
FT	DOMAIN 548
FT	GLUCAN BIND-1,3-BETA-D-GLUCOSIDASE.
FT	RICIN B-TYPE LECTIN.

DR EMBL; D10753; BAA01585.1; -.
 DR PIR; A45053; A45053.
 DR HSRP; P00778; A45053.
 DR XEROSE; S01276; -.
 DR ILEPPO; IPR001236; AL protease.
 DR ILEPPO; IPR001236; AL protease.
 DR InterPro; IPR000772; Ricin B lectin.
 DR InterPro; IPR001254; Ser protease_trp.
 DR Pfam; PF02883; AL protease; 1.
 DR Pfam; PF00652; Ricin B lectin; 3.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO0661; ALTYCEPTASE.
 DR SMART; SM00458; RICIN; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS02351; RICIN_B_Lectin; 1.
 DR PROSITE; PS02351; Ricin B lectin; 1.
 DR Hydrolase; Serine protease; Mannose-binding; Signal; Zymogen; 1.
 KW ILEPPO.
 FT SIGNAL 1 32
 FT PROPEP 33 211
 FT CHAIN 212 525
 FT DOMAIN 396 525
 FT DOMAIN 401 525
 FT DISTULID 223 239
 FT DISTULID 310 320
 FT DISTULID 316 376
 FT DISTULID 318 478
 FT DISTULID 453 472
 FT DISTULID 496 514
 FT ACT SITE 238 238
 FT ACT SITE 270 270
 FT ACT SITE 352 352
 FT ACT SITE 352 352
 SQ SEQUENCE 525 AA; 55654 MW; D42BCE7D330EB61 CRC64;
 Query Match 7.4%; Score 105; DB 1; Length 525;
 Best Local Similarity 30.2%; Pred. No. 0.12;
 Matches 32; Conservative 17; Mismatches 45; Indels 12; Gaps 5;
 QY 2 PHTCSASPTKATVRSKQKVDPRDDPHQNGQIQTPSKNDPQVLMITKRDNTIRSN 61
 DB 399 DVT-----TSYVGQGNCCIDVNSDPTDQQLAVNCKNGT--NQVSHFDITKIN 450
 QY 62 GSCD-FTYGYT-AGYVMIFPDQNTAVREATIQWIDNGIINPESN 105
 DB 451 GKCLDPAWMTNHTGEVQIANNNGHI--NQFTLNGAGDLVNVHAN 494
 RESULT 13
 ID 3896 STALI STANDARD; PRT; 475 AA.
 AC P6463;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).
 GN ABF9.
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomyces; Streptomyces; Streptomyces.
 RX NCBI_TaxID:1916;
 RP SOURCE FROM N.A.
 RC STRAIN=66 / 1326;
 RA MEDLINE=9720396; Pubmed=9148759;
 RT Vincent P., Shareck F., Dupont C., Morosoli P., Kluepfel D.;
 RT "new alpha-L-arabinofuranosidase produced by Streptomyces lividans:
 RT cloning and DNA sequence of the abf9 gene and characterization of the
 RT enzyme." J. 322:845-852(1997).
 RL EMBL; D10753; BAA01585.1; -.
 RP REVISIONS
 RC STRAIN=66 / 1326;

RA Shareck F.;
 RL Submitted (Jul-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: HAS A SPECIFIC ARABINOFURANOSIDE-BRANCHING ACTIVITY ON
 CC XYLAN FROM GRAMINEAE, ACTS SYNERGISTICALLY WITH THE XYLANASES AND
 CC BINDS SPECIFICALLY TO XYLAN. FROM SMALL ARABINOXYLO-OLIGOSIDES,
 CC IT LIBERATES ARABINOSE AND, AFTER PROLONGED INCUBATION, THE
 CC FORMER ENZYME EXHIBITS SOME XYLANOXYLYTIC ACTIVITY AS WELL.
 CC -1- CATALYZES THE HYDROLYTIC DEGRADATION OF ARABINOXYLO-OLIGOSIDES
 CC AND ARABINOFURANOSIDE RESIDUES IN alpha-L-arabinosides.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.
 CC -1- SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed, usage by and for commercial
 CC entities must be approved (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch)
 CC
 DR EMBL; X64551; AAC26524.1; -.
 DR InterPro; IPR005193; Glyco_hydro_62.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF03664; Glyco_hydro_62; 1.
 DR Pfam; PF00652; Ricin_B_lectin; 3.
 DR SMART; SM00458; RICIN; 1.
 DR PROSITE; PS02351; RICIN_B_Lectin; 1.
 DR PROSITE; PS02351; Ricin B lectin; 1.
 DR Hydrolase; Hydrolyase; POTENTIAL.
 KW ILEPPO.
 FT SIGNAL 38 475
 FT CHAIN 39 166
 FT DOMAIN 39 166
 FT DOMAIN 166 475
 SQ SEQUENCE 475 AA; 50369 MW; C1CB14EB7BF85A0 CRC64;
 Query Match 7.4%; Score 104.5; DB 1; Length 475;
 Best Local Similarity 23.6%; Pred. No. 0.12;
 Matches 51; Conservative 34; Mismatches 106; Indels 25; Gaps 10;
 QY 6 SASEFTVRYVSGKRVYRDPRDDPHQNGQIQTPSKNDPQVLMITKRDNTIRSN 64
 DB 37 AAGSGLAAGG-SNRCLVLAGSQDADLQITQWCGST--NQVSHFDITKIN 93
 QY 65 LITVGYTA-AGYVMIFPDQNTAVREATIQWIDNGIINPESNVL-AASGI-KGTILT 120
 DB 94 LDVPHATATAGTRVQVMSGSGNQ--MKNVNSGTVGVSGSLCLFAGATDPNGTAVQ 151
 QY 121 VQTLDTLQGVLAGNDTAPREVT-----TVGFDDCKESNQSQSVETCD-SSQKNGK 174
 DB 152 LMTGCGAGKQKWTGLTGPDPDQALPSTYMSSTGVLAQPSGAWALKDPFTYHNR 211
 QY 175 MLYVQDS-----IRNQKQCCITVGSQVS 201
 DB 212 HLYVSTSSGSSYSQSVNPSPTVMSDASHQNNAN 247
 RESULT 14
 ID 5946 ANASP STANDARD; PRT; 1526 AA.
 AC Q8YK11;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 GN A19346; 1321 WD-repeat protein a19346.
 OS Arabidopsis sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 RX NCBI_TaxID:109690;
 RP SOURCE FROM N.A.
 RC MEDLINE=21595285; Pubmed=1759840;
 RA Kaneo T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
 RA Kaneo T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iritschi W., Ishikawa K., Kawashima K., Kikuta T.,

Thu Dec 11 16:10:06 2003

us-09-601-667c-8.rsp

Page 12

PA	Kleibidei, Kohara M., Matsuno M., Muraki A., Nakazaki N., Shimo S., Sugimoto M., Yabuta M., Yabuta S.,	Matsuno A., Muraki A., Nakazaki N., Shimo S., Sugimoto M., Yabuta M., Yabuta S.,
RA	"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."	
RT	DNA Res. 8:205-213(2001).	
CC	CC -1. SIMILARITY: Contains 16 WD repeats.	
CC	CC -1. SIMILARITY: Contains 1 pentapeptide repeat domain.	
CC	CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.	
CC	CC the European Bioinformatics Institute. There are no restrictions on way CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.ebi.ac.uk/commerca or send an email to license@ebi-sib.ch).	
CC	CC EMBL, AF003593; BAB75165.1; -	
DR	DR ERL; AC2239; AC2239. Sequence repeat.	
DR	DR Interpro; IPR007116; WD40_1_repeat.	
DR	DR Interpro; IPR001680; WD40_1_repeat.	
DR	DR Pfam; PF00460; WD40_1.	
DR	DR PRINTS; PR00320; GPROTEINBRT.	
DR	DR ProDom; PD000018; WD40_15.	
DR	DR SMART; SMO0320; WD40_15.	
DR	DR PROSITE; PS00678; WD REPEATS 1; 11.	
DR	DR PROSITE; PS00678; WD REPEATS 2; 15.	
DR	DR PROSITE; PS00678; WD REPEATS REGION; 1.	
DR	DR PROSITE; PS00678; WD REPEATS REGION; 1.	
KW	Keywords: Repeat; WD repeat; Complete proteome.	
FT	FT REPEAT 137..171; Repeat; WD repeat; Complete proteome.	
FT	FT DOKAIN 823..862; PENTAPEPTIDE.	
FT	FT REPEAT 862..901; WD 2.	
FT	FT REPEAT 904..945; WD 3.	
FT	FT REPEAT 946..985; WD 4.	
FT	FT REPEAT 988..1027; WD 5.	
FT	FT REPEAT 1030..1069; WD 6.	
FT	FT REPEAT 1072..1111; WD 7.	
FT	FT REPEAT 1114..1153; WD 8.	
FT	FT REPEAT 1156..1195; WD 9.	
FT	FT REPEAT 1198..1237; WD 10.	
FT	FT REPEAT 1240..1279; WD 11.	
FT	FT REPEAT 1282..1321; WD 12.	
FT	FT REPEAT 1324..1363; WD 13.	
FT	FT REPEAT 1366..1405; WD 14.	
FT	FT REPEAT 1408..1447; WD 15.	
FT	FT REPEAT 1450..1491; WD 16.	
SO	SEQUENCE 1526 AA; 150376 MW; D5PFE27250B4738 CRC64;	
Query Match 6.5%; Score 91.5; DB 1; Length 1526;		
Best local Similarity 21.7%; P224 20.6; 47; Gaps 13;		
Matches 57; Conservative 35; Mismatches 84; Indels 97;		
QY	3 VTGSASPEPTVYRSGKGVDDDDPDDNDIOLMPSKSNDDPQWLTKDDYTRNSG 62	13
DB	900 LTKCKHNSWNSVFS-----QDCKL--ASGSDPLRLMI-----SSG 938	
DB	63 SCITTY-GTYAGVYVMPDCKNVAEATWQIMDNGITINRESNVTVAASGGITGLTV 121	
QY	939 QCKTKPKHNSVNSVSN-----SLDASGSS-----SVTV 972	
DB	122 QTLDTYLGQGLMAGNTPARFRTVITGFRDLCKMENGNSV-WST-----CPSSQNGKKA 176	
QY	973 RLMDSSSG-----CLYFQGHGMYSVAFNLDGSLATGS--1009	
DB	177 LVGDGSTRPKQ-NDQCKLTVGRSDSVTVINYSQS-----ASSQGRWTFNRYIAIKNS 231	
QY	1010 ---GGDTYVQMLNSGCFPIQGHSSCVNSVFSQGMALASGD-----DQTVLWDISS 1065	
DB	232 GLAMDVQMLNSGCFPIQGHSSCVNSVFSQGMALASGD-----DQTVLWDISS 1065	
DB	1064 GNCCLVTLQGHSSCVNSVFSQGMALASGD-----DQTVLWDISS 1086	

RESULT 15
PM20 CHLPP STANDARD; FRT: 1723 AA.
AC Q98612; GSKC1; C9R5B9;
ID PM20 CHLPP STANDARD; FRT: 1723 AA.
CC 098612; GSKC1; C9R5B9;
DT 16-OCT-2001 (Ref. 40, Created)
PT 16-OCT-2001 (Ref. 40, Sequence update)
PR 16-FEB-2003 (Ref. 41, Last annotation update)
DE Protein 20.
CS PM20 OR CPN0540 OR CPN212.
OS Chlamydia pneumoniae (Chlamydiophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiales; Chlamydiaceae; Chlamydiophila.
NC NCBI TaxId=33558;
LN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CWJ029;
RX MEDLINE=9920606; PubMed=10192388;
RA Kaiman S., Mitchell W., Marathe R., Lammé C., Fan J., Hyman R.W.,
RB "Hilber L., Grimwood J., Davis R.W., Stephens R.S."
RC "Chlamydia pneumoniae isolates from patients with pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RP SEQUENCE FROM N.A.
RC STRAIN=A339;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brumham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RB White O., Hickey E.K., Peterson J., Uetzback T., Berry K., Bass S.,
RC Linher K., Weidman D., Knorr H., Craven B., Bowman C., Dodson R.,
RD Gilmn M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
RE Eisen J., Fraser C.M.,
RF "Genomic analysis of Chlamydia trachomatis Nepr and Chlamydia
RG pneumoniae A339.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CJ38;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai W., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RB Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T.,
RC Comparison of whole genome sequences of Chlamydia pneumoniae J138
RD and J139 strains and their relationship to other Chlamydia pneumoniae
RE Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CJ38;
RX MEDLINE=20298986; PubMed=10839753;
RA Shirai W., Hirakawa H., Ouchi K., Tabuchi M., Kishi F., Kimoto M.,
RB Takeuchi H., Nishida Y., Shibata K., Fujinaga R., Yoneda H.,
RC Matsushina H., Tanaka C., Furukawa S., Miyata K., Nakazawa H.,
RD Shiba T., Shira T., Hattori M., Kohara S., Nakazawa T.,
RE "Whole genome sequencing of Chlamydia pneumoniae isolates from Japan and the
RF United States.";
RL J. Infect. Dis. 181 Suppl. 3:S524-S527(2000).
RN [-1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
RC (-POTENTIAL).
LN [-1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the EMBL European Bioinformatics Institute (EBI), the SIB Swiss Institute
CC for Bioinformatics and the EBC European Bioinformatics Centre. There are no restrictions on its use,
CC except that it may not be used for commercial purposes. The copyright for the
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sb.ch).
DR EMBL, AE001638; AB18660.1; -
DR EMBL, AE002181; AF938082.1; ALT_INT.
DR EMBL, AE002947; DA958746.1; -
DR EMBL, F02067; E72067.
DR EMBL, F02067; E72067.

DR PHCI-2DPAGE; Q92812; -
DR TIGR; CP0212; -
DR InterPro; IPR003368; Chlamydia_PMP.
DR InterPro; IPR006626; PHL.
DR Pfam; PF0212; DUF145; 1.
DR SMART; SM012; DUF145; 1.
DR TIGRfams; TIGR01376; POMP repeat; 24.
DR Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 21
FT CHAIN 22 1723 PROBABLE OUTER MEMBRANE PROTEIN PMP20.
FT DOMAIN 94 97 POLY-SER.
FT DOMAIN 140 144 POLY-SER.
FT DOMAIN 147 160 POLY-SER.
FT CONFLICT 1134 1134 I -> V (IN REF. 1).
SQ SEQUENCE 1723 AA; 179594 MW; 4507D5B8A0E3F01 CRC64;

Query Match 6.48; Score 90; DB 1; Length 1723;
Best Local Similarity 22.28; Pred No 10;
Matches 61; Conservative 32; Mismatches 86; Indels 96; Gaps 10;

QY 51 TIKEDNTIRNSGCLTYGYT--AGYVMIFDCNTA-----VREKTIQWMDN--- 96
DB 223 TFGNSQKSGGAYTEGALTTOAIVEAVFTGNTNSGCGALVYEKTELFNALDSIFE 282
QY 97 -----GTINPRSNLV-----AASGIGKTTITVOT 123
DB 283 KATSGQAGGAYTESITLITSNITKSLPTSNKASVPAPAPPTSPAPPSLINSITITDTST 342
QY 124 L-----DYTGQGLAGNDTARRYTYGFRDLCHESNQS 159
DB 343 LQTRASATPAVAPVAPVAPPTPTPTSTOTFANG--GAIYAKGISITFDLTPTNSNS 399
QY 160 VYVE-TCDSQKQKQKALYGDGSIIPKQNDQCL-----TVGRDSVATVI 204
DB 406 VDATLVDSSTIGESGALFPAADSIQDCTGTLTFSGNTANKSGGAYAVGQVTLEDIA 459
QY 205 NIV---SCSGASG--SQKVFTEVAIINLKSG 232
DB 460 NIKSTNTCKESGALITGKALTINGALITPFG 494

Search completed: December 11, 2003, 14:09:05
Job time : 5.6201 secs

Matches 242; Conservative 6; Mismatches 14; Indels 1; Gaps 1;
QY 1 DVTGASAPPTVIVSGKRVYVDDPHDQIOLAPSKSNDPNQMLTKEDNTIR 60
DB 269 DVTGASAPPTVIVSGKRVYVDDPHDQIOLAPSKSNDPNQMLTKEDNTIR 328
QY 61 NSGCTTGYAGVYVMEPCNIVBAATVQWNGTININRSNIVLAASGIGTIT 120
DB 329 NSGCTTGYAGVYVMEPCNIVBAATVQWNGTININRSNIVLAASGIGTIT 388
QY 121 VQTLDTYLGQGLAGNDAPREVTIYGFRLDQMSNGSWSVWETCDSSQKQKALYD 180
DB 389 VQTLDTYLGQGLAGNDAPREVTIYGFRLDQMSNGSWSVWETCDSSQKQKALYD 447
QY 181 GSIRPKNDQCLTVGRDSVSTIVIVSGSAGSQRWVFTNEVALIMLKSGLAMVQA 240
DB 448 GSIRPKNDQCLTVGRDSVSTIVIVSGSAGSQRWVFTNEVALIMLKSGLAMVQA 507
QY 241 NPKLRRIIIPATKRNQWMLPV 263
DB 508 NPKLRRIIIPATKRNQWMLPV 530

RESULT 2

Q8BK02 PRELIMINARY; FRT; 263 AA.
AC Q8BK02 (TREMURel. 22, Created)
DT 01-OCT-2002 (TREMURel. 22, Last sequence update)
DE 01-OCT-2002 (TREMURel. 22, Last sequence update)
DS 1-1. CATALYTIC ACTIVITY. ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC 1-1. SPECIFIC ADENOSINE ON THE 28S RRNA. INACTIVATING PROTEIN FAMILY.
CS Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2156752; PubMed=11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
DR PROSITE, PS50231; R1CIN_B_Lectin, 2.
KW Signal; toxin.
FT SIGNAL 1 22
FT CHAIN 23 278
FT CDS 23 278
FT TER 278
SQ SEQUENCE 565 AA; 62401 MW; 991E394D005F11 CRC64;
Query Match 76.2%; Score 1077.5; DB 10; Length 565;
Best Local Similarity 78.7%; Pred. No. 1.7e-87;
Matches 207; Conservative 15; Mismatches 36; Indels 5; Gaps 2;
QY 1 DVTGASAPPTVIVSGKRVYVDDPHDQIOLAPSKSNDPNQMLTKEDNTIR 60
DB 307 DVTGASAPPTVIVSGKRVYVDDPHDQIOLAPSKSNDPNQMLTKEDNTIR 362
QY 61 NSGCTTGYAGVYVMEPCNIVBAATVQWNGTININRSNIVLAASGIGTIT 120
DB 363 NSGCTTGYAGVYVMEPCNIVBAATVQWNGTININRSNIVLAASGIGTIT 422
QY 121 VQTLDTYLGQGLAGNDAPREVTIYGFRLDQMSNGSWSVWETCDSSQKQKALYD 180
DB 423 VQTLDTYLGQGLAGNDAPREVTIYGFRLDQMSNGSWSVWETCDSSQKQKALYD 481
QY 181 GSIRPKNDQCLTVGRDSVSTIVIVSGSAGSQRWVFTNEVALIMLKSGLAMVQA 240
DB 482 GSIRPKNDQCLTVGRDSVSTIVIVSGSAGSQRWVFTNEVALIMLKSGLAMVQA 541
QY 241 NPKLRRIIIPATKRNQWMLPV 263
DB 542 NPKLRRIIIPATKRNQWMLPV 564

QY 181 GSIRPKNDQCLTVGRDSVSTIVIVSGSAGSQRWVFTNEVALIMLKSGLAMVQA 240
DB 180 GSIRPKNDQCLTVGRDSVSTIVIVSGSAGSQRWVFTNEVALIMLKSGLAMVQA 239
QY 241 NPKLRRIIIPATKRNQWMLPV 263
DB 240 NPKLRRIIIPATKRNQWMLPV 262

RESULT 3

Q8W243 PRELIMINARY; FRT; 565 AA.
AC Q8W243;
DT 01-MAR-2002 (TREMURel. 20, Created)
DE 01-MAR-2002 (TREMURel. 20, Last sequence update)
DS 01-OCT-2002 (TREMURel. 22, Last sequence update)
DE VCA precursor (EC 3.2.2.22) (RNA N-glycosidase).
CS Viscum album susp. coloratum.
OC Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RA Park W.-B., Lyn S.;
RT Cloning of Viscum album subsp. coloratum (Korean mistletoe)."
RL Biochem. Biophys. Res. Commun. 0:0-(2002)
CC 1-1. CATALYTIC ACTIVITY. ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CS 1-1. SPECIFIC ADENOSINE ON THE 28S RRNA. INACTIVATING PROTEIN FAMILY.
DE Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=1800072; PubMed=18001574;
RA Park W.-B., Lyn S.;
DR PROSITE, PS50231; R1CIN_B_Lectin, 2.
KW Signal; toxin.
FT SIGNAL 1 22
FT CHAIN 23 278
FT CDS 23 278
FT TER 278
SQ SEQUENCE 565 AA; 62401 MW; 991E394D005F11 CRC64;

Query Match 76.2%; Score 1077.5; DB 10; Length 565;
Best Local Similarity 78.7%; Pred. No. 1.7e-87;
Matches 207; Conservative 15; Mismatches 36; Indels 5; Gaps 2;

QY 1 DVTGASAPPTVIVSGKRVYVDDPHDQIOLAPSKSNDPNQMLTKEDNTIR 60
DB 307 DVTGASAPPTVIVSGKRVYVDDPHDQIOLAPSKSNDPNQMLTKEDNTIR 362
QY 61 NSGCTTGYAGVYVMEPCNIVBAATVQWNGTININRSNIVLAASGIGTIT 120
DB 363 NSGCTTGYAGVYVMEPCNIVBAATVQWNGTININRSNIVLAASGIGTIT 422
QY 121 VQTLDTYLGQGLAGNDAPREVTIYGFRLDQMSNGSWSVWETCDSSQKQKALYD 180
DB 423 VQTLDTYLGQGLAGNDAPREVTIYGFRLDQMSNGSWSVWETCDSSQKQKALYD 481
QY 181 GSIRPKNDQCLTVGRDSVSTIVIVSGSAGSQRWVFTNEVALIMLKSGLAMVQA 240
DB 482 GSIRPKNDQCLTVGRDSVSTIVIVSGSAGSQRWVFTNEVALIMLKSGLAMVQA 541
QY 241 NPKLRRIIIPATKRNQWMLPV 263
DB 542 NPKLRRIIIPATKRNQWMLPV 564

RESULT 4

Q8BK01 PRELIMINARY; FRT; 263 AA.

AC	Q8LKO1	01-OCT-2002	(TREMBLrel. 22, Created)
DT	01-OCT-2002 <th>(TREMBLrel. 22, Last sequence update)</th> <td></td>	(TREMBLrel. 22, Last sequence update)	
DT	01-MAR-2003 <th>(TREMBLrel. 23, Last annotation update)</th> <td></td>	(TREMBLrel. 23, Last annotation update)	
DB	Lectin chain B isoform 3 (Fragment).		
OS	Viscum album subsp. coloratum.		
OC	Embryophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eudicotyledons, Vascularia, Vascularia, Eudicotyledons, core eudicots.		
CC	Stratigilys, Viscaceae, Viscum.		
NC	NCBI_TaxId=159976;		
LN	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=2156752; PubMed=11710524;		
RA	Do M.-S., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,		
RA	Do M.-S., Song S.-K.,		
RT	"cDNA cloning and sequence analysis of the lectin genes of the Korean		
RT	"mistlecote (Viscum album coloratum)."		
RI	Mol. Cells 12:215-220(2001).		
RP	SEQUENCE FROM N.A.		
RA	Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,		
RA	Do M.-S., Song S.-K.,		
RL	Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.		
RL	EMBL: AF508919; ANA46937.1; -		
DR	InterPro: IPR000772; Racin_B_lectin.		
DR	Pfam: PF00652; Racin_B_lectin. 6.		
DR	SMART, SM0458; Racin_B_lectin. 2.		
DR	PROSITE, PS50241; Racin_B_lectin. 2.		
FT	NON_TER		
FT	1		
FT	365		
FT	TER		
SC	SEQUENCE 263 AA; 29071 MW; 3F5C4AD8640F061D CnCr4;		
Query Match	74.9% Score 1058.5; DB 10; Length 263;		
Best Local Similarity	75.7%; Pred. No. 3, 1e-86;		
Matches 199; Conservative 24; Mismatches 39; Indels 1; Gaps 1			
QY	1 DDTVSASBPRTVTVASGSMGVVDVDDPFEDGNQIQAMPSSKSNPDQMTIKEDQNIHS 60		
DB	1 DDDCTCPBSPFTVTVAGSNLCVDRNGRFGDNPQAMFCSSNDPMDLITRRGTHS 60		
QY	61 NSGCTTGYGTGYGVYVITCDNAPRNTQYNDNTINPSNITVLAASGIGKITLT 120		
DB	121 GSPKPNQOGCTVAGSDSHPTVPEVTVYGRQLCEANSSSVYEVCSHRND-KVALYD 179		
DB	6. NSKCTITVGRDGMWVWVYCNTPRAREVITWQIMENQITVAPSSVVLGAASGSRITLT 120		
QY	121 VQTLDTVLTGGWMLKANDTIPSEVTVTGVFRLCMESNGSVWVETCDSSQSNQKMALYD 180		
QY	121 VGTSPKPNQOGCTVAGSDSHPTVPEVTVYGRQLCEANSSSVYEVCSHRND-KVALYD 240		
DB	180 GSRKQNRNQGLCTQCDSSVTVYVNSCSAASGSRVPTFNKGITLTNLDNLTVDVHGS 239		
QY	241 NPLKRRITIVPAKPGQWMTLV 263		
DB	240 NPLSRITIVPAKPGQWMTLV 262		
REMARK 5			
ID	Q8LKO3	PREDIMINARY; PRT; 266 AA.	
AC	Q8LKO3		
DT	01-OCT-2002	(TREMBLrel. 22, Created)	
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	
OS	Lectin chain B isoform 1 (Fragment).		
OS	Viscum album subsp. coloratum.		
OC	Embryophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eudicotyledons, Vascularia, Vascularia, Eudicotyledons, core eudicots.		
CC	Stratigilys, Viscaceae, Viscum.		
NC	NCBI_TaxId=159976;		
LN	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=2156752; PubMed=11710524;		

RA	D	Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA	A	Do M.-S., Song S.K.,
RT	"CDNA cloning and sequence analysis of the lectin genes of the Korean	
RT	mistletoe (<i>Viscum album coloratum</i>)."	
LN	Mol. Cells 12:215-220(2001).	
EN	[2]	
CC	SEQUENCE FROM N.A.	
RA	Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,	
RA	Submitted (May 2002) to the EMBL/Genbank/DDBB databases.	
RL	EMBL; AF089817; XMM6935.1;	
DR	InepPro; IPRO00772; Ricin B.Lectin.	
DR	Pfam; PF00652; Ricin B.Lectin; 5.	
DR	SMART; SMO0458; RICIN; 2.	
DR	PROSITE; PS50231; RICIN_B_LECTIN; 2.	
FT	NON TER	
FT	NON TER	
SO	SEQUENCE 266 AA; 29537 MW; 4A5147C37B94C73 CRC64;	
Query Match	68.3%; Score 965; DB 10; Length 266;	
Best local	Similarity 67.2%; Pctd No. 58-78;	
Matches 180;	Conservative 33; Mismatches 49; Indels 4; Gaps 2;	
QY	1 DVDTSSASPEFVATVRSGKRVADDDPHGNGQICMLPESKNSDPMQLMTRENDITRS 60	
Db	1 DVTCTTSPTFRVGRNGCLADVEEDVDHGDSIQMLPKSKSDMQMLTRIDDTIRS 60	
QY	61 NSGLTIVGTAGVYMIFDCNTAVREATIQTQINDGTTIMPSSNVL--ASSGIKGT 117	
Db	61 NSGLITIGTHASIMYIMIDONGKGNGLTQQINGGILIPRSMVLTGTSSKRITGT 120	
QY	118 TLTVQTLDTTGCGMAMNTAPAREATTIGSPRLCKENSNGSWTERCSSOKRGKHAL 177	
Db	121 TPLTQTVGSYGQMAMANTARERATTIGSRHDKERSGAKVGVTCVSQKQK-QWAL 179	
QY	178 YSGSGISPFKPNQDDCHTGYSDSYSTVINIVSCSGASGSGSWMTFNEALIKSGGLANDV 237	
Db	180 YSGGISPFPRPYDCHTGYSDSYSTVINIVSFCTASPRGKWTFNKALKALINKRLAMDV 239	
QY	238 AQAANKLRRIITITPATNCGRMPV 263	
Db	240 ASNPSLRLIIPISTVTPNQMWLPV 265	
RESULT 6		
ID	Q41174 PRELMINARY; FRT, 541 AA.	
CD	Q41174	
DT	01-MAY-1996 (TrEMBL), 01. Created.	
DT	01-JUN-1996 (TrEMBL), 01. (Sequence update)	
DT	01-MAR-2003 (TrEMBL), 23. (Last annotation update)	
DE	Prioritin A chain (EC 3.2.2.22) (RNA-N-glycosidase) (Prasman).	
OS	Ricinus communis (Castor bean).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC	eurosidia I; Malvales; Euphorbiaceae; Riciniaceae; Ricinus.	
OX	NCBI_TaxId=3989;	
OX	SEQUENCE FROM N.A.	
RX	MEDLINE=9238877; PubMed=133311;	
RX	Roberts L.M., Teegee J.M., Lloyd J.M.;	
RL	"Molecular cloning of ricin."	
RL	Targeted Diagn. Ther. 7:81-97(1992).	
CC	-; CATALYTIC ACTIVITY; ENOXYHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.	
CC	-; SIMILARITY; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
CC	EMBL; AF089817; Ricin B.Lectin.	
CC	HSSP; F02879; RIR,	
CC	InepPro; IPRO00772, RIR	
CC	InepPro; IPRO01574, RIR	
CC	InepPro; IPRO01574, Somatostatin.	
CC	Pfam; PF00652; Ricin B.Lectin; 6.	

DR PFAM: PF00161; RIP; 1.
 DR PRINTS: P000396; SHIGARICIN.
 DR SMART: SM00458; RICIN; 2.
 DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 DR PROSITE: PS00318; SOMATOTROPIN_2; 1.
 DR HYDROLASE; TOXIN.
 DR NON TER
 SQ SEQUENCE 541 AA; 60281 MW; 28732CDPFI2E3D9 CRC64;

Query Match 63.5%; Score 898.5; DB 10; Length 541;
 Best Local Similarity 63.5%; Pred. No. 1.4e-71;
 Matches 165; Conservative 34; Mismatches 60; Indels 1; Gaps 1;

QY 5 CSASEPTVAVIGSGMRYVDVDDFDHNOQIOMPSKSNDDPNOIWKIRNDITISNSGC 64
 DB 283 CMDEPTVAVIGSGMRYVDVDDFDHNOQIOMPSKSNDDPNOIWKIRNDITISNSGC 342
 QY 65 LTTTGTVAGTVYVMTFCNTAVREATVQIWDNGTIIIPRSNVLAAASGIGTLLVQTL 124
 DB 343 LTTTGTVAGTVYVMTFCNTAVREATVQIWDNGTIIIPRSNVLAAASGIGTLLVQTL 402
 QY 125 DYTLCQGMLAGNDPAPEVTVIGSRDLQMSNSGSGVWETDSSQKQKALYQDSIR 184
 DB 403 IVASQGMPLTNVTPFTTVIGVGLCLQNSGQVWETDSSQKQKALYQDSIR 461
 QY 185 PRONQDCLTVGRDSVSTVINIVSGSASGSRWFVTEVTAIINLKSGLAMVDAQNP 244
 DB 462 PQNRNDCLTVGRDSVSTVINIVSGSASGSRWFVTEVTAIINLKSGLAMVDAQNP 521
 QY 245 RLITVPAKGRNQKMLP 264
 DB 522 KQITVPAKGRNQKMLP 541

RESULT 7

Q1143 PRELIMINARY; PRT; 263 AA.

ID Q1143
 AC Q1143; PRELIMINARY; PRT; 263 AA.
 DT 01-NOV-1996 (TREMUR-rel. 01, Created)
 DT 01-NOV-1996 (TREMUR-rel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMUR-rel. 23, Last annotation update)
 DT 01-MAR-2003 (TREMUR-rel. 23, Last annotation update)
 GN RICIN B BETA CHAIN (fragment).
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
 NC NCBITaxID=3989;
 NX 111
 RF SEQUENCE FROM N.A.
 RA Leadin B.F., Murray E.E., Halling A.C., Halling K.C., Tlakarac N.,
 RA Leadin B.F., Murray E.E., Halling A.C., Halling K.C., Tlakarac N.,
 RT "Characterization of a cDNA encoding 'ricin B', a hybrid ricin-Ricinus
 RT communis agglutinin gene from the castor plant Ricinus communis.";
 RL Plant Mol. Biol. 9:287-295(1987).
 DR EMBL: M1631; AA04506.1; -.
 DR HSSP: P02879; 2M1.
 DR InterPro: IPR000772; Ricin_B_Lectin.
 DR InterPro: IPR001400; Somatotropin.
 DR Pfam: PF00652; Ricin_B_Lectin; 6.
 DR SMART: PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE: PS00318; SOMATOTROPIN_2; 1.
 DR PROSITE: PS00318; SOMATOTROPIN_2; 1.
 FT NON TER
 SQ SEQUENCE 263 AA; 29134 MW; AAB80PDDIDIE44 CRC64;

Query Match 61.0%; Score 863; DB 10; Length 263;
 Best Local Similarity 60.9%; Pred. No. 8.1e-69;
 Matches 159; Conservative 36; Mismatches 62; Indels 2; Gaps 2;

QY 5 CSASEPTVAVIGSGMRYVDVDDFDHNOQIOMPSKSNDDPNOIWKIRNDITISNSGC 64
 DB 283 CMDEPTVAVIGSGMRYVDVDDFDHNOQIOMPSKSNDDPNOIWKIRNDITISNSGC 342
 QY 65 LTTTGTVAGTVYVMTFCNTAVREATVQIWDNGTIIIPRSNVLAAASGIGTLLVQTL 124
 DB 343 LTTTGTVAGTVYVMTFCNTAVREATVQIWDNGTIIIPRSNVLAAASGIGTLLVQTL 402
 QY 125 DYTLCQGMLAGNDPAPEVTVIGSRDLQMSNSGSGVWETDSSQKQKALYQDSIR 184
 DB 403 IVASQGMPLTNVTPFTTVIGVGLCLQNSGQVWETDSSQKQKALYQDSIR 461
 QY 185 PRONQDCLTVGRDSVSTVINIVSGSASGSRWFVTEVTAIINLKSGLAMVDAQNP 244
 DB 462 PQNRNDCLTVGRDSVSTVINIVSGSASGSRWFVTEVTAIINLKSGLAMVDAQNP 521
 QY 245 RLITVPAKGRNQKMLP 264
 DB 522 KQITVPAKGRNQKMLP 541

DB 4 CMDEPTVAVIGSGMRYVDVDDFDHNOQIOMPSKSNDDPNOIWKIRNDITISNSGC 63
 QY 65 LTTTGTVAGTVYVMTFCNTAVREATVQIWDNGTIIIPRSNVLAAASGIGTLLVQTL 124
 DB 64 LTTTGTVAGTVYVMTFCNTAVREATVQIWDNGTIIIPRSNVLAAASGIGTLLVQTL 123
 QY 125 DYTLCQGMLAGNDPAPEVTVIGSRDLQMSNSGSGVWETDSSQKQKALYQDSIR 184
 DB 403 IVASQGMPLTNVTPFTTVIGVGLCLQNSGQVWETDSSQKQKALYQDSIR 461
 QY 185 PRONQDCLTVGRDSVSTVINIVSGSASGSRWFVTEVTAIINLKSGLAMVDAQNP 244
 DB 462 PQNRNDCLTVGRDSVSTVINIVSGSASGSRWFVTEVTAIINLKSGLAMVDAQNP 521
 QY 245 RLITVPAKGRNQKMLP 264
 DB 522 KQITVPAKGRNQKMLP 541

RESULT 8

Q1484 PRELIMINARY; PRT; 580 AA.

ID Q1484
 AC Q1484; PRELIMINARY; PRT; 580 AA.
 DT 01-DEC-2001 (TREMUR-rel. 19, Created)
 DT 01-DEC-2001 (TREMUR-rel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMUR-rel. 23, Last annotation update)
 DT 01-MAR-2003 (TREMUR-rel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein in cinamomoin II precursor
 DE (EC 3.2.2.22) (rRNA N-glycosidase).
 OS Cinamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinamomum.
 NC NCBITaxID=13429;
 NX 111
 RF SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinamomoin proteins and study of their expression
 RT patterns.";
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 CC -1. SPECIFIC ADenosINE ON THE 28S RRNA.
 CC -1. SPECIFIC ADenosINE ON THE 28S RRNA.
 CC EMBL: M1631; AA04506.1; -.
 DR EMBL: M1631; AA04506.1; -.
 DR InterPro: IPR000772; Ricin_B_Lectin.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00652; Ricin_B_Lectin; 6.
 DR Pfam: PF00652; Ricin_B_Lectin; 6.
 DR PRINTS: P000396; SHIGARICIN.
 DR SMART: PS00458; RICIN; 2.
 DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
 DR HYDROLASE; Signal; TOXIN.
 FT SIGNAL 33
 FT CHAIN 33
 SQ SEQUENCE 580 AA; 64265 MW; 37342892CEDECBF CRC64;

Query Match 59.3%; Score 839; DB 10; Length 580;
 Best Local Similarity 61.0%; Pred. No. 3.1e-66;
 Matches 161; Conservative 34; Mismatches 67; Indels 2; Gaps 2;

QY 1 DYTLCQGMLAGNDPAPEVTVIGSRDLQMSNSGSGVWETDSSQKQKALYQDSIR 184
 DB 317 RDYLCQGMLAGNDPAPEVTVIGSRDLQMSNSGSGVWETDSSQKQKALYQDSIR 180
 QY 65 LTTTGTVAGTVYVMTFCNTAVREATVQIWDNGTIIIPRSNVLAAASGIGTLLVQTL 120
 DB 64 LTTTGTVAGTVYVMTFCNTAVREATVQIWDNGTIIIPRSNVLAAASGIGTLLVQTL 123
 QY 377 NGKCLTVAGTVYVMTFCNTAVREATVQIWDNGTIIIPRSNVLAAASGIGTLLVQTL 436
 DB 121 VQNTVAVSRQGMLAGNDPAPEVTVIGSRDLQMSNSGSGVWETDSSQKQKALYQDSIR 180
 QY 437 VQNTVAVSRQGMLAGNDPAPEVTVIGSRDLQMSNSGSGVWETDSSQKQKALYQDSIR 180
 DB 181 GSIRPRONQDCLTVGRDSVSTVINIVSGSASGSRWFVTEVTAIINLKSGLAMVDAQ 239

RT	"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)		
RT	genes encoding cinnamomin proteins and study of their expression		
RT	patterns "		
RT	Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.		
CC	-1- CATALYTIC ACTIVITY: ENDOPEPTIDOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE		
CC	SPECIFIC ADENOSINE ON THE 26S RNA.		
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.		
CC	EMBL: AF039801; AAA82458.1; "		
DR	Interpro: IPR000772; Richin_B.lectin.		
DR	Interpro: IPR001574; RIP.		
DR	Pfam: PF00652; Richin_B.lectin. 5.		
DR	Pfam: pf00161; RIP. 1.		
DR	PRINTS: PR00356; SHIGARICIN.		
DR	SMART: SM00458; RICIN. 2.		
DR	PROSITE: PS50231; RICIN_B.LECTIN. 2.		
KW	Hydrolase; Signal; Toxin.		
KW	Signal.		
FT	Signal		
FT	1		
FT	3		
FT	32		
FT	1		
FT	3		
FT	581		
FT	CHAIN		
FT	POTENTIAL		
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN		
FT	CINNAMOMIN		
FT	SEQUENCE		
SC	581 AA;	64215 MW;	688575BSFASD196 CCKC4;

[illegible]

```

Q06076.12
Q06076 PRELIMINARY, FRT, 528 AA.
AC Q06076
AD 01-NOV-1996 (TRMBREL_01, Created)
AD 01-NOV-1996 (TRMBREL_01, Sequence update)
AD 01-MAR-2003 (TRMBREL_23, Last annotation update)
AD Abin-4 (BC 3.2.2.12) (RNA N-Glycosidase) (Fragment) .
OC Abrus precatorius (Indian Licorice) (Crab's Eye) .
OC Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosales;
OC Eucrotidae I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OC NCBI_Taxid=3916;
RX MEDLINE=93132798; PubMed=842133;
RX Hung C.-H., Lee M.-C., Lee T.-C., Lin Y.-Y.;
RX "Primary structure of three distinct isoenzymes determined by cDNA
RX sequencing: conservation and significance."
RX J. Mol. Biol. 123:263-267(1993).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL: M98346; AAA32626.1; "...
DR HSSP; P1140; IABR.
DR InterPro; IPRO00772; Rictin_B_fctlin.
DR InterPro; IPRO01574; RIB.

```

DR	Pfam:	PF00652;	Ricin_B_lectin; 6
DR	Pfam:	PF00161; RIP; 1.	
DR	PRINTS:	PR00396;	SHTGA_RICIN.
DR	SMART:	SM00458;	RKCTN; 2.
DR	PROSITE:	PS50231;	RICIN_B_LECTIN; 2.
DR	PROSITE:	PS00725;	SHTGA_RICIN; 1.
DR	PROSITE:	PS00456;	Toxin..
FT	NON TER	1.	
FT	NON TER	528	
SEQUENCE	528 AA;	58870 MW;	62ED42F58FE60FA CRC64;
Query Match	52.3%;	Score 740;	DB 10; Length 528;
Best Local Similarity	53.6%;	Pred. No. 1,be-57;	
Matches	140;	Conservative 43;	Mismatches 76; Indels 2; Gaps 2;
OY	5	CSEPTIATVSGCNRYVDDEPHDQIQALPSSXSNPNQMTXIEDNTIRNSGS	63
Dd	269	CSSRIETRTTRIGRDGDCVVYDDGDHKNMILIMKCRLREHQMTLTSADLTIRNSGK	128
OY	64	CLTGYTGAGYYVPDCAVAEENTITQINDGTITPPSNLYLAASSG;KGTLLVTQT	123
Dd	328	CLTFEGAAQGVWVIDGTSAVAETWEIMDNGTIIIPKSLALYSLESSSMGGTLVTQT	388
OY	124	LDTYGGMVLANDTPAEVITYGERDLCEMSNQSVVETFDSDSQNKAKLVYDGSI	183
Dd	389	NELIFRGGRKRNNTSPPTSISGLDLCMQNQSVLMDCKNKKED-QVALITDSGI	447
OY	184	RPKNQDGLCLTWDGVSIVTYNISSCGASGSGRWTFNRYVLIINKSLGMLNDPAQPK	243
Dd	448	RSYQVTCNLTKSKHNCSPLTVLACANCMASQWLFFNDQSISYSLYDMNDVYKSDPS	507
OY	244	LRRITLYPTGPNQMQLPVF	264
Dd	508	KRQILMFYTGKPEQIMTLTF	528
DESIGN 13			
OSBSA43			
ID OSBSA43	PRELIMINARY;	PRT;	382 AA.
AC OSBSA43			
DT	01-JUN-2002 (TREMBLrel. 21.	Created)	
DT	01-JUN-2002 (TREMBLrel. 21.	Last sequence update)	
DT	01-MAR-2003 (TREMBLrel. 23.	Last annotation update)	
Dd	Abrin isoform G (EC 3.2.2.22)	(tRNA N-glycosylase) (Fragment).	
Dd	Abrus precatorius (Indian licorice)	(Crab's eye)	
OC	Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophytes,		
CC	embryophyte, Fabales, Fabaceae, Papilionoidae, Abresee, Abrus;		
CC	ericoides, Babingtonia, Babingtonia, Babingtonia, Babingtonia;		
XX	NCBI_TaxID=4816;		
RM	SEQUENCES FROM N.A.		
RP	TISSUES=leaf;		
RA	Cook J.P., Roberts L.M., Lord M.;		
RU	New isoform of Abrin - Abrin G;		
RU	Submitted (JAN-2002) TO THE EMBL/GENB/CCDS databases		
CC	-1. SPECIFIC ABRINS ON THE 28S RNA.		
CC	-1. SIMILARITY: ALN77434.1; "		
CC	FEMU; A479626; BA177434.1; "		
DR	Interpro; IPR000172; Ricin_B_lectin.		
DR	Interpro; IPR001574; Ricin_B_lectin.		
DR	Pfam; PF00652; Ricin_B_lectin; 6.		
DR	Pfam; PRO0161; RIP; 1.		
DR	SMART; SM00458; RICIN; 2		
DR	PROSITE; PS00231; RICIN_B_LECTIN; 2.		
DR	PROSITE; PS00725; SHTGA_RICIN; 1.		
XX	Hydrolease; Toxin.		
PT	CHAIN	1	
FT	CHAIN	>105	ABRIN A CHAIN.
FT	NON TER	116	
FT	NON TER	382	
SEQUENCE	382 AA;	42743 MW;	B0BA834181ADZEE CRC64;

Query Match 52.3%; Score 739.5; DB 10; Length 382;
Best Local Similarity 53.5%; Pred. No. 1.3e-57;
Matches 137; Conservative 41; Mismatches 77; Indels 1; Gaps 1;
QY 9 EPTTRIVRSGRVYVDDDDPHDQIQQLWPSKSNDDPQQLWTKRNTKNSGCLTTF 68
DB 128 EPTTRIVRSGRVYVDDDDPHDQIQQLWPSKSNDDPQQLWTKRNTKNSGCLTTF 187
QY 63 GTTASGYVYVYPCNTAVREACTIQIWDNGITINPSNULVLAASGKGTTLVOTIDYTL 128
DB 188 GTTASGYVYVYPCNTAVREACTIQIWDNGITINPSNULVLAASGKGTTLVOTIDYTL 247
QY 123 GCGMLAGNDTAPREVTIYGFEDLCMESNQSQVWVETCDSSQKQKQKALYDGSIRPKQN 188
DB 248 RQKRTGNDTSPPTVSIAGYSDLCMAHESNMWLADEENKQO-QMALYDGSIRPKQN 306
QY 189 ODQCLTVGRDSVSTVINIVSGSGAGSGQVFTNVAIINLKSGLMDVQAQAPRLRII 248
DB 307 TNNCLSKDHQSGTIVKSGSNMAGQVFTNVAIINLKSGLMDVQAQAPRLRII 366
QY 249 IYPTATGKXNQMWLPVF 264
DB 367 LMPYTGKXNQMWLPVF 382
RESULT 14
QY 09M653 PRELIMINARY; FRT; 547 AA.
AC 09M653, 2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Preproglutinin (EC 3.2.2.22) (rRNA N-glycosidase).
GN AAG.
OS Abrus precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Abrease; Abrus.
OX NCBI_TaxId=3816;
RN 11
RS SEQUENCE FROM N.A.
RX MEDLINE=20102702; PubMed=10636890;
RA Liu C.T., Tsai C.C., Lin S.C., Wang L.I., Hsu M.J.,
RA Lin J.Y.;
RT "Primary Structure and Function Analysis of the Abrus precatorius
RT Agglutinin A Chain by Site-directed Mutagenesis: Pro199 of Amphiphilic
RT alpha-Helix H Impairs Protein Synthesis Inhibitory Activity.";
RL J. Biol. Chem. 275:1897-1901(2000)
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SPECIFIC ADENOSINE ON THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL: AF140733.2; AF28309.1; .
DB HSSP; P11403.1ABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50251; RICIN_B_LECTIN; 2.
DR PROSITE; PS50275; SHIGARICIN; 1.
SQ SEQUENCE: 547 AA; 61248 MW; 355A325C2354A1BD CRC64;

Query Match 51.8%; Score 733; DB 10; Length 547;
Best Local Similarity 53.3%; Pred. No. 8e-57;
Matches 139; Conservative 39; Mismatches 81; Indels 2; Gaps 2;
QY 5 CSAS-EPTTRIVRSGRVYVDDDDPHDQIQQLWPSKSNDDPQQLWTKRNTKNSG 63
DB 288 CSAS-EPTTRIVRSGRVYVDDDDPHDQIQQLWPSKSNDDPQQLWTKRNTKNSG 347
QY 64 CLITVGTAGYVYVYPCNTAVREACTIQIWDNGITINPSNULVLAASGKGTTLVOT 123
DB 348 CLITVGTAGYVYVYPCNTAVREACTIQIWDNGITINPSNULVLAASGKGTTLVOT 407
QY 124 LDYTLGGMLAGNDTAPREVTIYGFEDLCMESNQSQVWVETCDSSQKQKQKALYDGS 183
DB 408 LDYTLGGMLAGNDTAPREVTIYGFEDLCMESNQSQVWVETCDSSQKQKQKALYDGS 466
QY 184 RPKMOPQCLTVGRDSVSTVINIVSGSGAGSGQVFTNVAIINLKSGLMDVQAQAPK 243
DB 467 RPKMOPQCLTVGRDSVSTVINIVSGSGAGSGQVFTNVAIINLKSGLMDVQAQAPK 526
QY 244 LRRIIIVATGKXNQMWLPVF 264
DB 527 LKQIIIMPTGNNAMQWLPVF 547
RESULT 15
QY 09M258 PRELIMINARY; FRT; 573 AA.
AC 09M258;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2003 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Ribosome-inactivating protein IRat (EC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment).
GN LectinR.
OS Iris hollandica (Dutch iris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
OX NCBI_TaxId=35976;
RN 11
RS SEQUENCE FROM N.A.
RA Van Damme E.J.M., Pauwels W.J.;
RT "Iris (Iris hollandica var. 'Professor Blaauw') plants express both type
RT 1 and type 2 ribosome-inactivating proteins in bulb tissue.";
RT Submitted (Apr-2000) to the EMBL/Genbank/DBS databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SPECIFIC ADENOSINE ON THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL: AF140733.2; AF28309.1;
DB HSSP; P11403.1ABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50251; RICIN_B_LECTIN; 2.
DR PROSITE; PS50275; SHIGARICIN; 1.
RN HYDROLASE; Toxin.
SQ SEQUENCE: 573 AA; 63759 MW; 1444339AFCDA5C CRC64;
Query Match 47.1%; Score 666.5; DB 10; Length 573;
Best Local Similarity 49.8%; Pred. No. 7.1e-51;
Matches 132; Conservative 38; Mismatches 92; Indels 3; Gaps 3;
QY 1 DDTYASAEPTTRIVRSGRVYVDDDDPHDQIQQLWPSKSNDDPQQLWTKRNTKNSG 60
DB 311 DDTYASAEPTTRIVRSGRVYVDDDDPHDQIQQLWPSKSNDDPQQLWTKRNTKNSG 120
QY 61 NSGCTVGTAGYVYVYPCNTAVREACTIQIWDNGITINPSNULVLAASGKGTTLVOT 120
DB 371 NSGCTVGTAGYVYVYPCNTAVREACTIQIWDNGITINPSNULVLAASGKGTTLVOT 429
QY 121 VQYDLVYTLGGMLAGNDTAPREVTIYGFEDLCMESN-QSGVWVETCDSSQKQKQKALY 179
DB 430 VQYDLVYTLGGMLAGNDTAPREVTIYGFEDLCMESN-QSGVWVETCDSSQKQKQKALY 488
QY 180 DSGIRPKQK 239
DB 489 DSGIRPKQK 548

Thu Dec 11 16:10:07 2003

us-09-601-667c-8.rpt

Page 8

Oy 240 ANPCLRRITYPATGKNQWMLPVF 264
Db 549 SDBLQOIIWSTGNQWMTTF 573

Search completed: December 11, 2003, 14:01:02
Job time : 21.347 secs

PI Preparation of mistletoe lectins in heterologous systems,
PI particularly for use as anticancer agents and immunostimulants
XX
XX
PS Claim 9; Fig 9b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and activates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B2 protein.
SQ Sequence 264 AA;
Query Match 100.0%; Score 1414; DB 20; Length 264;
Best Local Similarity 100.0%; Pred. No. 5,9e-135;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVTGASSEPTVAVIGSGRVDVDDPHQNOIQLPKSNMDPQMTTKRNDTRS 60
DB 1 DVTGASSEPTVAVIGSGRVDVDDPHQNOIQLPKSNMDPQMTTKRNDTRS 60
QY 61 NSCLTGYTAGVYVWFPCNTAVREACTIQINDGTIINPSSWVLAASGKOTLT 120
DB 61 NSCLTGYTAGVYVWFPCNTAVREACTIQINDGTIINPSSWVLAASGKOTLT 120
QY 121 VQTLDTLGGMLAGNDTAPREVTIYGFEDLCMESNGSVMWETCDSSQKGMALYGD 180
DB 121 VQTLDTLGGMLAGNDTAPREVTIYGFEDLCMESNGSVMWETCDSSQKGMALYGD 180
QY 181 GSIRPNQDQCLTVGRDSVSTVNIYVSCGASGSGRWFTNEVAILNKSLAMDVAQA 240
DB 181 GSIRPNQDQCLTVGRDSVSTVNIYVSCGASGSGRWFTNEVAILNKSLAMDVAQA 240
QY 241 NPKLRILIIYPATKPNQMWLPVF 264
DB 241 NPKLRILIIYPATKPNQMWLPVF 264
RESULT 2
AAV25993
ID AAV25993 standard; Protein; 265 AA.
AC AAV25993;
XX
XX 18-OCT-1999 (first entry)
DB Mistletoe lectin B2 variant protein fragment.
XX
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform; lectin B2.
XX
XX Viscum album.
XX
XX DE19804210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX

PI Morris P. Stiefel T. Voelter W. Welters P;
XX
XX WPI; 1999-445335/38.
DR N-PSDB; AA209117.
XX
XX Preparation of mistletoe lectins in heterologous systems,
PI particularly for use as anticancer agents and immunostimulants
XX
XX
PS Disclosure; Fig 15b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC of the mistletoe lectin binds to, and activates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B2 protein.
SQ Sequence 265 AA;
Query Match 100.0%; Score 1414; DB 20; Length 265;
Best Local Similarity 100.0%; Pred. No. 5,9e-135;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVTGASSEPTVAVIGSGRVDVDDPHQNOIQLPKSNMDPQMTTKRNDTRS 60
DB 1 DVTGASSEPTVAVIGSGRVDVDDPHQNOIQLPKSNMDPQMTTKRNDTRS 60
QY 61 NSCLTGYTAGVYVWFPCNTAVREACTIQINDGTIINPSSWVLAASGKOTLT 120
DB 61 NSCLTGYTAGVYVWFPCNTAVREACTIQINDGTIINPSSWVLAASGKOTLT 120
QY 121 VQTLDTLGGMLAGNDTAPREVTIYGFEDLCMESNGSVMWETCDSSQKGMALYGD 180
DB 121 VQTLDTLGGMLAGNDTAPREVTIYGFEDLCMESNGSVMWETCDSSQKGMALYGD 180
QY 181 GSIRPNQDQCLTVGRDSVSTVNIYVSCGASGSGRWFTNEVAILNKSLAMDVAQA 240
DB 181 GSIRPNQDQCLTVGRDSVSTVNIYVSCGASGSGRWFTNEVAILNKSLAMDVAQA 240
QY 241 NPKLRILIIYPATKPNQMWLPVF 264
DB 241 NPKLRILIIYPATKPNQMWLPVF 264
RESULT 3
AAV25986
ID AAV25986 standard; Protein; 264 AA.
AC AAV25986;
XX
XX 18-OCT-1999 (first entry)
DB Mistletoe lectin B1 protein fragment.
XX
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform; lectin B1.
XX
XX Viscum album.
XX
XX DE19804210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX

XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Walters P;
XX MPI: 1999-44535/38.
XX N-FSDS; A4209110.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 9; Fig 8b; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MA) of
XX the mistletoe lectin binds to, and activates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B1 protein.
XX Sequence 264 Ab;
XX
XX Query Match 97.5%; Score 1379; DB 20; Length 264;
XX Best Local Similarity 97.7%; Pred. No. 2,1e-131;
XX Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 DVTTCASAPPTVAVIGSGMVDVDDDFDQNGQIQLPFSKNDPQQLMTIKEDITRS 60
XX 1 DVTTCASAPPTVAVIGSGMVDVDDDFDQNGQIQLPFSKNDPQQLMTIKEDITRS 60
XX 61 NSGCLTGYTAGVYVIMFDCTAVREATIQTNDNGTIINPESNLVLAASGKQTTLT 120
XX 61 NSGCLTGYTAGVYVIMFDCTAVREATIQTNDNGTIINPESNLVLAASGKQTTLT 120
XX 121 VQTLDTYLLQGMLAGNDTAPREVITYGPRDLCKESNQSQVWVETDSSQKNGKALYGD 180
XX 121 VQTLDTYLLQGMLAGNDTAPREVITYGPRDLCKESNQSQVWVETDSSQKNGKALYGD 180
XX 122 VQTLDTYLLQGMLAGNDTAPREVITYGPRDLCKESNQSQVWVETDSSQKNGKALYGD 180
XX 122 VQTLDTYLLQGMLAGNDTAPREVITYGPRDLCKESNQSQVWVETDSSQKNGKALYGD 180
XX 181 GSIRPKNQDQCLTSGRDSVSTVINIVSCGASGSGRWVFTNEGAILNLKSLAMOVQA 240
XX 181 GSIRPKNQDQCLTSGRDSVSTVINIVSCGASGSGRWVFTNEGAILNLKSLAMOVQA 240
XX 241 NPCLRRITIIYPATGKPNOMLVPF 264
XX 241 NPCLRRITIIYPATGKPNOMLVPF 264
XX
XX RESULT 4
XX AA25988
XX ID AA25988 standard; Protein; 264 AA.
XX
XX AA25988;
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B3 protein fragment.
XX
XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B3.
XX
XX Viscum album.

XX DB19604210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX Morris P, Stiefel T, Voelter W, Walters P;
XX MPI: 1999-44535/38.
XX N-FSDS; A4209112.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 9; Fig 10b; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MA) of
XX the mistletoe lectin binds to, and activates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B3 protein.
XX Sequence 264 Aa;
XX
XX Query Match 97.5%; Score 1379; DB 20; Length 264;
XX Best Local Similarity 97.7%; Pred. No. 2,1e-131;
XX Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 DVTTCASAPPTVAVIGSGMVDVDDDFDQNGQIQLPFSKNDPQQLMTIKEDITRS 60
XX 1 DVTTCASAPPTVAVIGSGMVDVDDDFDQNGQIQLPFSKNDPQQLMTIKEDITRS 60
XX 61 NSGCLTGYTAGVYVIMFDCTAVREATIQTNDNGTIINPESNLVLAASGKQTTLT 120
XX 61 NSGCLTGYTAGVYVIMFDCTAVREATIQTNDNGTIINPESNLVLAASGKQTTLT 120
XX 121 VQTLDTYLLQGMLAGNDTAPREVITYGPRDLCKESNQSQVWVETDSSQKNGKALYGD 180
XX 121 VQTLDTYLLQGMLAGNDTAPREVITYGPRDLCKESNQSQVWVETDSSQKNGKALYGD 180
XX 122 VQTLDTYLLQGMLAGNDTAPREVITYGPRDLCKESNQSQVWVETDSSQKNGKALYGD 180
XX 122 VQTLDTYLLQGMLAGNDTAPREVITYGPRDLCKESNQSQVWVETDSSQKNGKALYGD 180
XX 181 GSIRPKNQDQCLTSGRDSVSTVINIVSCGASGSGRWVFTNEGAILNLKSLAMOVQA 240
XX 181 GSIRPKNQDQCLTSGRDSVSTVINIVSCGASGSGRWVFTNEGAILNLKSLAMOVQA 240
XX 241 NPCLRRITIIYPATGKPNOMLVPF 264
XX 241 NPCLRRITIIYPATGKPNOMLVPF 264
XX
XX RESULT 5
XX AA25994
XX ID AA25994 standard; Protein; 265 AA.
XX
XX AA25994;
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B3 variant protein fragment.
XX
XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

Thu Dec 11 16:10:05 2003

us-09-601-667c-8-rag

Page 4

XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KV cancer; cytotoxicity; antigen; isoform; lectin B3.
XX Viscum album.
XX DEL9804210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welters P;
XX WPI: 1999-44535/38.
XX N-PSDB; AA209118.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Disclosure; Fig 14B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of the
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response against bacterial (or viral) infections. The method allows production of
XX humanized mistletoe lectins (I) and its fragments, and its individual isoforms
XX of mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B3 protein.
SQ Sequence 265 AA;
Query Match 97.5%; Score 1379; DB 20; Length 265;
Best Local Similarity 97.7%; Pred. No. 2.1e-131;
Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 DDTYCSASPTVAIVSGKRVYEDDDPHGNOQLWPKSKNDPNQLTIRKNTIS 60
DB 1 DDTYCSASPTVAIVSGKRVYEDDDPHGNOQLWPKSKNDPNQLTIRKNTIS 60
QY 61 NSGCLTGYTAGVYVIMPCQYVKEATIMQIMNGTIIIPRSNLVLAASGKIGTIT 120
DB 61 NSGCLTGYTAGVYVIMPCQYVKEATIMQIMNGTIIIPRSNLVLAASGKIGTIT 120
QY 121 VQTLVYLIGQWLAGNDTAPREVTIYGFRLDCHESNGSVWFTCDSSQKQKALYCD 180
DB 121 VQTLVYLIGQWLAGNDTAPREVTIYGFRLDCHESNGSVWFTCDSSQKQKALYCD 180
QY 181 GSIRPKQNDQCLTVGRDSVSTVINIVSGSGSSQSWFTNEGALINLKGALNDVPAQ 240
DB 181 GSIRPKQNDQCLTVGRDSVSTVINIVSGSGSSQSWFTNEGALINLKGALNDVPAQ 240
QY 241 NPKLRRIIYPATKKNQWMLPVF 264
DB 241 NPKLRRIIYPATKKNQWMLPVF 264
RESULT 6
AA25992
ID AA25992 standard; Protein; 265 AA.
AC AA25992;
XX
DT 18-OCT-1999 (first entry)

XX Mistletoe lectin B1 variant protein fragment.
DE
XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MLA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KV lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KV cancer; cytotoxicity; antigen; isoform; lectin B1.
XX Viscum album.
XX DEL9804210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welters P;
XX WPI: 1999-44535/38.
XX N-PSDB; AA209118.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Disclosure; Fig 14B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of the
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response against bacterial (or viral) infections. The method allows production of
XX humanized mistletoe lectins (I) and its fragments, and its individual isoforms
XX of mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B1 protein.
SQ Sequence 265 AA;
Query Match 97.5%; Score 1379; DB 20; Length 265;
Best Local Similarity 97.7%; Pred. No. 2.1e-131;
Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 DDTYCSASPTVAIVSGKRVYEDDDPHGNOQLWPKSKNDPNQLTIRKNTIS 60
DB 1 DDTYCSASPTVAIVSGKRVYEDDDPHGNOQLWPKSKNDPNQLTIRKNTIS 60
QY 61 NSGCLTGYTAGVYVIMPCQYVKEATIMQIMNGTIIIPRSNLVLAASGKIGTIT 120
DB 61 NSGCLTGYTAGVYVIMPCQYVKEATIMQIMNGTIIIPRSNLVLAASGKIGTIT 120
QY 121 VQTLVYLIGQWLAGNDTAPREVTIYGFRLDCHESNGSVWFTCDSSQKQKALYCD 180
DB 121 VQTLVYLIGQWLAGNDTAPREVTIYGFRLDCHESNGSVWFTCDSSQKQKALYCD 180
QY 181 GSIRPKQNDQCLTVGRDSVSTVINIVSGSGSSQSWFTNEGALINLKGALNDVPAQ 240
DB 181 GSIRPKQNDQCLTVGRDSVSTVINIVSGSGSSQSWFTNEGALINLKGALNDVPAQ 240
QY 241 NPKLRRIIYPATKKNQWMLPVF 264
DB 241 NPKLRRIIYPATKKNQWMLPVF 264
RESULT 7
AA25989

Thu Dec 11 16:10:05 2003

us-09-601-667c-8.rag

Page 5

```
ID  XX  AA25989 standard; Protein; 264 AA.
XX  XX  AA25989;
XX  XX  18-OCT-1999 (first entry)
XX  XX  Mistletoe lectin B4 protein fragment.
XX  XX  Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX  XX  ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX  XX  lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX  XX  cancer; cytotoxicity; antigen; isoform; lectin B4.
XX  XX  Viscum album.
XX  XX  DE19804210-A1.
XX  XX  12-AUG-1999.
XX  XX  03-FEB-1998; 98DB-1004210.
XX  XX  03-FEB-1998; 98DB-1004210.
XX  XX  03-FEB-1998; 98DB-1004210.
XX  XX  (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX  XX  Morris P, Stiefel T, Voelter W, Walters P;
XX  XX  WPI: 1999-44535/38.
XX  XX  N-PSDB; NA209113.
XX  XX  Preparation of mistletoe lectins in heterologous systems,
XX  XX  particularly for use as anticancer agents and immunostimulants
XX  XX  Claim 9; Fig 11B; 78pp; German.
XX  XX  This invention describes a novel mistletoe lectin (I) and its fragments
XX  XX  which have antitumor and immunostimulatory activity. The A-chain (MIA)
XX  XX  of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX  XX  ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX  XX  lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX  XX  fragments are used to treat uncontrolled cell growth (particularly of the
XX  XX  cancer) and if they lack cytotoxicity, to increase the strength of the
XX  XX  immune response, particularly to a co-administered antigen
XX  XX  (tumour-associated, bacterial or viral). The method allows production of
XX  XX  mistletoe lectin, and its individual chains, in many different isoforms
XX  XX  and on a large scale, at any time of the year. Recombinant products are
XX  XX  free from toxins present in natural mistletoe extracts. This sequence
XX  XX  represents a fragment of a mistletoe lectin B4 protein.
XX  XX  Sequence 264 AA:
XX  XX  Query Match 97.0%; Score 1371; DB 20; Length 264;
XX  XX  Best Local Similarity 97.3%; Pred. No. 1,36-13; Indels 0; Gaps 0;
XX  XX  Matches 257; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 DDVTCASSEPTVAVRVSQKAVDADDPDHGNQIQLPKSKNDPNQMLTKEDNTIRS 60
DB 1 DDVTCASSEPTVAVRVSQKAVDADDPDHGNQIQLPKSKNDPNQMLTKEDNTIRS 60
QY 61 NSGCLITTYGTYAGVYVIMFDCTANRERATVQWMDNTIINPRSNLYLAASGKGTIT 120
DB 61 NSGCLITTYGTYAGVYVIMFDCTANRERATVQWMDNTIINPRSNLYLAASGKGTIT 120
QY 121 VQIDLTGCGMLAGNDAPRATVQWMDNTIINPRSNLYLAASGKGTIT 180
DB 121 VQIDLTGCGMLAGNDAPRATVQWMDNTIINPRSNLYLAASGKGTIT 180
QY 122 VQIDLTGCGMLAGNDAPRATVQWMDNTIINPRSNLYLAASGKGTIT 180
DB 122 VQIDLTGCGMLAGNDAPRATVQWMDNTIINPRSNLYLAASGKGTIT 180
QY 181 GSIRPKONODCLTVGRDSVTVINIVSCGASGSGRWFTNEVALNLKGLAMDVQA 240
DB 181 GSIRPKONODCLTVGRDSVTVINIVSCGASGSGRWFTNEVALNLKGLAMDVQA 240
QY 241 NPLRRTITTPATCKPNQMLPVF 264
DB 241 NPLRRTITTPATCKPNQMLPVF 264
```

```
DB 241 NPLRRTITTPATCKPNQMLPVF 264
XX  XX  RESULT 8
XX  XX  AA25995
XX  XX  AA25995 standard; Protein; 265 AA.
XX  XX  AA25995;
XX  XX  18-OCT-1999 (first entry)
XX  XX  Mistletoe lectin B4 variant protein fragment.
XX  XX  Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX  XX  ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX  XX  lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX  XX  cancer; cytotoxicity; antigen; isoform; lectin B4.
XX  XX  Viscum album.
XX  XX  DE19804210-A1.
XX  XX  12-AUG-1999.
XX  XX  03-FEB-1998; 98DB-1004210.
XX  XX  03-FEB-1998; 98DB-1004210.
XX  XX  03-FEB-1998; 98DB-1004210.
XX  XX  (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX  XX  Morris P, Stiefel T, Voelter W, Walters P;
XX  XX  WPI: 1999-44535/38.
XX  XX  N-PSDB; NA209113.
XX  XX  Preparation of mistletoe lectins in heterologous systems,
XX  XX  particularly for use as anticancer agents and immunostimulants
XX  XX  Disclosure; Fig 17B; 78pp; German.
XX  XX  This invention describes a novel mistletoe lectin (I) and its fragments
XX  XX  which have antitumor and immunostimulatory activity. The A-chain (MIA)
XX  XX  of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX  XX  ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX  XX  lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX  XX  fragments are used to treat uncontrolled cell growth (particularly of the
XX  XX  cancer) and if they lack cytotoxicity, to increase the strength of the
XX  XX  immune response, particularly to a co-administered antigen
XX  XX  (tumour-associated, bacterial or viral). The method allows production of
XX  XX  mistletoe lectin, and its individual chains, in many different isoforms
XX  XX  and on a large scale, at any time of the year. Recombinant products are
XX  XX  free from toxins present in natural mistletoe extracts. This sequence
XX  XX  represents a fragment of a variant mistletoe lectin B4 protein.
XX  XX  Sequence 265 AA:
XX  XX  Query Match 97.0%; Score 1371; DB 20; Length 265;
XX  XX  Best Local Similarity 97.3%; Pred. No. 1,46-130; Indels 0; Gaps 0;
XX  XX  Matches 257; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 DDVTCASSEPTVAVRVSQKAVDADDPDHGNQIQLPKSKNDPNQMLTKEDNTIRS 60
DB 1 DDVTCASSEPTVAVRVSQKAVDADDPDHGNQIQLPKSKNDPNQMLTKEDNTIRS 60
QY 61 NSGCLITTYGTYAGVYVIMFDCTANRERATVQWMDNTIINPRSNLYLAASGKGTIT 120
DB 61 NSGCLITTYGTYAGVYVIMFDCTANRERATVQWMDNTIINPRSNLYLAASGKGTIT 120
QY 121 VQIDLTGCGMLAGNDAPRATVQWMDNTIINPRSNLYLAASGKGTIT 180
DB 121 VQIDLTGCGMLAGNDAPRATVQWMDNTIINPRSNLYLAASGKGTIT 180
QY 122 VQIDLTGCGMLAGNDAPRATVQWMDNTIINPRSNLYLAASGKGTIT 180
DB 122 VQIDLTGCGMLAGNDAPRATVQWMDNTIINPRSNLYLAASGKGTIT 180
QY 181 GSIRPKONODCLTVGRDSVTVINIVSCGASGSGRWFTNEVALNLKGLAMDVQA 240
DB 181 GSIRPKONODCLTVGRDSVTVINIVSCGASGSGRWFTNEVALNLKGLAMDVQA 240
```

DB 181 GSIRPKONQDCLTSGRDSVSTVINTVSCSAGSOGWVFNHGAJLNLKGPMDVQA 240
QY 241 NPKLRILITYPATKGNQWMLPVF 264
DB 241 NPKLRILITYPATKGNQWMLPVF 264

RESULT 9

AAV25990
ID AAV25990 standard; Protein: 264 AA.

AAV25990;
18-OCT-1999 (first entry)

XX Mistletoe lectin B5 protein fragment.

DE Mistletoe lectin B5 protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.

XX Viscum album.

OS Del19804210-A1.

XX Del19804210-A1.

PD 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelker W, Welters P;

DR WPI; 1999-44535/38.

XX N-PSDB; AA209114.

PT Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants

PS Claim 9; Fig 12B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MIA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly of the
CC tumour response, particularly to a co-administered antigen production of
CC immune-associated, bacterial or viral). The method allows production of
CC mistletoe lectin and its individual chains in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a mistletoe lectin B5 protein.

XX Sequence 264 AA;

QY Query Match 96.5%; Score 1364; DB 20; Length 264;
Best Local Similarity 96.6%; Pred. No. 6; 9e-130;

Matches 255; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVTYCSASEPTVRIYVGRGKRVYRDDPDHGNQIQLPKSKNDPNQWLTIKEDTIRS 60
DB 1 DVTYCSASEPTVRIYVGRGKRVYRDDPDHGNQIQLPKSKNDPNQWLTIKEDTIRS 60

QY 61 NSCLTYTGAGVYVIMFDCKTVAEATITWQMDNTITIPRSNIVLAASGIGKTLT 120
DB 61 NSCLTYTGAGVYVIMFDCKTVAEATITWQMDNTITIPRSNIVLAASGIGKTLT 120

QY 121 VQTLTYTLQCGWLANDTNAREVITVGRFLCHESNQSIVVETQSSQNGNCRNALVD 180
DB 121 VQTLTYTLQCGWLANDTNAREVITVGRFLCHESNQSIVVETQSSQNGNCRNALVD 180
QY 181 GSIRPKONQDCLTSGRDSVSTVINTVSCSAGSOGWVFNHGAJLNLKGPMDVQA 240
DB 181 GSIRPKONQDCLTSGRDSVSTVINTVSCSAGSOGWVFNHGAJLNLKGPMDVQA 240
QY 241 NPKLRILITYPATKGNQWMLPVF 264
DB 241 NPKLRILITYPATKGNQWMLPVF 264

RESULT 10

AAV25996
ID AAV25996 standard; Protein: 265 AA.

AAV25996;
18-OCT-1999 (first entry)

XX Mistletoe lectin B5 variant protein fragment.

DE Mistletoe lectin B5 variant protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.

XX Viscum album.

OS Del19804210-A1.

XX Del19804210-A1.

PD 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelker W, Welters P;

DR WPI; 1999-44535/38.

XX N-PSDB; AA209120.

PT Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants

PS Disclosure; Fig 18B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MIA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly of the
CC tumour response, particularly to a co-administered antigen production of
CC immune-associated, bacterial or viral). The method allows production of
CC mistletoe lectin and its individual chains in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a variant mistletoe lectin B5 protein.

XX Sequence 265 AA;

QY Query Match 96.5%; Score 1364; DB 20; Length 265;
Best Local Similarity 96.6%; Pred. No. 7e-130;

Matches 255; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVTYCSASEPTVRIYVGRGKRVYRDDPDHGNQIQLPKSKNDPNQWLTIKEDTIRS 60
DB 1 DVTYCSASEPTVRIYVGRGKRVYRDDPDHGNQIQLPKSKNDPNQWLTIKEDTIRS 60

Qy 61 NSGCLITGYVYGVYVIMFDQCNVAREATTWQIMNGTIIINPSNIVLAASSGIKGTTLT 120
Db 61 NSGCLITGYVYGVYVIMFDQCNVAREATTWQIMNGTIIINPSNIVLAASSGIKGTTLT 120
Qy 121 VQILDYTLGGQMLAGNDTAPREVTIYGFRLCMESNGSVWETCDSSQNGKALYGD 180
Db 121 VQILDYTLGGQMLAGNDTAPREVTIYGFRLCMESNGSVWETCDSSQNGKALYGD 180
Qy 181 GSIRPKONODQCLTVGRDSVSTVINIVSCGASGSGRMVFTNEVAIINTKSLAMDVAQA 240
Db 181 GSIRPKONODQCLTVGRDSVSTVINIVSCGASGSGRMVFTNEVAIINTKSLAMDVAQA 240
Qy 241 NPKLRKIIITTPANGKRNQMLPV 264
Db 241 NPKLRKIIITTPANGKRNQMLPV 264

RESULT 11
AAZ5985
ID AAZ5985 standard; Protein; 263 AA.
AC AAZ5985;
DT 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B protein fragment.
XX
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MAb; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B.
XX
XX Viscum album.
XX
XX DE19804210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX
XX Morris P, Stiefel T, Voelter W, Welters P;
XX WPI; 1999-445335/38.
XX N-PSDB; AAZ09109.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 9; Fig 7b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MA) of
XX the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of the
XX tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B protein.
XX
XX Sequence 263 AA;
XX
XX Query Match 92.4%; Score 1306.5; DB 20; Length 263;
XX Best Local Similarity 93.3%; Freq. No. 4,76-124;

Matches 247; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
Qy 1 DDTVTSASEPTVIRIVGRSGKRDVADDDPHQNGQIOLWFSKSNDDPNQMLTIXKNDITRS 60
Db 1 DDTVTSASEPTVIRIVGRSGKRDVADDDPHQNGQIOLWFSKSNDDPNQMLTIXKNDITRS 60
Qy 61 NSGCLITGYVYGVYVIMFDQCNVAREATTWQIMNGTIIINPSNIVLAASSGIKGTTLT 120
Db 61 NSGCLITGYVYGVYVIMFDQCNVAREATTWQIMNGTIIINPSNIVLAASSGIKGTTLT 120
Qy 121 VQILDYTLGGQMLAGNDTAPREVTIYGFRLCMESNGSVWETCDSSQNGKALYGD 180
Db 121 VQILDYTLGGQMLAGNDTAPREVTIYGFRLCMESNGSVWETCDSSQNGKALYGD 180
Qy 181 GSIRPKONODQCLTVGRDSVSTVINIVSCGASGSGRMVFTNEVAIINTKSLAMDVAQA 240
Db 181 GSIRPKONODQCLTVGRDSVSTVINIVSCGASGSGRMVFTNEVAIINTKSLAMDVAQA 240
Qy 241 NPKLRKIIITTPANGKRNQMLPV 263
Db 241 NPKLRKIIITTPANGKRNQMLPV 263

RESULT 12
AAZ5991
ID AAZ5991 standard; Protein; 264 AA.
AC AAZ5991;
DT 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin B variant protein fragment.
XX
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MAb; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B.
XX
XX Viscum album.
XX
XX DE19804210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX
XX Morris P, Stiefel T, Voelter W, Welters P;
XX WPI; 1999-445335/38.
XX N-PSDB; AAZ09115.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Disclosure; Fig 18b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumour and immunostimulatory activity. The A-chain (MA) of
XX the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of the
XX tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B protein.

XX Sequence 264 AA;
 SQ Query Match 92.4%; Score 1306.5; DB 20; Length 264;
 Best Local Similarity 93.9%; Pred. No. 4, 7e-124;
 Matches 247; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 DDTGSAEPTVRIYGRSGRVYRDDPHGNOIQIMPESKNDPQWLTKKNTIRS 60
 DB 1 DDTGSAEPTVRIYGRSGRVYRDDPHGNOIQIMPESKNDPQWLTKKNTIRS 60
 QY 61 NSCLITVGYTAGVYVMI FDCNTAVREATTIWIQNDGIIINPSNLVLAASGKKTTLT 120
 DB 61 NSCLITVGYTAGVYVMI FDCNTAVREATTIWIQNDGIIINPSNLVLAASGKKTTLT 120
 QY 121 VQTLDTLTGQWLAGNDYAFREATTIYGFRLCMESNGSVWVETCDSSQKQKALYGD 180
 DB 121 VQTLDTLTGQWLAGNDYAFREATTIYGFRLCMESNGSVWVETCDSSQKQKALYGD 180
 QY 122 VQTLDTLTGQWLAGNDYAFREATTIYGFRLCMESNGSVWVETCDSSQKQKALYGD 179
 DB 181 GSIRPKONODCLTVGRDSVSTVINIVCSGASGSGRVFTNEKALINIKSGLANDYAQA 240
 DB 180 GSIRPKONODCLTVGRDSVSTVINIVCSGASGSGRVFTNEKALINIKSGLANDYAQA 239
 QY 241 NPKLRRIIIYPATGKPNOMLPEV 263
 DB 240 NPKLRRIIIYPATGKPNOMLPEV 262

RESULT 13
 AA25979
 ID AAY25979 standard; Protein; 531 AA.
 AC AAY25979;
 DT 18-OCT-1999 (first entry)
 DE Mistletoe lectin I protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin I.
 OS Viscum album.
 PN DE19804210-A1.
 PD 12-AUG-1999.
 PE 03-FEB-1998; 98DB-1004210.
 PR 03-FEB-1998; 98DB-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelker W, Walters P;
 DR WPI; 1999-44535/38.
 DR N-PSDB; AA209106.
 XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX Claim 7, Fig 1B; 79pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a mistletoe lectin I protein fragment.
 XX Sequence 531 AA;
 SQ Query Match 92.4%; Score 1306.5; DB 20; Length 531;
 Best Local Similarity 93.9%; Pred. No. 4, 7e-123;
 Matches 247; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 DDTGSAEPTVRIYGRSGRVYRDDPHGNOIQIMPESKNDPQWLTKKNTIRS 60
 DB 269 DDTGSAEPTVRIYGRSGRVYRDDPHGNOIQIMPESKNDPQWLTKKNTIRS 328
 QY 61 NSCLITVGYTAGVYVMI FDCNTAVREATTIWIQNDGIIINPSNLVLAASGKKTTLT 120
 DB 329 NSCLITVGYTAGVYVMI FDCNTAVREATTIWIQNDGIIINPSNLVLAASGKKTTLT 388
 QY 121 VQTLDTLTGQWLAGNDYAFREATTIYGFRLCMESNGSVWVETCDSSQKQKALYGD 180
 DB 389 VQTLDTLTGQWLAGNDYAFREATTIYGFRLCMESNGSVWVETCDSSQKQKALYGD 447
 QY 181 GSIRPKONODCLTVGRDSVSTVINIVCSGASGSGRVFTNEKALINIKSGLANDYAQA 240
 DB 448 GSIRPKONODCLTVGRDSVSTVINIVCSGASGSGRVFTNEKALINIKSGLANDYAQA 507
 QY 241 NPKLRRIIIYPATGKPNOMLPEV 263
 DB 508 NPKLRRIIIYPATGKPNOMLPEV 530

RESULT 14
 AA25982
 ID AAY25982 standard; Protein; 532 AA.
 AC AAY25982;
 DT 18-OCT-1999 (first entry)
 DE Mistletoe lectin I (variant) protein fragment.
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin I.
 OS Viscum album.
 PN DE19804210-A1.
 PD 12-AUG-1999.
 PE 03-FEB-1998; 98DB-1004210.
 PR 03-FEB-1998; 98DB-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelker W, Walters P;
 DR WPI; 1999-44535/38.
 DR N-PSDB; AA209106.
 XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 4B; 79pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of

CC ribosomes. Non-cytotoxic forms of (1) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (1) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancer). (2) They lack cytotoxicity, but increase the strength of the
CC immune response against tumours. (3) They induce antigen production of
CC (tumour-associated bacterial or viral). The only different isoforms
CC mistletoe lectin, and its individual chains. In many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
CC represents a fragment of a mistletoe lectin I protein variant.
XX
SQ Sequence 532 AA:
Query Match 92.4%; Score 1306.5; DB 20; Length 532;
Best Local Similarity 93.5%; Pred. No. 1.9e-123;
Matches 247; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
OY 1 DDVTCASBPETVRIYGRGKRVVDVDDDFDQNGQIOLWPSKSNNDPQMLTKIKDITRS 60
DB DDVTCASBPETVRIYGRGKRVVDVDDDFDQNGQIOLWPSKSNNDPQMLTKIKDITRS 328
OY 61 NSCLITTYGTAGVYVIFDCNTAVREATVQIMDNGITINPSNVLVAASGKIGTIT 120
DB NSCLITTYGTAGVYVIFDCNTAVREATVQIMDNGITINPSNVLVAASGKIGTIT 388
OY 121 VQILDYTLGGMLAGNDTAPREVITVGRFDLCMESNGSVWVETCDSSQKQKVALYGD 180
DB VQILDYTLGGMLAGNDTAPREVITVGRFDLCMESNGSVWVETCDSSQKQKVALYGD 447
OY 181 GSIRPKQNDQCLTCGRDSVSTVINVSCASGSGRWFTNBYALINLKSGLMDVQA 240
DB GSIRPKQNDQCLTCGRDSVSTVINVSCASGSGRWFTNBYALINLKSGLMDVQA 507
OY 241 NPKLRILIIYPAKRNQMLPY 263
DB NPKLRILIIYPAKRNQMLPY 530
DB 508 NPKLRILIIYPAKRNQMLPY 530
RESULT 15
AA064662
ID AA064662 standard; Protein; 263 AA.
XX
AC AA064662;
XX
DN 23-OCT-1998 (first entry)
XX
DE Mistletoe rMLB variant protein.
XX
DE Lectin B-chain, mistletoe; rMLB; fusion protein; effector; cytotoxic;
XX internalized; processing module; protease recognition; targeting module;
XX internalized; observed; cell proliferation; activation;
XX autoimmune disease; allergy; tumour; ricin; translocation.
XX
OS Viscum album.
XX
FH Key
FH Protein 1..263 Location/Qualifiers
FT /note= "partial protein"
XX
XX MO9829540-A2.
XX
XX 09-JUL-1998.
XX
XX 02-JAN-1998; 98WD-EP00009.
XX
XX 02-JAN-1997; 97EP-0100012.
XX
XX (BRAT-) BRAIN BIOTECHNOLOGY RES & INFORMATION NZ.
XX
XX Eck J, Schmidt A, Zinke H;
XX
XX WPI: 1998-38022/33.
XX
XX N-PSDB; AA051344.

XX Nucleic acid encoding fusion protein containing mistletoe lectin A
XX chain - useful for treatment of proliferative and autoimmune
XX diseases, allergies and tumours
XX
XX Disclosure; Fig 11b'; 115p; German.
XX
XX This sequence represents a variant mistletoe lectin B-chain rMLB. This
XX sequence can be used in the construction of a fusion protein which
XX comprises an effector module that is cytotoxic intracellularly, a
XX processing module covalently bonded to the effector module and
XX containing a protease recognition sequence, and a targeting module
XX covalently bonded to the processing module, able to bind specifically to
XX the surface of a cell so as to mediate internalisation of the fusion
XX protein. Such a fusion protein can be used for treating disorders
XX involving proliferation and/or elevated activation of cells, especially
XX autoimmune disease, allergy and tumours. The proteins can be administered
XX e.g. by injection or topically but especially by intravenous injection,
XX and the fusion proteins can develop toxic activity in a wide range of target
XX cells. The processing module prevents extracellular dissociation and
XX fusion proteins based on mistletoe lectin A-chain are far more active
XX than those based on ricin and do have the associated problems of
XX non-specific toxicity. The protein may be expressed in a non-glycosylated
XX form that does not bind to sugar receptors in the liver, and which has a
XX long half-life in the blood. Where the mistletoe lectin B-chain is used,
XX it actively assists in translocation of the ML A-chain from the
XX endoplasmic reticulum to the cytoplasm.
XX
SQ Sequence 263 AA:
Query Match 92.0%; Score 1300.5; DB 19; Length 263;
Best Local Similarity 93.5%; Pred. No. 1.9e-123;
Matches 246; Conservative 4; Mismatches 12; Indels 1; Gaps 1;
OY 1 DDVTCASBPETVRIYGRGKRVVDVDDDFDQNGQIOLWPSKSNNDPQMLTKIKDITRS 60
DB DDVTCASBPETVRIYGRGKRVVDVDDDFDQNGQIOLWPSKSNNDPQMLTKIKDITRS 60
OY 61 NSCLITTYGTAGVYVIFDCNTAVREATVQIMDNGITINPSNVLVAASGKIGTIT 120
DB NSCLITTYGTAGVYVIFDCNTAVREATVQIMDNGITINPSNVLVAASGKIGTIT 120
OY 121 VQILDYTLGGMLAGNDTAPREVITVGRFDLCMESNGSVWVETCDSSQKQKVALYGD 180
DB VQILDYTLGGMLAGNDTAPREVITVGRFDLCMESNGSVWVETCDSSQKQKVALYGD 179
OY 181 GSIRPKQNDQCLTCGRDSVSTVINVSCASGSGRWFTNBYALINLKSGLMDVQA 240
DB GSIRPKQNDQCLTCGRDSVSTVINVSCASGSGRWFTNBYALINLKSGLMDVQA 239
OY 241 NPKLRILIIYPAKRNQMLPY 263
DB NPKLRILIIYPAKRNQMLPY 262
DB 240 NPKLRILIIYPAKRNQMLPY 262
Search completed: December 11, 2003, 14:07:44
Job time : 27.0864 secs

Thu Dec 11 16:10:05 2003

us-09-601-667c-8.rapb

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 11, 2003, 14:01:14 / Search time 17.0129 Seconds
2886.029 Million cell updates/sec

Title: US-09-601-667C-8
Perfect score: 1414
Sequence: 1 DVTCSASEPTVIVGRSGM.....RRIIIVPANGKPNQMLPVP 264

Scoring table: BLOSUM62
Gapop 10.0 / Gapext 0.5

Searched: 684280 seqs, 18593659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA*
1: /cgn2_6/prodata/1/pubpa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubpa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubpa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/1/pubpa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
12: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pep.*
13: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
15: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep.*
16: /cgn2_6/prodata/1/pubpa/US10_NEW_PUB.pep.*
17: /cgn2_6/prodata/1/pubpa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best hit being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1300.5	92.0	263	9	US-09-347-064-10 Sequence 10, Appl1
2	1292.5	92.0	567	12	US-09-347-064-10 Sequence 1, Appl1
3	1292.5	92.0	567	12	US-09-347-064-10 Sequence 17, Appl1
4	1291.1	12.6	46	15	US-10-017-327-5 Sequence 1470, A
5	128	11.9	145	14	US-10-074-527-5 Sequence 9724, A
6	152	10.7	420	15	US-10-156-761-4970 Sequence 9170, A
7	140.5	9.9	658	15	US-10-156-761-4970 Sequence 9170, A
8	131	9.3	536	15	US-10-156-761-4970 Sequence 9170, A
9	130	9.2	41	15	US-10-137-077-18 Sequence 1870, A
10	120.5	8.5	135	14	US-10-074-527-6 Sequence 8, Appl1
11	119.5	8.5	135	14	US-10-074-527-6 Sequence 8, Appl1
12	119.5	8.5	135	14	US-10-074-527-6 Sequence 8, Appl1
13	116.5	8.5	447	15	US-10-156-761-4970 Sequence 10246, A
14	116.5	8.5	447	15	US-10-156-761-4970 Sequence 10246, A
15	116.5	8.5	492	9	US-09-347-064-10 Sequence 4, Appl1

16	116.5	8.2	492	9	US-09-770-621-7 Sequence 7, Appl1
17	116.5	8.2	492	12	US-10-286-993-4 Sequence 4, Appl1
18	106	7.5	41	15	US-10-137-077-20 Sequence 20, Appl1
19	105	7.4	45	15	US-10-137-077-19 Sequence 19, Appl1
20	93.5	6.6	340	15	US-10-128-714-8037 Sequence 8037, Ap
21	93	6.6	625	15	US-10-128-714-8037 Sequence 15008, A
22	90.5	6.4	464	15	US-10-156-761-4970 Sequence 9647, Ap
23	90.5	6.4	464	15	US-10-156-761-4970 Sequence 9647, Ap
24	90	6.4	1723	9	US-09-841-132-395 Sequence 11831, A
25	89	6.2	2295	9	US-09-841-132-395 Sequence 11831, A
26	87	6.2	278	15	US-10-128-714-8037 Sequence 3037, Ap
27	84	5.9	1781	10	US-09-595-7494-2 Sequence 2, Appl1
28	83.5	5.9	579	14	US-10-001-851-29 Sequence 29, Appl1
29	83	5.9	770	9	US-09-815-656-11 Sequence 31, Appl1
30	83	5.8	833	9	US-09-815-656-11 Sequence 10951, A
31	82	5.8	2353	10	US-09-797-862-33 Sequence 33, Appl1
32	81.5	5.8	425	10	US-09-812-358-32 Sequence 32, Appl1
33	81.5	5.8	510	12	US-10-190-115-46 Sequence 25, Appl1
34	81	5.7	612	10	US-09-828-487-41 Sequence 41, Appl1
35	81	5.7	664	10	US-09-828-487-41 Sequence 41, Appl1
36	81	5.7	1032	11	US-09-733-643-16 Sequence 16, Appl1
37	81	5.7	1032	12	US-10-120-801-64 Sequence 64, Appl1
38	81	5.7	2771	10	US-09-808-602-82 Sequence 82, Appl1
39	81	5.7	2771	11	US-09-808-602-82 Sequence 70, Appl1
40	81	5.7	2771	11	US-09-808-602-82 Sequence 70, Appl1
41	80.5	5.7	293	15	US-10-137-077-2 Sequence 2, Appl1
42	80	5.7	434	9	US-09-770-621-6 Sequence 6, Appl1
43	79.5	5.6	165	12	US-10-252-896-126 Sequence 126, App
44	79.5	5.6	556	12	US-10-252-896-62 Sequence 62, Appl1
45	79.5	5.6	559	14	US-10-001-851-23 Sequence 23, Appl1

ALIGNMENTS

US-09-347-064-10	Application US/09347064A
Sequence 10, Appl1	
1	US-09-347-064-10
2	US-09-347-064-10
3	US-09-347-064-10
4	US-09-347-064-10
5	US-09-347-064-10
6	US-09-347-064-10
7	US-09-347-064-10
8	US-09-347-064-10
9	US-09-347-064-10
10	US-09-347-064-10
11	US-09-347-064-10
12	US-09-347-064-10
13	US-09-347-064-10
14	US-09-347-064-10
15	US-09-347-064-10
16	US-09-347-064-10
17	US-09-347-064-10
18	US-09-347-064-10
19	US-09-347-064-10
20	US-09-347-064-10
21	US-09-347-064-10
22	US-09-347-064-10
23	US-09-347-064-10
24	US-09-347-064-10
25	US-09-347-064-10
26	US-09-347-064-10
27	US-09-347-064-10
28	US-09-347-064-10
29	US-09-347-064-10
30	US-09-347-064-10
31	US-09-347-064-10
32	US-09-347-064-10
33	US-09-347-064-10
34	US-09-347-064-10
35	US-09-347-064-10
36	US-09-347-064-10
37	US-09-347-064-10
38	US-09-347-064-10
39	US-09-347-064-10
40	US-09-347-064-10
41	US-09-347-064-10
42	US-09-347-064-10
43	US-09-347-064-10
44	US-09-347-064-10
45	US-09-347-064-10

QY 121 VGLDYLGGWLAGNDIAPREVITVYGRDLCMESNGSWVETCDSSQKQKALYCD 180
DB 121 VGLDYLGGWLAGNDIAPREVITVYGRDLCMESNGSWVETCDSSQKQKALYCD 179
QY 181 GSIRPKQNDQCLTVGRDSVSTVINTVSCGASGSGQWFTNEVALINKSGIAMDVAQA 240
DB 180 GSIRPKQNDQCLTVGRDSVSTVINTVSCGASGSGQWFTNEVALINKSGIAMDVAQA 239
QY 241 NPKLRITIIYPATGKQNMALPV 263
DB 240 NPKLRITIIYPATGKQNMALPV 262

RESULT 2
US-09-347-064-4
Sequence 4, Application US/09347064A
Patent No. US20020045209A1
GENERAL INFORMATION:
APPLICANT: ECK, Jürgen
APPLICANT: Zimmermann, Rüdiger
APPLICANT: Zimmermann, Rüdiger
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the miscletoe viscum
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 267
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-4

Query Match 92.0%; Score 1300.5; DB 9; Length 267;
Best Local Similarity 93.5%; Pred. No. 2,1e-125;
Matches 246; Conservative 4; Mismatches 12; Indels 1; Gaps 1;
QY 1 DDTYCSASEPTVAVIGNSGKRVYDPPDHPDGNQIQLPFSKSNDDPNQIWTIKGGTIS 60
DB 1 DDTYCSASEPTVAVIGNSGKRVYDPPDHPDGNQIQLPFSKSNDDPNQIWTIKGGTIS 60
QY 61 NSGCLTGYAGVYVMPCKVAVENITWIMONGTIIINRSNLVLAASGIGTITL 120
DB 61 NSGCLTGYAGVYVMPCKVAVENITWIMONGTIIINRSNLVLAASGIGTITL 120
QY 121 VGLDYLGGWLAGNDIAPREVITVYGRDLCMESNGSWVETCDSSQKQKALYCD 180
DB 121 VGLDYLGGWLAGNDIAPREVITVYGRDLCMESNGSWVETCDSSQKQKALYCD 179
QY 181 GSIRPKQNDQCLTVGRDSVSTVINTVSCGASGSGQWFTNEVALINKSGIAMDVAQA 240
DB 180 GSIRPKQNDQCLTVGRDSVSTVINTVSCGASGSGQWFTNEVALINKSGIAMDVAQA 239
QY 241 NPKLRITIIYPATGKQNMALPV 263
DB 240 NPKLRITIIYPATGKQNMALPV 262

RESULT 3
US-10-083-336A-1
Sequence 1, Application US/10083336A
Publication No. US2003018165A1
GENERAL INFORMATION:
APPLICANT: Olsson, Mark A
APPLICANT: Willard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Mannmacher, Robert W

TITLE OF INVENTION: Rich Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (Raid 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 576
TYPE: PRT
ORGANISM: Ricinus communis
US-10-083-336A-1

Query Match 63.4%; Score 896.5; DB 12; Length 576;
Best Local Similarity 63.5%; Pred. No. 2.2e-83;
Matches 165; Conservative 33; Mismatches 61; Indels 1; Gaps 1;
QY 5 CSASEPTVAVIGNSGKRVYDPPDHPDGNQIQLPFSKSNDDPNQIWTIKGGTITL 124
DB 318 CSASEPTVAVIGNSGKRVYDPPDHPDGNQIQLPFSKSNDDPNQIWTIKGGTITL 124
QY 65 LTTGYAGVYVMPCKVAVENITWIMONGTIIINRSNLVLAASGIGTITL 124
DB 378 LTTGYAGVYVMPCKVAVENITWIMONGTIIINRSNLVLAASGIGTITL 124
QY 125 DYTLCGWMLAGNDIAPREVITVYGRDLCMESNGSWVETCDSSQKQKALYCD 184
DB 438 DYTLCGWMLAGNDIAPREVITVYGRDLCMESNGSWVETCDSSQKQKALYCD 184
QY 185 PKQNDQCLTVGRDSVSTVINTVSCGASGSGQWFTNEVALINKSGIAMDVAQA 244
DB 497 PKQNDQCLTVGRDSVSTVINTVSCGASGSGQWFTNEVALINKSGIAMDVAQA 244
QY 245 RIIITVYAGKQNMALPV 264
DB 557 RIIITVYAGKQNMALPV 264

RESULT 4
US-10-137-077-17
Sequence 17, Application US/10137077
Publication No. US20030092109A1
GENERAL INFORMATION:
APPLICANT: Zimmermann, Rüdiger
APPLICANT: Zimmermann, Rüdiger
APPLICANT: Zimmermann, Rüdiger
TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lect
FILE REFERENCE: UN-07124
CURRENT APPLICATION NUMBER: US/10/137,077
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 60/288,596
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/354,322
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 44
TYPE: PRT
ORGANISM: Ricinus communis
US-10-137-077-17

Query Match 12.8%; Score 181; DB 15; Length 44;
Best Local Similarity 75.0%; Pred. No. 2.4e-11;
Matches 33; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 12 VRIYVSGNLCVYVDRFHNGNAILCPFKSNTDPAQWLTIKED 55
DB 1 VRIYVSGNLCVYVDRFHNGNAILCPFKSNTDPAQWLTIKED 44

RESULT 5
US-10-074-527-5
Sequence 5, Application US/10074527

Thu Dec 11 16:10:05 2003

us-09-601-667c-8.rapb

Page 3

```
Publication No. US20020142426A1
GENERAL INFORMATION:
APPLICANT: Olander, Peter U.
APPLICANT: Olander, Rachel E.
APPLICANT: Olander, Rachel A.
APPLICANT: Millennium Pharmaceuticals Inc.
TITLE OF INVENTION: 33945. A human glycosyltransferase and
FILE REFERENCE: WI2001-018130P1 (W)
CURRENT APPLICATION NUMBER: US/10/074,527
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/269202
INVENTOR: SAKAKI, YOSHITAKI
INVENTOR: HATTORI, MASAHIRA
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 145
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus
US-10-074-527-5

Query Match
Best Local Similarity 11.9%; Score 168; DB 14; Length 145;
Matches 45; Conservative 19; Mismatches 59; Indels 14; Gaps 4;

QY 11 TTVAGTGGVYVAIFDCNTAVREATTWQINDGTTINP--KEDNTIRNS--NOSC 64
DB 7 TTVAGTGGVYVAIFDCNTAVREATTWQINDGTTINP--KEDNTIRNS--NOSC 64
DB 7 TTVAGTGGVYVAIFDCNTAVREATTWQINDGTTINP--KEDNTIRNS--NOSC 64
QY 65 LTTGYTGGVYVAIFDCNTAVREATTWQINDGTTINP--KEDNTIRNS--NOSC 116
DB 67 LTVANSPSEVYALVOCDSATSDVQKMLNDGLGKRLILNLTGVLADVAGSDTONG 126
QY 117 TTVTQVLDYTLTGQGMIL 133
DB 127 TTVTQVLDYTLTGQGMIL 143
```

```
RESULT 6
US-10-156-761-14970
Sequence 14970, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIZAKA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIWA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
INVENTOR: SAKAKI, YOSHITAKI
INVENTOR: HATTORI, MASAHIRA
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14970
LENGTH: 420
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-14970
```

```
Query Match
Best Local Similarity 10.7%; Score 152; DB 15; Length 420;
Matches 43; Conservative 20; Mismatches 68; Indels 10; Gaps 5;

QY 1 DD--VTCGAEPTTAVTGGVYVAIFDCNTAVREATTWQINDGTTINP--KEDNTIRNS--NOSC 58
DB 1 DD--VTCGAEPTTAVTGGVYVAIFDCNTAVREATTWQINDGTTINP--KEDNTIRNS--NOSC 58
```

```
DB 284 DVKVTGDSGAPITGLACKCVVAGSSSANGAPVQLY--DONGTIAKXTVASDGL 341
QY 59 RNSGSL--TTVAGTGGVYVAIFDCNTAVREATTWQINDGTTINP--KEDNTIRNS--NOSC 114
DB 342 RALGKCLDVTENGTDADSTVLDVOCGSANOK--WVTTAGDITVPOANWCLDVTGNSA 399
QY 115 KTTTLVQVLDYTLTGQGMIL 135
DB 400 NGTRLDQWGSAGANQWNG 420
```

```
RESULT 7
US-10-156-761-9724
Sequence 9724, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIZAKA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIWA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
INVENTOR: SAKAKI, YOSHITAKI
INVENTOR: HATTORI, MASAHIRA
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9724
LENGTH: 658
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-9724
```

```
Query Match
Best Local Similarity 9.8%; Score 140.5; DB 15; Length 658;
Matches 39; Conservative 17; Mismatches 56; Indels 9; Gaps 5;

QY 17 RSGWVYVDDPHDQDQVQKMLNDGLGKRLILNLTGVLADVAGSDTONG 596
DB 539 QSGRCADIVYVTTNGTQELM--DONGGNSWYTSKELVYQKCLDVTGNSA 399
QY 74 VYVAFCTAVREATTWQINDGTTINP--KEDNTIRNS--NOSC 116
DB 597 TKVYVWCGANOK--WNINSGITVMAGLDVAATVAGTSLVWVSCGTQDNG 654
QY 132 N 132
DB 655 N 655

RESULT 8
US-10-156-761-8170
Sequence 8170, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIZAKA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIWA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
```

Thu Dec 11 16:10:05 2003

us-09-601-667c-8.rapb

Page 4

;; PRIOR APPLICATION NUMBER: JP 2001-272697
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ ID NOS: 15109
;; SEQ ID NO 8170
;; LENGTH: 536
;; TYPE: PRT
;; ORGANISM: Streptomyces avermitilis
US-10-156-761-8170

Query Match
Best Local Similarity 30.1%, Pctd No. 0.000160, Indels 16, Gaps 6,
Matches 40; Conservative 17, Mismatches 60;

QY 14 IVRSGR-VVVDDEPHDNGIOLWPSKSNNDPQWLTIKEDNITRANG--SCITTY-- 68
DB 409 LVGASNRCLDAYDNGTAPGTKEIWDG--GGANQAVITTAGELIYGTQCLDAYN 465
QY 69 GTTAGVYVWIFDCNTAVRENTIWOIMNGTIIIPRSNLVY-----ASSGIRGTITVQ 122
DB 466 GTTSGTRVQLTTCNGANQR--WELNPNGVITSTGSLDVTGSDGNGVNGTALIM 523
QY 123 TDTTTCGCTAG 135
DB 524 TCGGANQWELD 536

RESULT 9
US-10-137-077-18
;; Sequence 18, Application US/10137077
;; Publication No. US2003092109X1
;; GENERAL INFORMATION:
;; APPLICANT: GlaxoSmith, Irwin J.
;; APPLICANT: GlaxoSmith, Irwin J.
;; APPLICANT: GlaxoSmith, Irwin J.
;; TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin
;; FILE REFERENCE: US-07124
;; CURRENT APPLICATION NUMBER: US/10/137,077
;; CURRENT FILING DATE: 2002-05-02
;; PRIOR APPLICATION NUMBER: 60/288,596
;; PRIOR FILING DATE: 2001-05-03
;; PRIOR APPLICATION NUMBER: 60/354,322
;; PRIOR FILING DATE: 2002-02-04
;; NUMBER OF SEQ ID NOS: 32
;; SOFTWARE: Patent version 3.1
;; SEQ ID NO 18
;; LENGTH: 41
;; TYPE: PRT
;; ORGANISM: Ricinus communis
US-10-137-077-18

Query Match
Best Local Similarity 9.2%, Score 130, DB 15, Length 41;
Matches 23; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 226 IINXSLAMDYQANPRLTITTPKGRKNOMTLPF 264
DB 3 IINXSLVLDVPAADPBLKQITITTPKGRKNOMTLPF 41

RESULT 10
US-09-973-457-5
;; Sequence 5, Application US/09973457
;; Publication No. US2002016746X1
;; GENERAL INFORMATION:
;; APPLICANT: Kappel, Liberman, Rosas
;; TITLE OF INVENTION: 47174, A NOVEL HUMAN GLYCOSYLTRANSFERASE
;; FILE REFERENCE: 10448-099001
;; CURRENT APPLICATION NUMBER: US/09/973,457
;; CURRENT FILING DATE: 2001-10-09
;; PRIOR APPLICATION NUMBER: 60/238,849
;; PRIOR FILING DATE: 2000-10-06
;; NUMBER OF SEQ ID NOS: 6

;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5
;; LENGTH: 135
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match
Best Local Similarity 29.1%, Pctd No. 0.000190, Indels 21, Gaps 8,
Matches 41; Conservative 19; Mismatches 60;

QY 14 IVRSGRVVDV--RDDPHDNGIOLWPSKSNNDPQWLTI--KRDNITRANGS-CLTT 67
DB 7 IGGNTGCLDVNGNSKSDNPNVLDHCGGG--NQLMKLYNESDGLAIRNSDCLTV 64
QY 68 YGTAGVYVWIFDCNTAVR--EATITWOIMNGTIIIPRSNLVYLAASGIRGTITVQ 125
DB 65 NG-----TVLVSDDGTGKNGDKQEVNNDGTTNRK-NKKGVDG-----LCDVVD 113
QY 126 YTGQGMALNDTPRETTI 146
DB 114 GNRQQLMTGNSGDHPNQKRI 134

RESULT 11
US-10-074-527-6
;; Sequence 6, Application US/10074527
;; Publication No. US20020142426A1
;; GENERAL INFORMATION:
;; APPLICANT: Bayer, Peter J. B.
;; APPLICANT: Bayer, Peter J. B.
;; APPLICANT: Bayer, Peter J. B.
;; TITLE OF INVENTION: 33945, A Human Glycosyltransferase and
;; FILE REFERENCE: MP12001-018PRCPI(M)
;; CURRENT APPLICATION NUMBER: US/10/074,527
;; CURRENT FILING DATE: 2002-02-12
;; PRIOR APPLICATION NUMBER: 60/269202
;; PRIOR FILING DATE: 2001-02-15
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6
;; LENGTH: 135
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: consensus
US-10-074-527-6

Query Match
Best Local Similarity 8.5%, Score 120.5, DB 14, Length 135;
Matches 41; Conservative 19; Mismatches 60; Indels 21; Gaps 8;

QY 14 IVRSGRVVDV--RDDPHDNGIOLWPSKSNNDPQWLTI--KRDNITRANGS-CLTT 67
DB 7 IGGNTGCLDVNGNSKSDNPNVLDHCGGG--NQLMKLYNESDGLAIRNSDCLTV 64
QY 68 YGTAGVYVWIFDCNTAVR--EATITWOIMNGTIIIPRSNLVYLAASGIRGTITVQ 125
DB 65 NG-----TVLVSDDGTGKNGDKQEVNNDGTTNRK-NKKGVDG-----LCDVVD 113
QY 126 YTGQGMALNDTPRETTI 146
DB 114 GNRQQLMTGNSGDHPNQKRI 134

RESULT 12
US-09-770-621-8
;; Sequence 8, Application US/09770621
;; Patent No. US20010024815A1

Thu Dec 11 16:10:05 2003

us-09-601-667c-8.ral

Page 2

```

US-08-776-059-33
Sequence 33, Application US/08776059B
Patent No. 6271168
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776,059B
CURRENT FILING DATE: 1999-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 564
MOLECULE TYPE: protein
ORGANISM: Viscum album

Query Match
Best Local Similarity 92.0%; Score 1300.5; DB 3; Length 264;
Matches 246; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 1 DDTGSASEPVTARIVSGKQVVDVDDPHQDQIQLPKSKMNDPQQLMTIKEDNTIRS 60
DB 2 DDTGSASEPVTARIVSGKQVVDVDDPHQDQIQLPKSKMNDPQQLMTIKEDNTIRS 61
QY 61 NSGCTTGTAGTGYWTFPCNTAVREATTIWIQWNGTIIINPESNLVLAASGIGKTLT 120
DB 62 NSGCTTGTAGTGYWTFPCNTAVREATTIWIQWNGTIIINPESNLVLAASGIGKTLT 121
QY 121 VQILDYTLQGWLAGNDTAPREVITYGFRLDQMSNGSWVETCDSSQKQKALYGD 180
DB 122 VQILDYTLQGWLAGNDTAPREVITYGFRLDQMSNGSWVETCDSSQKQKALYGD 180
QY 181 GSIRPKQNDQCLTVGRDSVSTVINIVSGASGSGQWVFTNEVAILINKSLAMDVAQA 240
DB 181 GSIRPKQNDQCLTVGRDSVSTVINIVSGASGSGQWVFTNEVAILINKSLAMDVAQA 240
QY 241 NPKLRRIIYPATKKNQMWLPV 263
DB 241 NPKLRRIIYPATKKNQMWLPV 263

RESULT 3
US-08-776-059-35
Sequence 35, Application US/08776059B
Patent No. 6271168
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776,059B
CURRENT FILING DATE: 1999-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 564
MOLECULE TYPE: protein
ORGANISM: Viscum album

Query Match
Best Local Similarity 92.0%; Score 1300.5; DB 3; Length 264;
Matches 246; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 1 DDTGSASEPVTARIVSGKQVVDVDDPHQDQIQLPKSKMNDPQQLMTIKEDNTIRS 60
DB 2 DDTGSASEPVTARIVSGKQVVDVDDPHQDQIQLPKSKMNDPQQLMTIKEDNTIRS 61
QY 61 NSGCTTGTAGTGYWTFPCNTAVREATTIWIQWNGTIIINPESNLVLAASGIGKTLT 120
DB 62 NSGCTTGTAGTGYWTFPCNTAVREATTIWIQWNGTIIINPESNLVLAASGIGKTLT 121
QY 121 VQILDYTLQGWLAGNDTAPREVITYGFRLDQMSNGSWVETCDSSQKQKALYGD 180
DB 122 VQILDYTLQGWLAGNDTAPREVITYGFRLDQMSNGSWVETCDSSQKQKALYGD 180
QY 181 GSIRPKQNDQCLTVGRDSVSTVINIVSGASGSGQWVFTNEVAILINKSLAMDVAQA 240
DB 181 GSIRPKQNDQCLTVGRDSVSTVINIVSGASGSGQWVFTNEVAILINKSLAMDVAQA 240
QY 241 NPKLRRIIYPATKKNQMWLPV 263
DB 241 NPKLRRIIYPATKKNQMWLPV 263

RESULT 4
US-08-378-761A-77
Sequence 77, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: ZIONSVILLE
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
INVENTOR: ANDREA T. BORUCKI
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 382728
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
STRANDNESS: acingie
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-378-761A-77

Query Match
Best Local Similarity 54.1%; Score 764.5; DB 1; Length 540;
Matches 143; Conservative 43; Mismatches 73; Indels 1; Gaps 1;
```

Thu Dec 11 16:10:05 2003

us-09-601-667c-8.rat

Page 3

QY 5 CSASEPTVRLVGRSGNRVDVDDDFHGNQIQWPSKSNNDPNQWLTIKEDNTIRNSGSC 64
DB 282 CMDEPTVRLVGRNGLCVDVTGEFFDGNPIQWPCCKSNTPNQWLTIRKSTIRNSGKC 341
QY 65 LITVGTAGVYVMIFDCTAVRELTQWINDGTLINPSNLVLAASGSKETLLVYOTL 124
DB 342 LITKSSPRQGVYVINCSTAVGATRMQWINDGTLINPSNLVLAASGSKETLLVYOTN 401
QY 125 DYTIGQWLAGNDPAPEAVTIGFRDLQMSNGSVWVETCSQSQGQWALYGDGSR 184
DB 402 IYVSGQWLPNTNTPPTVITVGLYGMCLQANSQWLEDC-TSEKACQWALYADGSR 460
QY 185 PRONODCLTVGRDSVSTVITIVSCSASQSGQWVFTNEVALINKSGLAMDVQANPEL 244
DB 461 PQMRDNCULTDANIKGTIVKILGCPASSGQWRFNDGTLINLVNGLVDRSDPEL 520
QY 245 RRIITVPATGKPNQWMLPVF 264
DB 521 KQIIVHPFHQNLQWMLPVF 540

RESULT 5

US-08-485-286-77
; Sequence 77, Application US/08485286
; Patent No. 5646028
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; STATE: INDIANAPOLIS
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY INFORMATION DATA: US 08/378761
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-485-286-77

Query Match 54.1%; Score 764.5; DB 1; Length 540;
Best Local Similarity 55.0%; Pred. No. 7.3e-69;
Matches 143; Conservative 43; Mismatches 73; Indels 1; Gaps 1;

QY 5 CSASEPTVRLVGRSGNRVDVDDDFHGNQIQWPSKSNNDPNQWLTIKEDNTIRNSGSC 64
DB 282 CMDEPTVRLVGRNGLCVDVTGEFFDGNPIQWPCCKSNTPNQWLTIRKSTIRNSGKC 341
QY 65 LITVGTAGVYVMIFDCTAVRELTQWINDGTLINPSNLVLAASGSKETLLVYOTL 124
DB 342 LITKSSPRQGVYVINCSTAVGATRMQWINDGTLINPSNLVLAASGSKETLLVYOTN 401
QY 125 DYTIGQWLAGNDPAPEAVTIGFRDLQMSNGSVWVETCSQSQGQWALYGDGSR 184
DB 402 IYVSGQWLPNTNTPPTVITVGLYGMCLQANSQWLEDC-TSEKACQWALYADGSR 460
QY 185 PRONODCLTVGRDSVSTVITIVSCSASQSGQWVFTNEVALINKSGLAMDVQANPEL 244
DB 461 PQMRDNCULTDANIKGTIVKILGCPASSGQWRFNDGTLINLVNGLVDRSDPEL 520
QY 245 RRIITVPATGKPNQWMLPVF 264
DB 521 KQIIVHPFHQNLQWMLPVF 540

RESULT 6

US-09-512-342-14
; Sequence 14, Application US/09512342
; Patent No. 6388068
; GENERAL INFORMATION:
; APPLICANT: SATOH, SHINROU
; APPLICANT: MASUDA, SUSUMU
; TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT
; FILE REFERENCE: 081356/0142
; CURRENT APPLICATION NUMBER: US/09/512,342
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Cucumis sativus
US-09-512-342-14

Query Match 12.7%; Score 179; DB 4; Length 293;
Best Local Similarity 26.6%; Pred. No 4.7e-10;
Matches 65; Conservative 36; Mismatches 103; Indels 40; Gaps 11;

QY 14 IYVRSGNRVDVDDDFHGNQIQWPSKSNNDPNQWLTIRKSTIRNSGSC 59
DB 41 LIVERGICLQNSP-----VYKQGIPTPLPCDEKQOTQWLTIVGQGIIRPM 89
QY 60 SNGSLT---YGTAGVYVMIFDCTAVRELTQWINDGTLINPSNLVLAASGSKG 116
DB 90 NDFPCLAAEYFQVIA--KAVSBCGVSDPKKWKQKNDGTLALVDSRVLTQDLDY-- 145
QY 117 TLTIVGTLVYTLGGWLAGNDPAPEAVTIGFRDLQMSNGS--VWETCSQSQGQW 174
DB 146 --VTQGNKRTPSQSWETLSNSKVNTEMLNMLDQSTDSNVGNCNTNXXQ-R 202
QY 175 WLYVDSIRFPRONODCLTVGRDSVSTVITIVSCSASQSGQW-VFTNEVALINKSG 233
DB 203 WLYVDSIRFPRONODCLTVGRDSVSTVITIVSCSASQSGQW-VFTNEVALINKSG 233
QY 234 AMDV 237
DB 261 VDVV 264

RESULT 7

US-09-159-106-15
; Sequence 15, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: FETTER, PAU
; APPLICANT: DIERS, IVAN

Thu Dec 11 16:10:05 2003

us-09-601-667c-8.ra1

Page 4

```

/ APPLICANT: Halkier, Torben
/ TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
/ FILE REFERENCE: 4693.204-US
/ CURRENT APPLICATION NUMBER: US/09/159.106
/ EARLIER FILING DATE: 1998-09-23
/ EARLIER FILING DATE: 1998-12-04
/ EARLIER FILING DATE: 1996-08-23
/ EARLIER FILING DATE: 1997-04-14
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 15
/ LENGTH: 132
/ TYPE: FRT
/ ORGANISM: Oerskovia xanthineolytica
US-09-159-106-15

```

```

Query Match
8.8%; Score 125; DB 3; Length 132;
Best Local Similarity 34.7%; Pred. No. 4,3e-05;
Matches 43; Conservative 12; Mismatches 53; Indels 16; Gaps 6;

```

```

Qy 18 SQMVDVDDDFDNDQIQMPKSKNDPNQMTIKNDITISNGSCUTTY--GYTAGYV 75
Db 14 NMGCVVPMADPFDNPEVQVTCGN--AQWTGSDQTFVALGKCDVRGSGTSGAA 71
Qy 76 VAFPCNTVRENTIMQIW--DNCT--IINRSNIVLAASGI--KSTTLVQTLDTL 128
Db 72 VQWVTCN-----GTGAKNVAIDAGSKALNPQSLCDATGAPLRDQQLQWTCNGTT 126
Qy 129 GQGW 132
Db 127 AQGW 130

```

```

RESULT 8
US-09-159-106-11
/ Sequence 11, Application US/09159106
/ Patent No. 6284100
/ GENERAL INFORMATION:
/ APPLICANT: Farkner, Pau
/ APPLICANT: Dietz, Ivan
/ APPLICANT: Halkier, Torben
/ APPLICANT: Hedegaard, Lisbeth
/ TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
/ FILE REFERENCE: 4693.204-US
/ CURRENT APPLICATION NUMBER: US/09/159.106
/ EARLIER FILING DATE: 1998-09-23
/ EARLIER FILING DATE: 1998-12-04
/ EARLIER FILING DATE: 1996-08-23
/ EARLIER FILING DATE: 1997-04-14
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 11
/ LENGTH: 435
/ TYPE: FRT
/ ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11

```

```

Query Match
8.8%; Score 125; DB 3; Length 435;
Best Local Similarity 34.7%; Pred. No. 0.00024;
Matches 43; Conservative 12; Mismatches 53; Indels 16; Gaps 6;
Qy 18 SQMVDVDDDFDNDQIQMPKSKNDPNQMTIKNDITISNGSCUTTY--GYTAGYV 75
Db 317 NMGCVVPMADPFDNPEVQVTCGN--AQWTGSDQTFVALGKCDVRGSGTSGAA 374

```

```

Qy 76 VAFPCNTVRENTIMQIW--DNCT--IINRSNIVLAASGI--KSTTLVQTLDTL 128
Db 375 VQWVTCN-----GTGAKNVAIDAGSKALNPQSLCDATGAPLRDQQLQWTCNGTT 429
Qy 129 GQGW 132
Db 430 AQGW 433

```

```

RESULT 9
US-08-468-812-8
/ Sequence 8, Application US/08468812
/ Patent No. 5935836
/ GENERAL INFORMATION:
/ APPLICANT: Vehmaanger, Jari
/ APPLICANT: M neyl, Arja
/ APPLICANT: Fagerstr m, Richard
/ APPLICANT: Lantto, Ralfja
/ APPLICANT: Palomaa, Marja
/ APPLICANT: Lominen, Pirkko
/ APPLICANT: Keskitalo, Pauli
/ TITLE OF INVENTION: Actinomodula Xylanase Sequences and Methods
/ NUMBER OF SEQUENCES: 25
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: STERN, KESSLER, GOLSTEIN & FOX
/ STREET: 1100 New York Ave., N.W.
/ CITY: Washington
/ COUNTRY: U.S.A.
/ DTD: 200008
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/468.812
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA: US 08/322,412
/ FILING DATE: 31-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/282,001
/ FILING DATE: 29-JUL-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Larry B.
/ REGISTRATION NUMBER: 35,086
/ REGISTRATION DATE: 1980-03-04
/ TRIAL/INVENTION INFORMATION:
/ TELEPHONE: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 491 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FUNCTION: 11,000
/ CHROMOSOME/SEGMENT: NC4551
US-08-468-812-8

```

```

Query Match
8.5%; Score 119.5; DB 2; Length 491;
Best Local Similarity 28.6%; Pred. No. 0.001;
Matches 40; Conservative 19; Mismatches 62; Indels 19; Gaps 6;
Qy 7 ASEP-----TVAIVGSGNRYVDVDDDFDNDQIQMPKSKNDPNQMTIKND 55

```

Db 354 SSEPXXXXXADGQIGVG-SGRCLDPDASTSDGTOLQIMDCHSGT--NQOMATDA 410
Qy 56 NTRISNG-SCLTGYGTAGVYVMIPEICNTAVREATIWCIMDGTIINRSNVLAA--SS 112
Db 411 GELVYGDKLDAAATNSGKQIIVSCMGDNQK--WINSDSVVGVGSLCLDAVNG 468
Qy 113 GIKGTTLVQTLDPYTLGGQW 132
Db 469 TANGTLIQLYTCSNGSNQPM 488

RESULT 10
US-08-590-563-8
Sequence 8, Application US/08590563
Accession: 620114
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vehmanper, Jari
APPLICANT: Pagarst m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-771-2600
TELEFAX: 202-771-2600
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: 8:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
GENES/EXONS/SEGMENT: M64551
US-08-590-563-8
Query Match 8.5%; Score 119.5; Db 4; Length 491;

Best Local Similarity 28.6%; Pred. No. 0.001,
Matches 40; Conservative 19; Mismatches 62; Indels 19; Gaps 6;
Qy 7 ASEP-----TVATVGRSGNRVYRDDDPDHQNOQLWPSKSNNDPVQLATIKRD 55
Db 354 SSEPXXXXXADGQIGVG-SGRCLDPDASTSDGTOLQIMDCHSGT--NQOMATDA 410
Qy 56 NTRISNG-SCLTGYGTAGVYVMIPEICNTAVREATIWCIMDGTIINRSNVLAA--SS 112
Db 411 GELVYGDKLDAAATNSGKQIIVSCMGDNQK--WINSDSVVGVGSLCLDAVNG 468
Qy 113 GIKGTTLVQTLDPYTLGGQW 132
Db 469 TANGTLIQLYTCSNGSNQPM 488

RESULT 11
US-09-770-621-8
Sequence 8, Application US/09770621
Accession: 620114
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vehmanper, Jari
APPLICANT: Pagarst m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-771-2600
TELEFAX: 202-771-2600
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: 8:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: No. 6506593 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:

Thu Dec 11 16:10:05 2003

us-09-601-667c-8.ra1

Page 6

CHROMOSOME/SEGMENT: M64551

Query Match 8.5%; Score 119.5; DB 4; Length 491;
Best Local Similarity 28.6%; Pred. No. 0.001;
Matches 40; Conservative 19; Mismatches 62; Indels 19; Gaps 6;

Qy 7 ASEP-----TVLVRSQNRVYRDDPHDGNQIOLWPSKSNPNQWLTIXD 55
Db 354 SSEPXXXXXXXXXADGQIRNGV-SGRCLDVPASTDSGTQLDMDCHSST--NQOMATDA 410
Qy 56 NTIRSNQ-SCLTGYGTAGVYVYVPCNTNATREATIQTWNGTIRSNVLA--SS 112
Db 411 GELVYGVQKCLDAAGTNSGKXVQYSCWGDNOK--WRLNSDGSVVGQGLDVGANG 468
Qy 113 GIKGTVLVQTLDTYTLQGM 132
Db 469 TANGTLLQLYTCSNSNQRW 488

RESULT 12

US-08-392-828C-39
Sequence 39, Application US/08392828C
Patent No. 5795962

GENERAL INFORMATION:
APPLICANT: IMANAGA, SADAAKI
APPLICANT: MOTA, TATSUSHI
APPLICANT: SEKI, NORIAKI
APPLICANT: ODA, TOSHIO
TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING
NUMBER OF SEQUENCES: 39
TITLE OF INVENTION: THREASOP
ADDRESS: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESS: THIBRAULT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,828C
FILING DATE: 28-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FOM-033
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..127
OTHER INFORMATION: /note= "XIN A SEQUENCE (FIGURE 4)"

Query Match 8.4%; Score 119; DB 1; Length 127;
Best Local Similarity 29.8%; Pred. No. 0.00016;
Matches 37; Conservative 18; Mismatches 61; Indels 8; Gaps 5;

Qy 12 VELVRSQNRVYRDDPHDGNQIOLWPSKSNPNQWLTIXDNTIRSNQ-SCLTGY 70
Db 6 IKGVG-SGRCLDVPASTDSGTQLDMDCHSST--NQOMATDAEELRYVGDKCLDAAGT 62
Qy 71 TAGVYVYVPCNTNATREATIQTWNGTIRSNVLA--SSGIKGTTLVQTLDTYL 128
Db 63 SNOSKXVQYSCWGDNOK--WRLNSDGSVVGQGLDVGANGTANGTLLQLYTCSNGS 120
Qy 129 GQGM 132
Db 121 NQGM 124

RESULT 13

US-09-330-945-39
Sequence 39, Application US/09330945
Patent No. 6077946

GENERAL INFORMATION:
APPLICANT: IMANAGA, SADAAKI
APPLICANT: MOTA, TATSUSHI
APPLICANT: SEKI, NORIAKI
APPLICANT: ODA, TOSHIO
TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: ANTIBODY LYCAT FACTOR C SUBUNIT A
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESS: THIBRAULT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,945
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDWARD R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FOM-032DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..127
OTHER INFORMATION: /note= "XIN A SEQUENCE (FIGURE 4)"

Query Match 8.4%; Score 119; DB 3; Length 127;
Best Local Similarity 29.8%; Pred. No. 0.00016;
Matches 37; Conservative 18; Mismatches 61; Indels 8; Gaps 5;

Qy 12 VELVRSQNRVYRDDPHDGNQIOLWPSKSNPNQWLTIXDNTIRSNQ-SCLTGY 70
Db 6 IKGVG-SGRCLDVPASTDSGTQLDMDCHSST--NQOMATDAEELRYVGDKCLDAAGT 62

Thu Dec 11 16:10:05 2003

us-09-601-667c-8.ra1

Page 7

QY 71 TAAYVWIMPECTATVREATIMQINDGRIIPRSVLAA--SSGKXTLLVQLELYTL 128
:::|:::|
Db 63 SINSKMQYSCTGSDGNK--RRLNSDSVVGQSLDLANGNTANETLIQVYTCNSG 120
QY 129 GGGM 132
| |
Db 121 NQRM 124

```

RESULT 14
US-08-468-812-5
Sequence 5, Application US/08468812
Patent No. 5938936
GENERAL INFORMATION:
APPLICANT: Vannanper, Jari
INVENTOR: Vannanper, Jari
APPLICANT: Regeritz, Mark Richard
APPLICANT: Tanton, Ralfja
APPLICANT: Paloheimo, Marka
APPLICANT: Suominen, Pirkko
APPLICANT: Lahnen, Taina
APPLICANT: Kistio, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
TYPE OF INVENTION: of use
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLSTEIN & FOX
SPEER, 100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA/08/468,812
PENDING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-OCT-1994
CLASSIFICATION: 435
ACTION/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050 0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
STRANDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-08-468-812-5

```

```

Query Match      8.2%; Score 116.5; DB 2; Length 480;
Best Local Similarity   31.4%; Pred.No.0.002;
Matches    32; Conservative   16; Mismatches   49; Indels     5; Gaps     3
QY      22 VDVEDDFHDAQOLTPKSNKDNDPDLATLRDNTIRNGS-CLTGYGTAGVAVIID 80
       ::::|::|::|::

```

Db 379 IDVPNGTADTQVQJZCHSSS--NQWPTTSSGFEI FKKCLDAGSSNGNVAIYS 4366

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

```

Query Match      8.2%  Score 116.5  DB  4;  Length 480;
Best Local Similarity 31.4%;  Pred. No. 0.002149;
Matches 32;  Conservative 16;  Mismatches 16;  Gaps 5;  Gaps 3
22 VVYDDDDPDDDDGICGMMSSNNDDGNCWTTCXNDNTTSSNGS-CLTGYVYVATGYVYVMD FD 80

```

Thu Dec 11 16:10:05 2003

us-09-601-667c-8.ra1

Page 8

Db 379 IVPNGNTADGTQVQVLDCHSGS--NQWYTSGBRIFGNKCLDAGSSNGAVQIYS 436
Qy 81 CNTAVRENTIWOIMDNGTIINPRSNVLAASGIGKTTLTVO 122
Db 437 CWGANNOK--WEIADGTIIVQVSGICLDVAGGCTGNGTRIQ 476

Search completed: December 11, 2003, 14:11:34
CPU time : 10.1403 secs

506330
 ricin B - castor bean (fragment)
 N:Contains: chain B; rRNA N-glycosidase (EC 3.2.2.22) (chain A)
 C:Species: Ricinus communis (castor bean)
 C:Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text change 20-Aug-1999
 C:Accession: S06330, J05381
 K:Label: B, E; Murray, J.E.; Halling, A.C.; Halling, K.C.; Tlakaratne, N.; Long, G.L.;
 J. Biol. Chem. 265:6846-6852, 1990
 A:Title: Characterization of a cDNA encoding ricin B, a hybrid ricin-Ricinus communis ag-
 A:Reference number: S06330
 A:Accession: S06330
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-263 <IAD>
 A:Cross-references: EMBL:M17631; NID:G169714; PDB:AAA63506.1; PDB:G169715
 K:Mark: T.; Funatsu, G.
 A:Title: The complete amino acid sequence of the B-chain of ricin E isolated from small-
 A:Reference number: J05381, PMID:87101106, PMID:3801493
 A:Accession: J05381
 A:Molecule type: protein
 A:Residues: 1-69, 'P', 'S', '72-209, 'A', '211-241, '243-250, 'V', '252-263 <ABA>
 A:Experimental source: seed
 C:Superfamily: ricin; rRNA N-glycosidase homology
 C:Keywords: duplication; ricin B #status experimental <ECH>
 F:1-263/Product: ricin B chain B #status experimental <ECH>
 F:17-59/60-100, 103-141, 168-183, 187-228, 229-263/Region: 40-residue repeats
 F:17-59/60-100, 103-141, 168-183, 187-228, 229-263/Region: 40-residue repeats
 F:95,135/Binding site: carbohydrate (asn) (covalent) #status experimental
 Query Match 61.5% Score 871; DB 2; Length 263;
 Best Local Similarity 61.3%; Pred. No. 1e-65;
 Matches 160; Conservative 37; Mismatches 62; Indels 2; Gaps 2;
 QY 5 CSASEPTATVGNNGRYVDRDDPDQNOIOLWFSKSNDDNQMTTKEDFTTSNSQC 64
 DB 4 GMDPEPTVIVNGKGCVDKQFRTNMGALQWFCSSNDLWHLTKDKRTTSGNC 63
 QY 65 LFTYGTAGVWVWIPCKPKNRATWQINNGITTPSNVLAASSGKXKTLTYQGL 124
 DB 64 LFTYGVSPVWVWVYDCTATDPTWQINNGITTPSNVLAASSGKXKTLTYQGL 123
 QY 125 DYLGGQNTAGNTAPREVTIYGPRLCSESNGSVWETCSSQDQCKMALYDQDSIR 184
 DB 124 IVASQGMPTNNVTPFTIIVGVYKCLQANSGVWLEDC-TSEASQGMALYDQDSIR 182
 QY 185 PRKQDQCTISGDSVSTVIVTCGASGSGQVFTNKGALIMLTGLANDYDQANP-K 243
 DB 183 PRKRDNCITIDANIKGVTKVILCQPSVSGQWFWFNGDTIMLVINELVDYDRSPSS 242
 QY 244 LRRIIVPATGKXNQWLPF 264
 DB 243 LRQIVVPHFGNINQWLPF 263

RESULT 5
 A:Title: A precursor - Indian jatropha (fragment)
 N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C:Species: Abrus precatorius (Indian jatropha)
 C:Date: 31-Dec-1999 #sequence revision 01-Aug-1997 #text change 16-Jul-1999
 C:Accession: S32429, J02022, A39761, J01398, S14472, S24133, S74110, S74111
 J. Mol. Biol. 229: 263-267, 1993
 A:Title: Primary structure of three distinct isoforms determined by cDNA sequencing.
 A:Reference number: S32429; PMID:8332798; PMID:8421313
 A:Accession: S32429, J02022, A39761, J01398, S14472, S24133, S74110, S74111
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 'E', '2-528 <HUN>
 A:Cross-references: GIM:89344; NID:G166294; PDB:AAA36234.1; PDB:G166295
 A:Note: the coding region for the sequence shown is preceded by an ATG codon
 A:Note: residues 1-8 were derived from the synthesized primer

R:Funatsu, G.; Taguchi, Y.; Kanemoto, M.; Yanaka, M.
 Agric. Biol. Chem. 52, 1095-1097, 1988
 A:Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein f
 A:Reference number: J02022
 A:Accession: J02022
 A:Molecule type: protein
 A:Residues: 1-201, 203-251 <FDR>
 A:Note: The amino acid sequence of the A-chain of abrin-a, a toxic protein f
 J. Biol. Chem. 265: 6846-6852, 1990
 A:Title: Direct molecular cloning and expression of two distinct abrin A-chains.
 A:Reference number: A39761; PMID:91201329; PMID:3016300
 A:Accession: A39761
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 'B', '2-251 <EVB>
 A:Cross-references: EMBL:3243872
 A:Title: The complete amino acid sequence of the B-chain of abrin-a and abrin-b, tox
 R:Funatsu, G.; Taguchi, Y.; Kanemoto, M.; Yanaka, M.
 Agric. Biol. Chem. 52, 1095-1097, 1988
 A:Title: The complete amino acid sequence of the B-chain of abrin-a and abrin-b, tox
 A:Reference number: J01398; PMID:93169023; PMID:7763442
 A:Accession: J01398
 A:Status: not compared with conceptual translation
 A:Molecule type: protein
 A:Residues: 261-347, 'T', '349-351, 'A', '353-357, 'L', '359-528 <KIM>
 A:Experimental source: seed
 C:Superfamily: ricin; rRNA N-glycosidase homology
 C:Keywords: duplication; ricin B #status experimental <ECH>
 F:1-263/Product: ricin B chain B #status experimental <ECH>
 F:17-59/60-100, 103-141, 168-183, 187-228, 229-263/Region: 40-residue repeats
 F:17-59/60-100, 103-141, 168-183, 187-228, 229-263/Region: 40-residue repeats
 F:95,135/Binding site: carbohydrate (asn) (covalent) #status experimental
 Query Match 55.0% Score 779; DB 1; Length 528;
 Best Local Similarity 55.6%; Pred. No. 1.3e-57;

Matches 145; Conservative 43; Mismatches 71; Indels 2; Gaps 2;
QY 5 CAS8-EPTVATVGRKGRVYVDDDDPHDNOICLWPSKSNDDPPQALMTIRKGTIRSN63
DB 269 CSRREPTVRIIGRDGKCVDDVYDGHGKRNRIIMKCKRLEENQWLTKSDKTRSNK 328
QY 64 CLTYGYTAVGVYVIFDCTAVREATTIWMNDGIIINRSNVLAAASGIGKTLTVOT 123
DB 329 CLTYGYTAVGVYVIFDCTAVREATTIWMNDGIIINRSNVLAAASGIGKTLTVOT 388
QY 124 LDYTLGGKTLAAGNDPRAEVITVGRDLCKESNGSWYERCCSGKQKXALYKGS1 183
DB 389 NEYLMKQKRTGNTTSPVTSISGYSDLCQQAQGSNVMADDSNKKEQ-QVALYDGS1 447
QY 184 RPKNODCLTSGRDSVTVINIVSCGASGSGRWFTVSGALINIKTGLADVAQANPK 243
DB 448 RSVQNTNCKLTSDHKQSGTILMGCSGNVAGSOFWRFKDDSIYSLYDVMVYDGS1 507
QY 244 LRKILTYPTGKRNQMLPVF 264
DB 508 LRKILTYPTGKRNQMLPVF 528

RESULT 6

RLCSAG
Agglutinin precursor - castor bean
N/Contains: RNA N-glycosidase (EC 3.2.2.22)
C/Species: Ricinus communis (castor bean)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
A/Accession: A24261, A24210
N/RefSeq: U.N. #amino acid sequence: Pappin, D.J.C.; Lord, J.M.
N/RefSeq: U.N. #amino acid sequence: Pappin, D.J.C.; Lord, J.M.
A/Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
A/Reference number: A24261, PMID:8605449; PMID:2993130
A/Accession: A24261
A/Molecule type: mRNA
A/Residues: 1-564 <R08>
A/Cross-references: GB:M12089; NID:9169700; PIDN:AAA3869.1; PID:G169701
R/Araki, T.; Yoshikawa, Y.; Funatsu, G.
B/ochim. Biophys. Acta 872, 277-285, 1986
A/Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
A/Reference number: A24210
A/Accession: A24210
A/Molecule type: protein
A/Residues: 303-325, 'P', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-564
C/Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C/Superfamily: ricin; RNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F/1-25/Domain: signal sequence #status predicted <SIG>
F/25-290/Product: agglutinin chain A #status predicted <ACH>
F/35-281/Domain: RNA N-glycosidase homology <RNS>
F/303-564/Product: agglutinin chain B #status experimental <BCH>
F/3125/2562-402, 405-413, 450-485, 489-528, 531-564/Region: 40-residue repeats
F/104, 147, 231, 232/Binding site: carbohydrate (Oxyanion) #status predicted
F/200, 203/Active site: Glu, Arg #status predicted
F/282-306, 322-341, 365-382, 453-466, 492-509/Disulfide bonds: #status predicted
F/324, 337, 348/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status predicted
F/397, 437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/536, 537/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 54.38; Score 777.5; DB 1; Length 564;
Best Local Similarity 55.88; Pval. No. 1.9e-577

Matches 145; Conservative 41; Mismatches 73; Indels 1; Gaps 1;
QY 5 CAS8-EPTVATVGRKGRVYVDDDDPHDNOICLWPSKSNDDPPQALMTIRKGTIRSN63
DB 269 CSRREPTVRIIGRDGKCVDDVYDGHGKRNRIIMKCKRLEENQWLTKSDKTRSNK 328
QY 64 CLTYGYTAVGVYVIFDCTAVREATTIWMNDGIIINRSNVLAAASGIGKTLTVOT 123
DB 329 CLTYGYTAVGVYVIFDCTAVREATTIWMNDGIIINRSNVLAAASGIGKTLTVOT 388
QY 124 LDYTLGGKTLAAGNDPRAEVITVGRDLCKESNGSWYERCCSGKQKXALYKGS1 183
DB 389 NEYLMKQKRTGNTTSPVTSISGYSDLCQQAQGSNVMADDSNKKEQ-QVALYDGS1 447
QY 184 RPKNODCLTSGRDSVTVINIVSCGASGSGRWFTVSGALINIKTGLADVAQANPK 243
DB 448 RSVQNTNCKLTSDHKQSGTILMGCSGNVAGSOFWRFKDDSIYSLYDVMVYDGS1 507
QY 244 LRKILTYPTGKRNQMLPVF 264
DB 508 LRKILTYPTGKRNQMLPVF 528

QY 125 DYTLGGKTLAAGNDPRAEVITVGRDLCKESNGSWYERCCSGKQKXALYKGS1 184
DB 426 IYVSGQWLPFTNTPQPTVITVGLYKMCQANSGKWLKED-TESEKQGMALYDGS1 484
QY 185 RPKNODCLTSGRDSVTVINIVSCGASGSGRWFTVSGALINIKTGLADVAQANPK 244
DB 448 RSVQNTNCKLTSDHKQSGTILMGCSGNVAGSOFWRFKDDSIYSLYDVMVYDGS1 507
QY 245 LRKILTYPTGKRNQMLPVF 264
DB 545 LRKILTYPTGKRNQMLPVF 564

RESULT 7

abrin-b precursor - Indian licorice (fragrant)
N/Contains: RNA N-glycosidase (EC 3.2.2.22)
C/Species: Abrus precatorius (Indian licorice)
C/Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
A/Accession: S32430, UCL139
N/RefSeq: U.N. #amino acid sequence: T.C.; Lin, J.Y.
N/RefSeq: U.N. #amino acid sequence: T.C.; Lin, J.Y.
A/Title: Primary structure of three distinct isoforms determined by cDNA sequencing.
A/Reference number: S32430; PMID:9313279; PMID:8423113
A/Accession: S32430
A/Molecule type: mRNA
A/Residues: 1-527 <R08>
A/Cross-references: GB:M98345; NID:9166296; PIDN:AAA3263.1; PID:G166297
R/Kimura, M.; Sumikawa, T.; Funatsu, G.
B/ochim. Biotechnol. Blochem. 57, 186-189, 1993
A/Title: The complete cDNA sequence of the B-chains of abrin-a and abrin-b, tox
A/Reference number: UCL139; PMID:9313279; PMID:7763422
A/Accession: UCL139
A/Molecule type: protein
A/Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'W', 427, 'D', 429-4;
A/Experimental source: seed
C/Superfamily: ricin; RNA N-glycosidase homology
C/Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin;
F/1-250/Product: abrin-b chain A #status predicted <ACH>
F/250-527/Product: abrin-b chain B #status experimental <BCH>
F/280-527/Domain: RNA N-glycosidase homology <RNS>
F/280-527/Region: 40-residue repeats
F/104, 147, 231, 232/Binding site: carbohydrate (Oxyanion) #status predicted
F/200, 203/Active site: Glu, Arg #status predicted
F/282-306, 322-341, 365-382, 453-466, 492-509/Disulfide bonds: #status predicted
F/324, 337, 348/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status predicted
F/397, 437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/449, 520/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 54.38; Score 769; DB 2; Length 527;
Best Local Similarity 55.24; Pval. No. 7e-577

Matches 144; Conservative 42; Mismatches 73; Indels 2; Gaps 2;
QY 5 CAS8-EPTVATVGRKGRVYVDDDDPHDNOICLWPSKSNDDPPQALMTIRKGTIRSN63
DB 269 CSRREPTVRIIGRDGKCVDDVYDGHGKRNRIIMKCKRLEENQWLTKSDKTRSNK 327
QY 64 CLTYGYTAVGVYVIFDCTAVREATTIWMNDGIIINRSNVLAAASGIGKTLTVOT 123
DB 329 CLTYGYTAVGVYVIFDCTAVREATTIWMNDGIIINRSNVLAAASGIGKTLTVOT 387
QY 124 LDYTLGGKTLAAGNDPRAEVITVGRDLCKESNGSWYERCCSGKQKXALYKGS1 183
DB 389 NEYLMKQKRTGNTTSPVTSISGYSDLCQQAQGSNVMADDSNKKEQ-QVALYDGS1 446
QY 184 RPKNODCLTSGRDSVTVINIVSCGASGSGRWFTVSGALINIKTGLADVAQANPK 243
DB 448 RSVQNTNCKLTSDHKQSGTILMGCSGNVAGSOFWRFKDDSIYSLYDVMVYDGS1 506
QY 244 LRKILTYPTGKRNQMLPVF 264
DB 507 LRKILTYPTGKRNQMLPVF 527

RESULT 9
S32431
abrin-d precursor - Indian licoice (fragment)
N:Contains: RNA N-glycosidase (IPC 3.2.2.922)
C:Species: Abrus precatorius (Indian licoice)
C>Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
C/Accession: S32431, S34408
R:Hung, C.H.; Lee, M.C.; Lin, J.Y.
A:Title: Primary structure of three distinct abrinins determined by cDNA sequencing. C
A:Accession: S32431, S32439, M01D:9132798, F01D:842313
A:Molecule type: mRNA
A:Residues: 1-528 <RIN>

Query Match
Best Local Similarity 54.0%; Score 765; DB 2; Length 562;
Matches 143; Conservative 43; Mismatches 73; Indels 2; Gaps 2;

5 CSAS-EPYRIVGNKGRVYRDDPHDNGQOLMBSKSNNDPQVLTIRKDTIRSNIS 63
303 CSRYEPTVIGSRDCKVDYDDGNGRILIMKCKORLENDWTLSSKTIKSNK 362
64 CLTGYGAGVYVMPDCTVRENTIYQVINGTINPNSNTYLAASGIGTTLTQT 123
363 CLTTEGAPGVYVYDCTSAVEMTWIENGTINPNSNTYLAASGIGTTLTQT 422
124 LDTYLGQWLAGNDTAPREVTIYGRDLQESNGSVWVETCSSQKQKALYDPSI 183
423 NEYLNQGNNTNNISFPVTSISGSDLCQAGQSNWVLADCKNKKEQ-QVALYDPSI 481
184 RPKNOQDCLTSGRDSVTYVNIYSGSGASGSRWFNFGALINLKTGLADVAQAPK 243
482 RSYQNTNNCLTSKDKQSGSPIVACSNWAGQWLFNDGSIYTLHDWVDYKSDPS 541
244 LRIIITPAGKPNQWMLPFV 264
542 LKRIITPAGKPNQWMLTF 562

A:Cross-references: EMBL:X55667; NID:916084; PID:CA39202.1; PID:916085
A:Comment: Abria consists of an A chain, which inhibits protein synthesis by inactivat
The A and B chains are linked by a single disulfide bond, which is essential for toxic
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid
F:23-265/Product: abrin-c chain A #status predicted <RCH>
F:235-260/Product: abrin-c chain B #status predicted <RCH>
F:317-359/360-400/402-444/Region: 317-359, 360-400, 402-444 (in mature form) #status predicted
F:335/Modified site: pyrrolidone carbonyl site (Tyr, Tyr, Glu, Asn) #status predicted
F:108, 147, 229, 230/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:198, 201/active site: Glu, Arg #status predicted
F:234, 287, 395, 435, 436/Binding site: carbonyl site (Asn) (covalent) #status predicted
F:281-303, 320-339, 363-380, 451-464, 490-507/Disulfide bonds: #status predicted
F:322, 346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F:534, 555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

A:Cross-references: GB:M96346
R:Hung, C.; Lee, M.; Lee, T.; Lin, J.
Submitted to the EMBL Data Library, March 1993
A:Reference number: S34408
A:Accession: S34408
A:Molecule type: mRNA
A:Residues: 1-169, C, 171-320, T, 322-528 <R02>
A:Cross-references: GB:M96346
C:Comment: Abria consists of an A chain, which inhibits protein synthesis by inactivat
The A and B chains are linked by a single disulfide bond, which is essential for toxic
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin;
F:1-251/Product: abrin-d chain A #status predicted <RCH>
F:7-246/Domain: RNA N-glycosidase homology <RNG>
F:261-328/Product: abrin-d chain B #status predicted <RCH>
F:283-325, 336-366, 407, 414-449, 453-493, 495-528/Region: 40-residue repeats
F:1/Modified site: pyrrolidone carbonyl site (Glu) #status predicted
F:112, 125, 196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:140, 283, 351, 401, 505, 508, 510, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000
F:247-269, 286-305, 323-345, 417-430, 456-473/Disulfide bonds: #status predicted
F:287, 312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F:500, 521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match
Best Local Similarity 53.9%; Score 764; DB 2; Length 528;
Matches 143; Conservative 44; Mismatches 72; Indels 2; Gaps 2;

5 CSAS-EPYRIVGNKGRVYRDDPHDNGQOLMBSKSNNDPQVLTIRKDTIRSNIS 63
269 CSRYEPTVIGSRDCKVDYDDGNGRILIMKCKORLENDWTLSSKTIKSNK 328
64 CLTGYGAGVYVMPDCTVRENTIYQVINGTINPNSNTYLAASGIGTTLTQT 123
329 CLTTEGAPGVYVYDCTSAVEMTWIENGTINPNSNTYLAASGIGTTLTQT 388
124 LDTYLGQWLAGNDTAPREVTIYGRDLQESNGSVWVETCSSQKQKALYDPSI 183
389 NEYLNQGNNTNNISFPVTSISGSDLCQAGQSNWVLADCKNKKEQ-QVALYDPSI 447
184 RPKNOQDCLTSGRDSVTYVNIYSGSGASGSRWFNFGALINLKTGLADVAQAPK 243
448 RSYQNTNNCLTSKDKQSGSPIVACSNWAGQWLFNDGSIYTLHDWVDYKSDPS 507
244 LRIIITPAGKPNQWMLPFV 264
508 LKRIITPAGKPNQWMLTF 528

RESULT 10
S62627
agglutinin I precursor - European elder
C:Species: Sambucus nigra (European elder)
C:Accession: S62627, S62619
R:van Damme, B.J.M.; Barry, A.; Ruge, P.; van Leeuwen, F.; Peumans, W.J.
A:Title: The NeuAc(alpha-2,6)-Gal(GalNAc-binding lectin from elderberry (Sambucus nigra)
A:Reference number: S62619; M01D:96209926; F01D:8631339
A:Accession: S62627
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-570 <VAN>
A:Cross-references: EMBL:U07122; NID:9141772; PID:AAQ9158.1; PID:9141773
A:Accession: S62627
A:Molecule type: protein
A:Residues: 29-39,309-319 <VA2>
C:Superfamily: ricin; RNA N-glycosidase homology
F:37-283/Domain: RNA N-glycosidase homology <RNG>

Query Match
Best Local Similarity 38.5%; Score 545; DB 2; Length 570;
Matches 143; Conservative 45.9%; Pred. No. 6, 2e-38;

Matches 119; Conservative 33; Mismatches 95; Indels 12; Gaps 6;
QY 5 CSASEPTVAVGNKGRVYRDDDFDQNGQIQLMPSKSNNDPQMLTKRQGTIRSNASC 64
DB 316 CSVSEVTRISGMDGLCVDRGCHYIDNPOLAR--CGNECDQLTFRTGTIRMGK 373
QY 65 LTTGTTCATVYVMTFPCNTAVKNTIWIQNDGTTINPSNTVYLAASGIGTTLVOTL 124
DB 374 L-----TASSVWIDQNTVPEAKNTVVISIDGILNHSGLVILNPAQAGTALSLEN 428
QY 125 DYTGGQMLAGNDLAFREVTYIGRDLCKMENGSG--VWERTCSQKQKQKALYDPS 182
DB 429 IHARQGMVVG-DVEELVTFIVGKQKCLRNENNEFWLEDCVLRVQ--EWALYGR 486
QY 183 IPRQNDQCLTSGNDVSFTVINTVSCSAGSGQWVFTNEGATLILKTGLADYQAQNP 242
DB 487 IKVNSNSLCVTSDEHSPDLVLKCGE--SGNQKRWVNTNCTISNPAKLMDVQAQDV 545
QY 243 KRLRIIVATGKPNQML 261
DB 546 SIKKILVPTGPNQML 564

RESULT 11.

UC7535
Chitinase (EC 3.2.1.14) 35 - Streptomyces thermoviolaceus
C/Species: Streptomyces thermoviolaceus
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C/Accession: UC7535
R/Author: J. O'Malley, T. J. Hateno, N. Miyamoto, K. Matsumoto, M. J. Inanc
BioSci. Biotechnol. Biochem. 64: 2445-2453 (2000)
A/Title: Family 19 chitinases from Streptomyces thermoviolaceus OPC-520: Molecular cloni
A/Reference number: UC7535; MUID:21036907; PMID:11193414
A/Accession: UC7535
A/Molecule type: DNA
A/Residues: 1-377 <TSU>
A/Cross-references: DDBJ:AB016842
A/Experimental source: strain OPC-520
A/Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin degr
A/Keywords: chitin-binding domain that is important in the efficient hydrolysis of insoluble c
A/Genes: ch15
C/Keywords: glycosidase; hydrolase

Query Match 10.1%; Score 142.5; DB 2; Length 377;
Best Local Similarity 21.6%; Pred. No. 0.00022;
Matches 64; Conservative 33; Mismatches 110; Indels 89; Gaps 10;
QY 7 ASBPYVAVGNKGRVYRDDDFDQNGQIQLMPSKSNNDPQMLTKRQGTIRSNASC 66
DB 33 KALISITIGDKCKLQKABSGKTPVQIDCNQGN--AQGVVSGSGIHALGCLD 90
QY 67 TGYVTA--GVYVMTFPCNTAVKNTIWIQNDGTTINPSNTVYLAAS--SGIGTTLV 122
DB 91 VDRSTADQAVQVQMDCTGSAQK--VYVTAHDVMPADKCLDTPRNSANGRQVQ 148
QY 123 TLDTTLCQGWLA-----GNDTAFEVTLI-----TGPRLCKESNGSVAW 162
DB 149 TGTGSSNQKMAATGAGSTPAPSGVVSQAQNPFRNPFYVQGLVQALSPFGSA 208
QY 163 ETCDSQKQNO-----GNALTRGG 181
DB 209 NTGDDTTKQGAALFANVHETGQVQVYELMTANFTYQCMQSGYCGCRQALHYSG 266
QY 182 SIRPKNDQCLTSGRDSVSTVIVYVSGASG--SGRWTFNGGAILNLTGL 233
DB 269 PTLQSWN-----YVYRAGAGIQLVILNMPVLPVNDPAIA--KTL 308

RESULT 12
J50589
endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Streptomyces lividans
N/Alternate names: xylanase A

C/Species: Streptomyces lividans
C/Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999
C/Accession: J50589; F50238
R/Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
Gene 107, 75-82, 1991
A/Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A/Reference number: J50589; MUID:92077439; PMID:1743521
A/Accession: J50589
A/Molecule type: DNA
A/Cross-references: GB:W64551
A/Accession: F50238
A/Molecule type: protein
A/Residues: 42-92 <SH2>
C/Genetics:
A/Genes: xlnA
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-xylan
C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F42-477/Protein: signal sequence #status predicted <SIS>
F174-341/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>
F169,277/Active site: Glu #status predicted

Query Match 8.9%; Score 125.5; DB 1; Length 477;
Best Local Similarity 29.9%; Pred. No. 0.0079;
Matches 40; Conservative 20; Mismatches 61; Indels 13; Gaps 6;
QY 7 ASBP-----TVAVGNKGRVYRDDDFDQNGQIQLMPSKSNNDPQMLTKRQGTIRSN 61
DB 346 SSFPAQAGQILKVG--SGKCLDVPASTGQVQLQMGCHST--NQGMATDAGELRY 402
QY 62 G-SCLTYGTAGVYVMTFPCNTAVKNTIWIQNDGTTINPSNTVYLAAS--SGIGT 118
DB 403 GDCSCDAAGSGSKVQIYSCWCGDNK--VRLNSGSVGVQSGCLDAVNGTAGTL 460
QY 119 LVYQTLDTYTGQW 132
DB 461 IQLYTCSNSGNRW 474

RESULT 13

T34603
Xylanase A - Streptomyces coelicolor (fragment)
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 28-Jul-2000
C/Accession: T34603
R/Murphy, L.; Harris, D.; Parthill, J.; Barrett, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, January 1998
A/Reference number: Z21548
A/Accession: T34603
A/Molecule type: translated from GB/EMBL/DDB
A/Residues: 1-383 <MR>
A/Cross-references: EMBL:AL021529; PIRN:CAI6466.1; GSPDB:GN00070; SCODB:SCI0A5.36C
A/Experimental source: strain A3(2)
C/Genetics:
A/Genes: xlnA; SCODB:SCI0A5.36C
C/Superfamily: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-xylan
F11-247/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>

Query Match 8.6%; Score 122.5; DB 2; Length 383;
Best Local Similarity 29.9%; Pred. No. 0.011; 62; Indels 13; Gaps 6;
Matches 40; Conservative 19; Mismatches 62; Indels 13; Gaps 6;
QY 7 ASBP-----TVAVGNKGRVYRDDDFDQNGQIQLMPSKSNNDPQMLTKRQGTIRSN 61
DB 252 SSFPAQAGQILKVG--SGKCLDVPASTGQVQLQMGCHST--NQGMATDAGELRY 308
QY 62 G-SCLTYGTAGVYVMTFPCNTAVKNTIWIQNDGTTINPSNTVYLAAS--SGIGT 118

Thu Dec 11 16:10:08 2003

us-09-601-667c-9.rpr

Db 309 GPKCLDAAGTNSKVVQYSCNGEDNOK--RLNSDGSVGVQSGCLDVGNGTANQTL 366
QY 119 LTVQTLDTYLAQGM 132
Db 367 IQLYTCNSGNSNRM 380

RESULT 14

135697
arabinofuranosidase - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Accession: 135697 #sequence_revision 05-Nov-1999 #text_change 03-Dec-1999
P/Function: 135697, D. Parkhill, J. Barrall, B.G. Rajandream, M.A.
submitted to the EMBL Data Library, January 1999
A/Reference number: 221548
A/Accession: 135697
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-475 <MOR>
A/Cross-references: EMBL:AL021411; EMBL:CAAL6189.1; GSPDB:GN00070; SCOPDB:SC7H1.02
A/Experimental source: strain A3(2)
C/Genetics:
A/Genes: adeB; SCOPDB:SC7H1.02

Query Match 8.2% Score 115.5; DB 2; Length 475;
Best Local Similarity 24.1%; Read No. 0.064; Indels 25; Gaps 10;
Matches 52; Conservative 35; Mismatches 104;

QY 6 SASPEVTVIRVGNRGNVDVDDDFHDSNQIOLWPSKSNDPQOLATIKNDGTIRANG-SC 64
Db 37 AAGSGALNRGAGNRCLDVLZSGSDDBALLQLDYCKGGT--NOQWTSPTDRLTVYGKX 93
QY 65 LTTVGYTA--GVYWIPEQNTAVREATINQIMNGIINPRSNLV--AASSG--IKGTLTV 120
Db 94 LDVPEHATNPEGRVQWMSGSAQNC--WRVNSDGVVGVSGCLERAGAGNGTAVQ 151
QY 121 VQIDLYTLAGQNLAKGNTAREVT-----YGRDLCKSSNGSSWVETCP--SSQAKCK 174
Db 152 LWTGNGGNGQWQVGLGTPPTDGTCLPSTYKSSSTGTLAQPKSGWYALNDFTVTNRSR 211
QY 175 WALYGDGS-----IREKONODCLTSGRDSVS 201
Db 212 HLVYGSYSSGSGSYGNVFSPTNMSDMASAGQANAN 247

RESULT 15

133094
endo-1,3-beta-glucosidase (EC 3.2.1.-) precursor - Oerskovia xanthineolytica
C/Species: Oerskovia xanthineolytica
C/Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 22-Oct-1999
C/Accession: A39094
R/Shen, S.H.; Chretien, P.; Bastien, L.; Siliaty, S.N.
J. Biol. Chem. 266, 1058-1063, 1991
A/Title: Primary sequence of the glucanase gene from Oerskovia xanthineolytica. Express
A/Reference number: A39094; PMID:91093212; PMID:1985933
A/Accession: A39094
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-488
A/Cross-references: GDB:M60926; GB:M8734; NID:G150444; EMBL:AAA25520.1; FID:G150445
C/Keywords: glycosidase; hydrolase

Query Match 8.0% Score 114; DB 2; Length 548;
Best Local Similarity 31.3%; Read No. 0.087; Indels 20; Gaps 7;
Matches 41; Conservative 18; Mismatches 52;

QY 16 GGNQWRY-----DYRDDPHQNGQIOLWPSKSNNDPQOLATIKNDGTIRNSGCL--TT 67
Db 422 GGNALISSTLCIDPMDADPTNVOVL--ATCSGNAQQWTRGTGTVPALGKCLDVAR 479
QY 68 YGTAGVYVMTEDCK--TARENTINQIMNGT--INPRSNLVLAASSGI--KQTLTV 121

Db 480 SGTAADGTAVITVTCNGTGAQKKT----YDARTKALRNPSGKCLDAQGAFLNDQKVVOL 535
QY 122 QTLDTYLAQGM 132
Db 536 WTCQTEAQRW 546

Search completed: December 11, 2003, 13:55:44
Job time : 8.20622 secs

Thu Dec 11 16:10:08 2003

us-09-601-667c-9.rfp

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18 ; Search time 4.53677 Seconds

Title: US-09-601-667C-9 (without alignments)
Sequence: 1 DDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264

Perfect score: 1417

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: Swissprot_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Match	Length	DB ID	Description
1	1412	99.6	264	1 M1A VIRSL	P81830 vicium albu
2	907.5	64.0	576	1 R1C1 R1C1C	P02879 ricinus coo
3	779	55.0	528	1 ABR1 ARBR	P11410 abrus prec
4	777.5	54.9	564	1 AGOL ARICCO	P06570 ricinus com
5	769	54.3	527	1 ABR1 ARBR	P06577 abrus prec
6	765	54.0	562	1 ABR1 ARBR	P28590 abrus prec
7	528.5	37.3	563	1 N1B1 SM1	P33183 sambucus ni
8	477	8.9	477	1 K1M1 STR1	P26514 streptococ
9	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
10	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
11	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
12	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
13	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
14	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
15	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
16	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
17	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
18	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
19	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
20	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
21	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
22	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
23	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
24	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
25	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
26	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
27	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
28	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
29	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
30	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
31	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
32	473	8.2	473	1 ABR1 ARBR	P05146 streptococ
33	473	8.2	473	1 ABR1 ARBR	P05146 streptococ

ALIGNMENTS

Result 1	US-09-601-667C-9	STANDARD	PRT	264 AA
1	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
2	P81830			
3	28-SEP-2003 (Rel. 41, Created)			
4	28-SEP-2003 (Rel. 41, Last sequence update)			
5	15-SEP-2003 (Rel. 42, Last annotation update)			
6	Galactose specific lectin I B chain (MLB) (ML-I B)			
7	Vicia album (European mistletoe)			
8	Spentolophyta; Magnoliophyta; eudicotyledons; core eudicot;			
9	Santalales; Santalaceae; Viscum.			
10	NCBI_TaxID=3972;			
11	SEQUENCE			
12	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
13	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
14	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
15	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
16	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
17	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
18	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
19	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
20	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
21	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
22	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
23	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
24	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
25	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
26	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
27	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
28	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
29	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
30	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
31	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
32	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			
33	MDVTCASAEPTVRIKVENGM.....RRIIVPATGRKNQWLPVF 264			

FT VARIANT 231 231 N -> S OR T.
FT VARIANT 231 233 NGL -> KGP.
FT VARIANT 232 235 GLDM -> SLWV.
SQ SEQUENCE 264 AA: 28991 WW: 7DDDC326CC6F5A4 CRC64:
Query Match 99.6%; Score 1412; DB 1; Length 264;
Best Local Similarity 99.6%; Pred. No. 1.le-112;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDTYCSASPTTRIVGNGKRVGVDDPFDGNGQIDLPKESNDPNQALTTTGGTIRG 60
DB 1 DDTYCSASPTTRIVGNGKRVGVDDPFDGNGQIDLPKESNDPNQALTTTGGTIRG 60
QY 61 NSCLTYGYTAGVYVNI-FPCNTNVPREATTQIMDKTINPRSNVYLAASSGIGTTLT 120
DB 61 NSCLTYGYTAGVYVNI-FPCNTNVPREATTQIMDKTINPRSNVYLAASSGIGTTLT 120
QY 121 VQIDYTLTGQMLAGNDTAPREVTLYGFEDLCWESNGSVWETCDSSOXKQKVALYGD 180
DB 121 VQIDYTLTGQMLAGNDTAPREVTLYGFEDLCWESNGSVWETCDSSOXKQKVALYGD 180
QY 181 GSIRPKNDQCLTSGDSYGVYTNIVYCSGASGSGKRVTFMEALINKTGLAMGVYQA 240
DB 181 GSIRPKNDQCLTSGDSYGVYTNIVYCSGASGSGKRVTFMEALINKTGLAMGVYQA 240
QY 241 NPQLRRITIVPANGKPNQMLPVF 264
DB 241 NPQLRRITIVPANGKPNQMLPVF 264
RESULT 2
TITLE: RICC
AUTHOR: RICC
JOURNAL: RICC
AC P02879; P02880; PRT; 576 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-AUG-1987 (Rel. 05, Last sequence update)
DE 13-SEP-2003 (Rel. 42, Last annotation update)
DE Ricin precursor [Contains: Ricin A chain (RNA N-glycosidase)
(BC 3.2.2.22); Ricin B chain).
OS Ricinus communis (Castor bean).
OC Euphorbiaceae; Stereophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
OC Euphorbiales; Euphorbiaceae; Ricinus.
OC NCBI TaxID:3986;
RN [1] TextID:3986;
RP SEQUENCE FROM N.A.
RX MEDLINE=6067214; PubMed=2999712;
RA Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,
Weaver R.P.;
RT "Genomic cloning and characterization of a ricin gene from Ricinus
communis.";
RL Nucleic Acids Res. 13:8019-8033(1985).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=9216317; PubMed=1711405;
RA Tregear J.W., Roberts L.M.;
RT "The lectin gene family of Ricinus communis: cloning of a functional
ricin gene and three lectin pseudogenes.";
RL Plant Mol. Biol. 18:515-525(1992).
RN [3]
RP SEQUENCE OF 12-576 FROM N.A.
RX MEDLINE=85179479; PubMed=383723;
RA Lamb A., Roberts L.M., Lord J.M.;
RT "Nucleotide sequence of cloned cDNA coding for preproricin.";
RN [4]
RN J. Biochem. 148:265-270(1985).
RP SEQUENCE OF 36-302
RA Yoshitake S., Funatsu G., Funatsu M.;
RT "Isolation and sequences of peptic peptides, and the complete
sequence of the chain of ricin-D.";
RL Agric. Biol. Chem. 42:1267-1274(1978).
RN [5]
RP SEQUENCE OF 315-576.

RA Funatsu G., Kimura M., Funatsu M.;
RT "Primary structure of A1a chain of ricin D.";
RN [6]
RN J. Biol. Chem. 43:2221-2224(1979).
RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
RX MEDLINE=90344223; PubMed=136817;
RA Kimura Y., Kusuku H., Tada M., Takagi S., Funatsu G.;
RT "Structural analyses of sugar chains from ricin A-chain variant.";
RL Agric. Biol. Chem. 54:157-162(1990).
RN [7]
RP REVIEW.
RX MEDLINE=21480122; PubMed=1195634;
RA Oleses S., Kozlov J.V.;
RT "Toxicity 39:1723-1728(2001).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=87165983; PubMed=1558397;
RA Montfort W., Villafraña J.E., Monzinger A.F., Ernst S.R., Katzin B.,
Rutember E., Xiong N.H., Hamlin R., Robertus J.D.;
RT "The three-dimensional structure of ricin at 2.8 A.";
RL J. Biol. Chem. 262:5398-5405(1987).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=9352011; PubMed=168081;
RA Katzin B., Collins E., Robertus J.D.;
RT "Structure of ricin A-chain at 2.5 A.";
RL Proteins 10:251-259(1991).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
RX MEDLINE=91352005; PubMed=1881882;
RA Rutember E., Robertus J.D.;
RT "Structure of ricin B-chain at 2.5-A resolution.";
RL Proteins 10:260-269(1991).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=95082010; PubMed=7990130;
RA Weston S.A., Tucker A.D., Thatcher D.F., Darbyshire D.J.;
RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.";
RL J. Mol. Biol. 244:410-421(1994).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HTS-215.
RX MEDLINE=96374222; PubMed=870513;
RA Day F.J., Ernst S.R., Frankel A.E., Monzinger A.F., Pascal J.M.,
Rutember E., Xiong N.H., Robertus J.D.;
RT "Structure and activity of an active site substitution of ricin A
chain.";
RL Biochemistry 35:11098-11103(1996).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=97240820; PubMed=9086180;
RA Yan X., Hollis T., Swinich M., Day P., Monzinger A.F., Milne G.W.,
Robertus J.D.;
RT "Structure-based identification of a ricin inhibitor.";
RL J. Mol. Biol. 266:1043-1049(1997).
RN [14]
RP WITHINDBSIS.
RX MEDLINE=93165632; PubMed=1287657;
RA Kin Y., Robertus J.D.;
RT "Analysis of several key active site residues of ricin A chain by
mutagenesis and X-ray crystallography.";
RL Protein Eng. 5:775-779(1992).
RN [15]
RP -1- FUNCTION: Ricin is highly toxic to animal cells and to a less
extent to plant cells. The A chain is responsible for inhibiting
protein synthesis through the catalytic inactivation of 60S
ribosomal subunits. It acts as a glycosylase that removes a
specific adenine residue from an exposed loop of 28S ribosomal
RNA. The loop is involved in the binding of elongation
factors. The loop is able to support protein
synthesis. The A chain can
per minute, thus inactivating them faster than the cell can make
new ones. A single A-chain molecule can therefore kill an animal

	.DIST.FID	377	384	
FT	DIST.FID	465	478	
FT	DIST.FID	504	521	
FT	CARBOHYD	45	45	N-LINKED (GLCNAC. . .)
PT	CARBOHYD	271	271	/FID-CAR 00090.
FT	CARBOND	409	409	N-LINKED (GLCNAC. . .) (IN MINOR FORM).
FT	CARBOND	449	449	/FID-CAR 00091.
FT	CARBOND	452	452	N-LINKED (GLCNAC. . .)
FT	CONFLICT	55	55	N-LINKED (GLCNAC. . .)
FT	STRAND	43	47	E -> D (IN REF. 3).
FT	TURN	49	50	A -> R (IN REF. 3).

Query Match 64.0%; Score 907.5; Db 1; Length 576;
Base Local Similarity 63.8%; Pred. No. 1.ee-69;
Matches 166; Conservative 33; Mismatches 60; Indels 1; Gaps 1;

```

5 CAAAGPCTTATTCGKCRVDYRDDFDHGNQIQALMPSSKNDDPNQMTIRDGTTIRNSGC 64
Db   QMDPEVYAIYRNQSCLDQGRFRNQAQLMPCSNISDNWQNTNITSNGKC 377
Oy   LTTGYGAYGVYVMEPCNKVEVETIMOTXMGITTIIPRSENIVLAASGGITLTVQTL 124
Db   LTTYVSPPGVYVMKYDNTAATAIRAQIOWINGIIIRRSSTVLAANSQSGITLLVQIA 437
Oy   125 DYTGQGMLAGNDAPRAEVITYIGFPDLCAENSGSYVWEVCSSQXNQAKMALYPDSIR 184
Db   438 IYRTHGCVLPFNNOGTPVTITVIGLYGLCNSQGVWTEIC-SSEAEQNALPAADNRKI 496
Oy   185 PRONDCCTCGSDPSYVPTVVITVIGLYGLCNSQGVWTEIC-SSEAEQNALPAADNRKI 244
Db   497 PQRNDNCCTGSDPSIEHVYVKILISQPHASQGRMFNRINDGTILNVSGLVADPRASDHS 556
Oy   245 RRITTYPATGEPMQMLPFV 264
Db   557 KQILTYELHGDPQIMLEF 576

```

RESULT 3
ABRA ABRR STANDARD; PRT; 528 AA.
ID ABRA ABRR
AC P1110; P28589;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Abtin-a precursor [contains: Axtin-a B chain]
DE Ec 3.2.2.23; Abtin-a B chain.
DB Abrus precatorius (Andean locoweed) (Embryophyta; Tracheophyta;
OC Saururales; Vitaceae); Streptocarpus; Streptocarpaceae;
OC eumetazoa; Eukaryota; Embryodivisions; core eudicots; Rosidae;
OC eumetazoa; Eukaryota; Embryodivisions; core eudicots; Rosidae;
OC NCBI_Taxid=3816;
LN [1]
RN SEQUENCE FROM N.A.
RA MEDLINE=3132798; PubMed=8421313;
RX Hung C.-H., Lee M.-C., Lee T.C., Lin Y.-Y.;
RT "Primary structure of three distinct isoforms determined by cDNA
sequencing. Conservation and significance."
RL (2) Mol. Biol. 229:1283-1287(1993).
RN [2]
RN SEQUENCE OF 1-251.
RA TTISUB-Seel;
RC Funatsu G., Taguchi Y., Kamemoto M., Yanaka M.;
RT "The complete amino acid sequence of the A-chain of abtin-a, a toxic
protein from the seeds of Abrus precatorius.";
RL Agric. Biol. Chem. 52:1095-1097(1988).
RN [3]
RN SEQUENCE OF 1-251 FROM N.A.
RA MEDLINE=3132798; PubMed=20163007;
RX Funatsu G., Taguchi Y., Kamemoto M., Yanaka M.;
RT "Direct molecular cloning and sequencing of two distinct abtin-

RT A-chains.";
RT J. Biol. Chem. 266:6848-6852(1991).
RN [4]
RP MEDLINE=92571656; PubMed=1505674;
RA "Chen I.-H., Chow L.-P., Tsugita A., Lin J.-Y.,
RT "Crystal structure of abrin-a B chain";
RL FBS Lett. 309:115-116(1992).
RN [5]
RP X-RAY CRYSTALOGRAPHY (2.14 ANGSTROMS).
RX MEDLINE=95333188; PubMed=7609980;
RA Tahirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;
RT "Crystal structure of abrin-a at 2.14 A";
RL J. Mol. Biol. 250:354-367(1995).
CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC SYNTHESIS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
CC -1- FUNCTION: THE B CHAIN IS RESPONSIBLE FOR FACILITATING THE
CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
CC PRECEDES ENDOCYTOSIS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.
CC -1- SIMILARITY: contains 2 ricin B-type lectin domains.
CC This SWISS-PROT entry is a copyright material produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M98344; AAA2624.1; ALT INIT.
DR GENB; J59822; NOT ANNOTATED CDS.
DR KJ; S7423; T438395.
DR PDB; 1ABR; 07-FEB-95.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR SMART; PS00231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGARICIN; 1.
DR K01908; Ricin_B_lectin; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; 3D-struc; disulfide carboxylic acid.
KW CHAIN
FT CHAIN 1 251
FT PEPTIDE 252 261
FT CHAIN 262 528
FT DOMAIN 273 400
FT DOMAIN 403 527
FT REPEAT 283 325
FT REPEAT 326 366
FT REPEAT 369 401
FT REPEAT 404 443
FT REPEAT 444 483
FT REPEAT 484 528
FT ACT SITE 164 164
FT ACT SITE 164 164
FT DISULFID 247 269
FT DISULFID 286 305
FT DISULFID 329 346
FT DISULFID 417 430
FT DISULFID 456 473
FT DISULFID 361 361
FT CARBOHYD 401 401
FT CARBOHYD 401 401
FT CONFLICT 202 202

FT CONFLICT 298 298
FT CONFLICT 427 427
FT CONFLICT 467 467
FT CONFLICT 483 483
FT TURN 5 8
FT TURN 10 11
FT STRAND 12 28
FT STRAND 12 32
FT TURN 32 32
FT STRAND 34 34
FT STRAND 42 42
FT STRAND 42 43
FT STRAND 47 49
FT STRAND 51 57
FT STRAND 63 69
FT TURN 70 72
FT STRAND 75 79
FT STRAND 83 86
FT TURN 88 89
FT TURN 92 93
FT HELIX 94 101
FT TURN 103 103
FT STRAND 103 106
FT TURN 113 114
FT TURN 115 119
FT TURN 124 126
FT STRAND 129 129
FT HELIX 131 142
FT TURN 143 144
FT HELIX 148 167
FT STRAND 168 168
FT HELIX 169 180
FT STRAND 182 182
FT STRAND 182 182
FT HELIX 189 196
FT TURN 197 197
FT HELIX 198 207
FT STRAND 212 220
FT TURN 222 223
FT STRAND 226 231
FT TURN 232 233
FT TURN 235 239
FT STRAND 240 240
FT STRAND 248 248
FT STRAND 268 268
FT STRAND 276 277
FT STRAND 279 280
FT HELIX 282 284
FT STRAND 286 289
FT STRAND 290 292
FT TURN 296 297
FT STRAND 299 303
FT STRAND 315 315
FT TURN 315 315
FT STRAND 319 320
FT STRAND 322 325
FT TURN 326 327
FT STRAND 328 332
FT TURN 337 338
FT STRAND 340 344
FT TURN 346 348
FT TURN 351 353
FT HELIX 351 353
FT STRAND 353 355
FT TURN 355 355
FT TURN 360 361
FT STRAND 364 366
FT TURN 367 370
FT STRAND 371 374
FT TURN 380 381
FT STRAND 383 383
FT STRAND 385 387
FT HELIX 393 395
FT STRAND 398 399

N -> Y (IN REF. 4).
M -> L (IN REF. 4).
T -> P (IN REF. 4).
V -> L (IN REF. 4).

Thu Dec 11 16:10:08 2003

us-09-601-667c-9.rsp

Page 6

Db	306	CMPPEFLVIRVGRNGLCDVYVGRSFFPDGNTLVMPCKSTPDNQLTTRFDDSTIRNSMGC	368
Qy	65	LITVYVYAGVYVMAFDONTAREKATVQIMWDGVIIMPESKLVYLAASGKREGLVYQTL	124
Db	366	LITSSSRQGVVIVINSSTAVAKRQIMDKRITINPESGLVLAATSGSGKGLVYQVN	428
Qy	125	DTYLGCGMAGMDTAPREITVYSPDQDNLSNGSGVWMTDSCQNGKALVYDSTR	184
Dy	426	IVYVSGQMLTNPVQPFVITVIVLVYKQVLQANSGLWLEDC-TSEKQGMVLVYDOSTR	484
Qy	185	PKONDDQLTNSGRGVSIVIVIVYSCGASGSGRWVFNFSNGAILNLTCTLMAMDVAQNPGL	244
Dy	485	FOONDDQLTNPVQPFVITVIVLVYKQVLQANSGLWMTDSCQNGKALVYDSTR	544
Qy	245	RRIITVYAPCKRQNMALPYV 264	
Dy	545	KQITVYVPHGRLNQMILPYV 564	

```
CC RESULT 5
CC ABRB_ABRBP
CC ID ABRB_ABRBP STANDARD; PRT; 527 AA.
CC Q06077; B81374;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Abri-n precursor [Contains: Abri-n b chain (rRNA N-glycosidase)]
CC DS Abri-n b (2.22), Abri-n b chain
CC OS Abus pectinase
CC OS Eukaryota; Viridiplantae; Sciericeae (Crab's eye)
CC SC Spermatophyta; Magnoliopsida; eudicots; Rosidae;
CC eucotsids I; Fabales; Fabaceae; Papilionoideae; Abrsee; Abri-.
CC NCBI_TaxId=3816;
CC RN
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=93127298; PubMed=84231313;
CC RA Hung C.-H., Lee M.-C., Lee T.C., Lin Y.-Y.;
CC RT Secondary structure of three distinct isobutins determined by CDNA
CC RT RT
CC RL J Mol. Biol. 229:1263-1267(1993).
CC RM [2]
CC RP SEQUENCE OF 260-527.
CC RP TISSUE=Seed;
CC RX MEDLINE=93169023; PubMed=7763422;
CC RA Kimura M., Sumizawa T., Funatsu G.;
CC RT "The complete amino acid sequences of the B-chains of abrin-a and
CC RT abrin-b, toxic proteins from the seeds of Abrus precatorius.",
CC RS Biochemistry. Biophys. 57:156-165(1993).
CC CC FUNCTION THROUGH THE CATALYTIC SITE FOR ANHYDROLYSING PROTEIN
CC CC SYNTHESIS THROUGH THE CATALYTIC SITE FOR ANHYDROLYSING PROTEIN
CC CC STUDENTS BY REMOVING AMINO ACIDS FROM POSITION 4,224 OF 26 S RNA.
CC CC ABRI-N-A IS MORE TOXIC THAN RICIN.
CC -1 FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
CC -1 FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
CC PRECEDES ENDOCYTOSIS.
CC -1 CATALYTIC ACTIVITY: Anhydrolcylsis of the N-glycosidic bond at one
CC specific asidesine on the 26S RNA.
CC -1 SUBUNIT: DISULFIDE-LINKED DIMER OF TWO DOMAINS, EACH DOMAIN
CC CONSISTS OF 3 HOMOLOGOUS STRANDS (HELIXES, SHEETS, GRABN).
CC -1 SIMILARITY: IN THE N-TERMINAL SECTION HELICES, SHEETS, GRABN.
CC -1 INACTIVATING PROTEIN FAMILY: TYPE 2 RII SUPRANALY.
CC -1 SIMILARITY: Contains 2 ricin B-type lectin domains.
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the swiss institute of bioinformatics and the EMBL outstation
CC at the European bioinformatics institute. There are no restrictions on its
CC usage by non-profit institutions as long as its content is in no way
CC mislead and this statement is not removed. Usage by and for commercial
CC entities and for profit making purposes requires a separate agreement
CC or send an email to license@ebi.ac.uk. See http://www.isb-sib.ch/announce.
```

[illegible]

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for Commercial
CC entities requires a license agreement (See <http://www.lsb-slb.ch/annouche/>)
CC or send an email to license@lsb-slb.ch)

DR EMBL; AL639125; CNA16189.1; -
DR PIR; T35697; T35697;
DR InterPro; IPR005193; Glyco_Hydro_62;
DR InterPro; IPR007722; Ricin_B lectin;
DR Pfam; PF03664; Glyco_Hydro_62;
DR Pfam; PF00652; Ricin_B lectin; 1;
DR SMART; SM00453; Ricin_B lectin; 1;
DR SMART; SM00453; Ricin_B lectin; 1;
KW Xylan degradation, Hydrolase, Glycosidase, Signal, Lectin;
KW Complete proteome.
KW SIGNAL. 37
KW POTENTIAL.
KW ALPHA-L-ARABINOFURANOSIDASE.
KW CHAIN 38 475
KW DOMAIN 39 166
KW RICIN B-TYPE LECTIN.
KW SEQUENCE 475 AA; 50045 MW; 47E07FE543C60D CRC64.

Best Local Similarity 24.1%; Pred. No. 0.18;
Matches 15; Conservative 35; Mismatches 104; Indels 25; Gaps 10;

QY 6 SASEPTVIRVNGVYVDEDDFHGNIQIDLVSKSNDDPQWLMTIKDQTRISNG-SC 64
DB 37 MARGALAKRKRNR-C-LDVAGSGDDHALLDLIDMGCT--NQQNSITDLRLVYENK 93
QY 65 LITVGTGA--GVYVPECNIVTEATITMOINQNTIINPESRNV--AASG-IKQTLE 120
DB 94 LDVGHARAPETVIVINSGSGAQOQ--WRVNSDDTVVGVSGICLAAAGSGANQNTVVO 151

	RESULT 10	
	E13B ARTSP	
	ID E13B ARTSP STANDARD: PRG: 548 AA.	
	AC Q69146:	
Dt	15-JUL-1998 (Rel. 36, Created)	
Dt	15-JUL-1998 (Rel. 36, Last sequence update)	
Qy	175 WATYAGDS-----IREXONODQLTSSRPASVS 201 ::: :	
Db	212 HLYGTSTGSGSYGSVMFSPFTNMSDMAAQAQAAW 247	

DE Glucan endo-1,3-beta-glucanase precursor (EC 3.2.1.39) (1,3-)-beta-
 DE glucan endohydrolase (1,3-)-beta-glucanase).
 GN GLC1.
 GN Arthrobacter sp. (strain VCM33).
 OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Micrococcaceae; Arthrobacter.
 OX NCBI_TaxId:167.
 RN 111
 RS SEQUENCE FROM N.A.
 RS Submitted (JAN1993) to the EMBL/Genbank/DBJ databases.
 RA Submitted (JAN1993) to the EMBL/Genbank/DBJ databases.
 CC -1 FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETO-1,3-GLUCANS.
 CC IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS (BY
 CC SIMILARITY).
 CC -1 CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
 CC in 1,3-beta-D-glucans.
 CC -1 SUBCELLULAR LOCATION: Periplasmic (by similarity).
 CC -1

CC -1-SIMILARITY: Contains 1 richin B-type lectin domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way that is modified and this statement is not removed. Usage by and for commercial

Thu Dec 11 16:10:08 2003

us-09-601-667c-9.rsp

Page 13

FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 363 363 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 545 AA; 60148 MW; 2DC5A710CE9D59C CRC64;

Query Match

Best Local Similarity 7.1%; Score 100.5; DB 1; Length 545;

Matches 46; Conservative 43; Mismatches 97; Indels 45; Gaps 8;

QY 22 VDVRRDDPFDGNOICLSPSKNNNDNQLWIKRGTIRNSGCLTYGTA----- 72
DB 342 LDIILRLANDRLTLVANKNT-----TVRLIPVQW/LGLETDCYFIEDLMDGKTQ 395
QY 73 ---GVYWIPEGNTAVEATWQ---IMNGTIIIPRSLVLAASGKGTLLVQTL 124
DB 396 KISDHKIELASHNIVFRSLPQGSVYFTGLVNTASGCLTAS--NSVAFQSC 452
QY 125 DYLGGQMLANDAPAEVITYGRDLCHNSGSGWTEGDSQKQKQKALYAGSTR 184
DB 453 NERTSQIMQYTESKTRPVG--QTGLAADNLYLQKDSIDSDGKKTVPVTSGLK 509
QY 185 PKWQDQCLTSGSDSVTVINIVSCGASGSGSQWPTNIGALINLKTGLAM 235
DB 510 -NAKTDGCLTBES-----VQWKSQ-----LYERIDQYFGLPSGVOL 544

Search completed: December 11, 2003, 14:09:06
Job time : 5.6201 secs

Thu Dec 11 16:10:09 2003

us-09-601-667c-9.rpt

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protease search, using sw model

Run on: December 11, 2003, 13:53:19 / Search time 20.3487 Seconds

(without alignment)

Title: US-09-601-667C-9

Sequence: 1 DVTGSAEPTVRIYVNGM.....RRIITPNTKPKYQMLPVF 264

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: SP_ARCHAEA:
2: SP_BACTERIA:
3: SP_FUNGI:
4: SP_HUMAN:
5: SP_INVERTEBRATE:
6: SP_MAMMAL:
7: SP_MUS:
8: SP_MUS_MELLE:
9: SP_DBASE:
10: SP_PLANT:
11: SP_RECENT:
12: SP_VIRUS:
13: SP_VIRTEBRATE:
14: SP_UNCLASSIFIED:
15: SP_VIRUS:
16: SP_BACTERIA:
17: SP_ARCHAEA:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1310.5	92.5	531 10 Q8RXK6	Q8RXK6 vitiscum albu
2	1119.5	79.0	263 10 Q8KX02	Q8KX02 vitiscum albu
3	1106.5	78.1	565 10 Q8KX03	Q8KX03 vitiscum albu
4	1085.5	76.6	263 10 Q8KX01	Q8KX01 vitiscum albu
5	999.5	70.5	266 10 Q8KX03	Q8KX03 vitiscum albu
6	909.5	64.2	541 10 Q41174	Q41174 ricinus com
7	871.5	61.5	263 10 Q41174	Q41174 ricinus com
8	870.5	61.4	580 10 Q94B84	Q94B84 cinnamomum
9	870.5	61.4	580 10 Q94B84	Q94B84 cinnamomum
10	824.5	58.2	549 10 Q94B85	Q94B85 cinnamomum
11	824.5	58.2	581 10 Q94B85	Q94B85 cinnamomum
12	782.5	53.8	528 10 Q96076	Q96076 abrus preca
13	748.5	52.8	382 10 Q96A43	Q96A43 abrus preca
14	748.5	52.8	547 10 Q96A43	Q96A43 abrus preca
15	679.5	48.0	573 10 Q8WZ68	Q8WZ68 iris hollan
16	679.5	48.0	592 10 Q8WZ67	Q8WZ67 iris hollan

ALIGNMENTS

RESULT 1	Q8RXK6	PRELIMINARY:	PT:	531 AA.
1D Q8RXK6	1310.5	92.5	531 AA.	Q8RXK6
2D Q8KX02	1119.5	79.0	263 10 Q8KX02	Q8KX02
3D Q8KX03	1106.5	78.1	565 10 Q8KX03	Q8KX03
4D Q8KX01	1085.5	76.6	263 10 Q8KX01	Q8KX01
5D Q8KX03	999.5	70.5	266 10 Q8KX03	Q8KX03
6D Q41174	909.5	64.2	541 10 Q41174	Q41174
7D Q41174	871.5	61.5	263 10 Q41174	Q41174
8D Q94B84	870.5	61.4	580 10 Q94B84	Q94B84
9D Q94B84	870.5	61.4	580 10 Q94B84	Q94B84
10D Q94B85	824.5	58.2	549 10 Q94B85	Q94B85
11D Q94B85	824.5	58.2	581 10 Q94B85	Q94B85
12D Q96076	782.5	53.8	528 10 Q96076	Q96076
13D Q96A43	748.5	52.8	382 10 Q96A43	Q96A43
14D Q96A43	748.5	52.8	547 10 Q96A43	Q96A43
15D Q8WZ68	679.5	48.0	573 10 Q8WZ68	Q8WZ68
16D Q8WZ67	679.5	48.0	592 10 Q8WZ67	Q8WZ67

Q8RXK6: PRELIMINARY: PT: 531 AA.
Q8KX02: 1310.5, 92.5, 531 AA.
Q8KX03: 1119.5, 79.0, 263 10 Q8KX02
Q8KX01: 1106.5, 78.1, 565 10 Q8KX03
Q8KX03: 1085.5, 76.6, 263 10 Q8KX01
Q8KX03: 999.5, 70.5, 266 10 Q8KX03
Q41174: 909.5, 64.2, 541 10 Q41174
Q41174: 871.5, 61.5, 263 10 Q41174
Q94B84: 870.5, 61.4, 580 10 Q94B84
Q94B84: 870.5, 61.4, 580 10 Q94B84
Q94B85: 824.5, 58.2, 549 10 Q94B85
Q94B85: 824.5, 58.2, 581 10 Q94B85
Q96076: 782.5, 53.8, 528 10 Q96076
Q96A43: 748.5, 52.8, 382 10 Q96A43
Q96A43: 748.5, 52.8, 547 10 Q96A43
Q8WZ68: 679.5, 48.0, 573 10 Q8WZ68
Q8WZ67: 679.5, 48.0, 592 10 Q8WZ67

Matches 246; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 1 DVTGSAEPTVRIYGNMRYVDDPHDQNOIQLPKSKNDPQWLTKREDGTIRS 60
 DB 269 DVTGSAEPTVRIYGNMRYVDDPHDQNOIQLPKSKNDPQWLTKREDGTIRS 328
 QY 61 NSGCLTYGTAGYVYMFECNTAREATIQWKGITINPRSNVLAASSGKGTIT 120
 DB 329 NSGCLTYGTAGYVYMFECNTAREATIQWKGITINPRSNVLAASSGKGTIT 388
 QY 121 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMESNGSGSVWETCDSSQKQKALYGD 180
 DB 389 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMESNGSGSVWETCDSSQKQKALYGD 447
 QY 181 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWVTFNEGALINKTGLAMDVAQA 240
 DB 448 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWVTFNEGALINKTGLAMDVAQA 507
 QY 241 NPKLRRIIYPATGKPKQWMLPV 263
 DB 508 NPKLRRIIYPATGKPKQWMLPV 530

RESULT 2

QBLK02 PRELIMINARY; PRT; 263 AA.

ID QBLK02
 DT 01-OCT-2002 (Tremblrel, 22, Created)
 DT 01-OCT-2002 (Tremblrel, 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)
 DE Lectin chain B isoform 2 (Fragment).
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 OX NCBI_TaxID=159976;
 RN [1]
 RA Do M.-S., Song S.K., Pubmed:1170524.
 RA Park C.-H., Song S.K., Kang I.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 "cDNA cloning and sequence analysis of the lectin genes of the Korean
 RT mistletoe (Viscum album coloratum)."
 RL Mol. Cells 12:215-220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 Do M.-S., Song S.K.,
 Submitted (MAY-2002) to the EMBL/GenBank/DBD databases.
 DB 121 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMESNGSGSVWETCDSSQKQKALYGD 180
 DB 389 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMESNGSGSVWETCDSSQKQKALYGD 447
 DB 181 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWVTFNEGALINKTGLAMDVAQA 240
 DB 448 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWVTFNEGALINKTGLAMDVAQA 507
 DB 241 NPKLRRIIYPATGKPKQWMLPV 263
 DB 508 NPKLRRIIYPATGKPKQWMLPV 530

Query Match 79.0%; Score 119.5; DB 10; Length 263;
 Best Local Similarity 79.1%; Pred. No. 2, Le-86;
 Matches 208; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

QY 1 DVTGSAEPTVRIYGNMRYVDDPHDQNOIQLPKSKNDPQWLTKREDGTIRS 60
 DB 1 DVTGSAEPTVRIYGNMRYVDDPHDQNOIQLPKSKNDPQWLTKREDGTIRS 60
 QY 61 NSGCLTYGTAGYVYMFECNTAREATIQWKGITINPRSNVLAASSGKGTIT 120
 DB 61 NSGCLTYGTAGYVYMFECNTAREATIQWKGITINPRSNVLAASSGKGTIT 120
 QY 121 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMESNGSGSVWETCDSSQKQKALYGD 180
 DB 121 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMESNGSGSVWETCDSSQKQKALYGD 180

RESULT 3

QBLK01 PRELIMINARY; PRT; 263 AA.

ID QBLK01
 DT 01-OCT-2002 (Tremblrel, 20, Created)
 DT 01-MAR-2002 (Tremblrel, 20, Last sequence update)
 DT 01-OCT-2002 (Tremblrel, 22, Last annotation update)
 DE VLA precursor (EC 3.2.2.22) (RNA N-glycosylase).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 OX NCBI_TaxID=159976;
 RN [1]
 RA Park W.-B., Lyu S.,
 Cloning of Viscum album subsp. coloratum (Korean mistletoe)."
 CC - SIMILARITY ACTIVITY: ENDORIBONUCLEASE OF THE N-GLYCOSIDIC BOND AT ONE
 DE - SIMILARITY: BEYOND TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL: A536961; AL40417.1;
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR Pfam: PF00652; Ricin_B_lectin; 6.
 DR PRINTS: PR00396; SHIGRICIN.
 DR SMART: SM00453; RICIN_B_LLECTIN; 2.
 DR PROSITE: PS00231; RICIN_B_LLECTIN; 2.
 RN HYDROLASE; Signal; Toxin.
 RN CHAIN 1
 FT CHAIN 309 565
 FT CHAIN VCA BETA CHAIN.
 SO SEQUENCE 565 AA; 62401 MW; 991E399AD005F11 CRC64;

Query Match 78.1%; Score 1106.5; DB 10; Length 565;
 Best Local Similarity 80.2%; Pred. No. 6, 7e-85;
 Matches 211; Conservative 15; Mismatches 32; Indels 5; Gaps 2;

QY 1 DVTGSAEPTVRIYGNMRYVDDPHDQNOIQLPKSKNDPQWLTKREDGTIRS 60
 DB 307 DVTGSAEPTVRIYGNMRYVDDPHDQNOIQLPKSKNDPQWLTKREDGTIRS 362
 QY 61 NSGCLTYGTAGYVYMFECNTAREATIQWKGITINPRSNVLAASSGKGTIT 120
 DB 363 NSGCLTYGTAGYVYMFECNTAREATIQWKGITINPRSNVLAASSGKGTIT 422
 QY 121 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMESNGSGSVWETCDSSQKQKALYGD 180
 DB 422 VQTLDTYTCQGLAGNDTAPPEVTIYGRDLQMESNGSGSVWETCDSSQKQKALYGD 481
 QY 181 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWVTFNEGALINKTGLAMDVAQA 240
 DB 482 GSIRPKONQDCLTSGRDSVSTVINIVSCGASGSGRWVTFNEGALINKTGLAMDVAQA 541
 QY 241 NPKLRRIIYPATGKPKQWMLPV 263
 DB 542 NPKLRRIIYPATGKPKQWMLPV 564

AC 091K01;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Lectin chain B subsp. coloratum.
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 OX NCBI_TaxID=159976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.,
 RA Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF508919; AA046937.1;
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR SMART: SM00458; Ricin_B_lectin; 6.
 DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
 FT NON TER 1
 FT NON TER 263
 SQ SEQUENCE 263 AA; 29071 MW; 3F9CADAD860F61D CRC64;
 Query Match 76.6%; Score 1085.5; DB 10; Length 263;
 Best Local Similarity 77.2%; Pred. No. 1.5e-83;
 Matches 203; Conservative 22; Mismatches 37; Indels 1; Gaps 1;
 QY 1 DDTVCSAEPPTVATVGNKAKVYDDPHDQGLMPSKSNDDPQGLTTRDGTIS 60
 DB 1 DDTVCSAEPPTVATVGNKAKVYDDPHDQGLMPSKSNDDPQGLTTRDGTIS 60
 QY 61 NSCLTGYGTAGVYVIFPCNTAVERTTQINDGTIINPRSNLYL--AASGIGKT 120
 DB 61 NSCLTGYGTAGVYVIFPCNTAVERTTQINDGTIINPRSNLYL--AASGIGKT 120
 QY 61 NSCLTGYGTAGVYVIFPCNTAVERTTQINDGTIINPRSNLYL--AASGIGKT 120
 DB 61 NSCLTGYGTAGVYVIFPCNTAVERTTQINDGTIINPRSNLYL--AASGIGKT 120
 QY 121 VQTLDTYLGQGLMAGNDTAPREVTIYGFDDCMESNGSVWETCDSSQKQKVALYD 180
 DB 121 VQTLDTYLGQGLMAGNDTAPREVTIYGFDDCMESNGSVWETCDSSQKQKVALYD 180
 QY 121 VQTLDTYLGQGLMAGNDTAPREVTIYGFDDCMESNGSVWETCDSSQKQKVALYD 180
 DB 121 VQTLDTYLGQGLMAGNDTAPREVTIYGFDDCMESNGSVWETCDSSQKQKVALYD 180
 QY 181 GEIRKQNDQCTLSGRDSVSTVNIYVSCGASGQKRWFTNKGALINLTGLADVAQK 240
 DB 181 GEIRKQNDQCTLSGRDSVSTVNIYVSCGASGQKRWFTNKGALINLTGLADVAQK 240
 QY 180 GSIRPKQNDQCTLSGRDSVSTVNIYVSCGASGQKRWFTNKGALINLTGLADVAQK 239
 DB 180 GSIRPKQNDQCTLSGRDSVSTVNIYVSCGASGQKRWFTNKGALINLTGLADVAQK 239
 QY 241 NPKLRRIIIPATCKENQMLPV 263
 DB 241 NPKLRRIIIPATCKENQMLPV 263
 QY 240 NPKLRRIIIPATCKENQMLPV 262
 DB 240 NPKLRRIIIPATCKENQMLPV 262
 RESULT 5
 QY 091K03
 ID 091K03 PRELIMINARY; FRT; 266 AA.
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Lectin chain B isoform 1 (fragment).
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 OX NCBI_TaxID=159976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.,
 RA Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF508919; AA046937.1;
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR SMART: SM00458; Ricin_B_lectin; 5.
 DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
 FT NON TER 1
 FT NON TER 266
 SQ SEQUENCE 266 AA; 29537 MW; 4A51473C7B94C73 CRC64;
 Query Match 70.5%; Score 999; DB 10; Length 266;
 Best Local Similarity 69.5%; Pred. No. 3e-76;
 Matches 185; Conservative 21; Mismatches 46; Indels 4; Gaps 2;
 QY 1 DDTVCSAEPPTVATVGNKAKVYDDPHDQGLMPSKSNDDPQGLTTRDGTIS 60
 DB 1 DDTVCSAEPPTVATVGNKAKVYDDPHDQGLMPSKSNDDPQGLTTRDGTIS 60
 QY 61 NSCLTGYGTAGVYVIFPCNTAVERTTQINDGTIINPRSNLYL--AASGIGKT 117
 DB 61 NSCLTGYGTAGVYVIFPCNTAVERTTQINDGTIINPRSNLYL--AASGIGKT 117
 QY 61 NSCLTGYGTAGVYVIFPCNTAVERTTQINDGTIINPRSNLYL--AASGIGKT 117
 DB 61 NSCLTGYGTAGVYVIFPCNTAVERTTQINDGTIINPRSNLYL--AASGIGKT 117
 QY 118 TLTQTLDTYLGQGLMAGNDTAPREVTIYGFDDCMESNGSVWETCDSSQKQKVALY 177
 DB 118 TLTQTLDTYLGQGLMAGNDTAPREVTIYGFDDCMESNGSVWETCDSSQKQKVALY 177
 QY 121 TLTQTLDTYLGQGLMAGNDTAPREVTIYGFDDCMESNGSVWETCDSSQKQKVALY 179
 DB 121 TLTQTLDTYLGQGLMAGNDTAPREVTIYGFDDCMESNGSVWETCDSSQKQKVALY 179
 QY 178 YQDSIRPKQNDQCTLSGRDSVSTVNIYVSCGASGQKRWFTNKGALINLTGLADVAQK 237
 DB 178 YQDSIRPKQNDQCTLSGRDSVSTVNIYVSCGASGQKRWFTNKGALINLTGLADVAQK 239
 QY 180 YQDSIRPKQNDQCTLSGRDSVSTVNIYVSCGASGQKRWFTNKGALINLTGLADVAQK 239
 DB 180 YQDSIRPKQNDQCTLSGRDSVSTVNIYVSCGASGQKRWFTNKGALINLTGLADVAQK 239
 QY 238 AANPRLRIIIPATCKENQMLPV 263
 DB 238 AANPRLRIIIPATCKENQMLPV 263
 QY 240 AANPRLRIIIPATCKENQMLPV 265
 DB 240 AANPRLRIIIPATCKENQMLPV 265
 RESULT 6
 QY 041174
 ID 041174 PRELIMINARY; FRT; 541 AA.
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Protein A chain (EC 3.2.2.22) (rRNA N-glycosylase)
 OS Homo sapiens (Caenorhabditis).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosidae; Malpighiales; Euphorbiaceae; Riciniaceae; Ricinus.
 OX NCBI_TaxID=3988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE:9338377; PubMed:163311;
 RA Roberts L.M., Tregear U.M., Lord U.M.,
 RA Molecular cloning of ficin."
 RL Targeted Disgn. Ther. 7:81-97(1992).
 CC -1- CHLORALHYDRATE-INDUCED DEGRADATION OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SITE OF THE PROTEIN ENCODING THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL: 540165; JAB22582.1;
 DR HSPB: P02879; 18R6
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR InterPro: IPR001574; RIP.
 DR SMART: SM00458; Ricin_B_lectin; 6.
 DR PROSITE: PS50231; RICIN_B_LECTIN; 5.

DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SMO0459; RICIN. 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN. 1.
DR PROSITE: PS00339; SOMATROPIN_2; 1.
DR PROSITE: PS00339; SOMATROPIN_2; 1.
FT NOW RES. 1.
SQ SEQUENCE 541 AA; 60281 MW; 29782CCEP1PZBD9 CRC64;

Query Match 64.2%; Score 909.5; DB 10; Length 541;
Best Local Similarity 63.8%; Pred. No. 2, se-68;
Matches 166; Conservative 34; Mismatches 59; Indels 1; Gaps 1;

QY 5 CSASEPTVIVGNNGRVYVADDDPDHGNQIQIMPESKNDPNOIWLTIKEDGTIRNSGSC 64
DB CMDEPTVIVGNGLCVVDSDSFHNGNAIQMPCKNSNTDANQIWLTKRNTIRNSGKC 342
QY 65 LITVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 124
DB LITVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 124
QY 343 LITVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 402
DB LITVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 402
QY 125 DYTIGGMLAGNDTAPREVITYGFRDLCSNNGSGVWETCCSSQKMGKALYGDGSR 184
DB 403 IYVSGMLPTNNTQPFVTTIVGLGCLQANSQVWIEDC-TSEKAEQWALYADGSR 461
QY 185 PKQNDQCLTSGRDSVSTVNIIVSGASGSGQVFTNEGALINIKTGLANDVQANPKL 244
DB 462 PQKNDQCLTSGRDSVSTVNIIVSGASGSGQVFTNEGALINIKTGLANDVQANPKL 244
QY 245 RRIIVYATGKNGMPLV 264
DB 522 KQIIVHFGNINQIWLPLF 541

RESULT 7

ID 041143 PRELIMINARY; RT; 263 AA.
AC 041143
QY 01-NOV-1996 (TRENHARL 01, Created)
DT 01-NOV-1996 (TRENHARL 01, Last sequence update)
DE 01-MAR-2003 (TRENHARL 23, Last annotation update)
GN RICIN E beta chain (fragment).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
OC eucotids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RA Laitin, J.F., Murray, E.Z., Halling, A.C., Halling, K.C., Tikkanen, N.,
RT "Characterization of a cDNA encoding a hybrid ricin-ricinus
RT communis agglutinin gene from the castor plant Ricinus communis".
RT Plant Mol. Biol. 9:287-295(1987).
DR EMBL: M17631; AA063506.1; --
DR HSSP: P02879; 2A1.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR SMART: SMO0458; RICIN_2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00339; SOMATROPIN_2; 1.
FT NON TER. 1.
SQ SEQUENCE 263 AA; 29134 MW; AAB0PDD1D1E144 CRC64;

Query Match 61.5%; Score 871; DB 10; Length 263;
Best Local Similarity 61.3%; Pred. No. 1, se-65;
Matches 160; Conservative 37; Mismatches 62; Indels 2; Gaps 2;

QY 5 CSASEPTVIVGNNGRVYVADDDPDHGNQIQIMPESKNDPNOIWLTIKEDGTIRNSGSC 64
DB CMDEPTVIVGNGLCVVDSDSFHNGNAIQMPCKNSNTDANQIWLTKRNTIRNSGKC 342
QY 65 LITVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 124
DB LITVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 124
QY 343 LITVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 402
DB LITVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 402
QY 125 DYTIGGMLAGNDTAPREVITYGFRDLCSNNGSGVWETCCSSQKMGKALYGDGSR 184
DB 403 IYVSGMLPTNNTQPFVTTIVGLGCLQANSQVWIEDC-TSEKAEQWALYADGSR 461
QY 185 PKQNDQCLTSGRDSVSTVNIIVSGASGSGQVFTNEGALINIKTGLANDVQANPKL 244
DB 462 PQKNDQCLTSGRDSVSTVNIIVSGASGSGQVFTNEGALINIKTGLANDVQANPKL 244
QY 245 RRIIVYATGKNGMPLV 264
DB 522 KQIIVHFGNINQIWLPLF 541

DB 4 CMDEPTVIVGNGLCVVDSDSFHNGNAIQMPCKNSNTDANQIWLTKRNTIRNSGKC 63
QY 65 LITVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 124
DB 64 LITVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 123
QY 125 DYTIGGMLAGNDTAPREVITYGFRDLCSNNGSGVWETCCSSQKMGKALYGDGSR 184
DB 124 IYVSGMLPTNNTQPFVTTIVGLGCLQANSQVWIEDC-TSEKAEQWALYADGSR 182
QY 183 PKQNDQCLTSGRDSVSTVNIIVSGASGSGQVFTNEGALINIKTGLANDVQANPKL 243
DB 462 PQKNDQCLTSGRDSVSTVNIIVSGASGSGQVFTNEGALINIKTGLANDVQANPKL 242
QY 244 RRIIVYATGKNGMPLV 264
DB 243 KQIIVHFGNINQIWLPLF 541

RESULT 8

ID 04484 PRELIMINARY; RT; 580 AA.
AC 04484
QY 01-DEC-2001 (TRENHARL 19, Created)
DT 01-DEC-2001 (TRENHARL 19, Last sequence update)
DE 01-MAR-2003 (TRENHARL 23, Last annotation update)
GN Type 2 ribosome-inactivating protein cinnaomnin II precursor
DE (BC 3.2.2.22) (rRNA N-glycosylase).
OS Cinnaomnin camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnaomnin.
OX NCBI_TaxID=19429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang, O., Gong, Z., Liu, X.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnaomnin proteins and study of their expression
RT patterns".
RT Submitted (Jun-2001) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDORIBONUCLEASE ACTIVITY.
CC -1- SPECIFIC ACIDOSOME ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
GN EMBL: AF099802; AA092459.1; --
DR InterPro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF001400; Somatotropin.
DR SMART: SMO0458; RICIN_2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00339; SOMATROPIN_2; 1.
FT SIGNAL. 1 32
FT CHAIN. 33 580
FT POTENTIAL.
FT CINAOMNIN II.
SQ SEQUENCE 580 AA; 64265 MW; 3784289CEBCEBF CRC64;

Query Match 61.4%; Score 870; DB 10; Length 580;
Best Local Similarity 62.9%; Pred. No. 5, se-65;
Matches 166; Conservative 32; Mismatches 64; Indels 2; Gaps 2;

QY 1 DDTVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 120
DB 317 NDFTGADDEPTVIRISGNGLCVVDSDSFHNGNAIQMPCKNSNTDANQIWLTKRNTIRNSGKC 376
QY 61 NGSTVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 120
DB 377 NGSTVGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 120
QY 121 VGLTGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 180
DB 437 VGLTGTAGVYVWIPDQNVARETITNDQNTINRNSNLTAASSGKGTITVTL 180
QY 181 GSRFQNDQCLTSGRDSVSTVNIIVSGASGSGQVFTNEGALINIKTGLANDVQANPKL 243

DB 496 GSIRPHODRCLSTDMHSGSIIISCSFSGSQQWFWFNDOTLNLKGLVADYK 555
 QY 240 ANPKLRRIIYPATGKQWMLPV 263
 DB 556 SNPSLHQLIWPATGKQWMLPV 579

RESULT 9

094BM3 PRELIMINARY; PRT; 580 AA.
 ID 094BM3
 AC 094BM3; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinamomoin III precursor
 DE EC 3.2.2.22 (EC N-Glycosylase)
 OS Cinamomum camphora (Camphor tree)
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 NX NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinamomoin proteins and study of their expression
 RT patterns; (2001) to the EMBL/GenBank/DBJ databases.
 RT Submitted (2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC -1- SPECIFIC ADPOSING ON THE 28S RRNA
 DR EMBL; A039803; A039803.1; R1CIN_B_LECTIN.
 DR Interpro; IPR000772; R1CIN_B_LECTIN.
 DR Interpro; IPR001574; R1P.
 DR Pfam; PF00652; R1CIN_B_LECTIN; 6.
 DR Pfam; PF00161; R1P; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; R1CIN; 2.
 DR PROSITE; PS0231; R1CIN_B_LECTIN; 2.
 DR PROSITE; PS0231; R1CIN_B_LECTIN; 2.
 KM Hydrolyase; Signal; Toxin.
 FT SIGNAL 1
 FT CHAIN 33 580
 FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CINAMOMOIN III.
 SQ SEQUENCE 580 AA; 64421 MW; 940010F0L87B558 CRC64;

Query Match 60.5%; Score 863; DB 10; Length 580;
 Best Local Similarity 62.5%; Pred. No. 2,36-64;
 Matches 165; Conservative 33; Mismatches 64; Indels 2; Gaps 2;

QY 1 DVTGASAPTYRIVGKNGKIVVDDDFDQNGIQLPKSKNDPQGLMTIKDCTTIS 60
 DB 317 NDPTCADPEFTYRISGNGLCVDYDCKXNNGNFIQLPFCQKQSDVWQMLTARDCTIS 376
 QY 61 NSGCLTGYTAGYVYMI FDCQAVREATIQIWDNGIILNPSNVLAAAGSISKTTLT 120
 DB 377 NGKCLTNGSAGDYVMIDRPTVLAASIQFANGIILNPSALVLAAGSINPPTLT 436
 QY 121 VQTLDTYLGQWLAGNDTAPREVTLYGFDLQENSGSVWVETDSQKQGNALYD 180
 DB 437 VQADTYASRQWLAGNTEPVTISVFNDCQWQAMWVBCSSFAED KMLVYD 495
 QY 181 GSIRPHODRCLSTDMHSGSIIISCSFSGSQQWFWFNDOTLNLKGLVADYK 239
 DB 496 GSIRPHODRCLSTDMHSGSIIISCSFSGSQQWFWFNDOTLNLKGLVADYK 555
 QY 240 ANPKLRRIIYPATGKQWMLPV 263
 DB 556 SNPSLHQLIWPATGKQWMLPV 579

RESULT 10

094BM3 PRELIMINARY; PRT; 549 AA.
 ID 094BM3

AC 094BM3; 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Type II ribosome-inactivating protein cinamomoin (EC 3.2.2.22) (RNA
 DE N-glycosylase) (fragment)
 OS Cinamomum camphora (Camphor tree)
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 NX NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xie L., Liu W.-Y., Wang E.-D.;
 RT Molecular cloning of cinamomoin A-, B-chain and the expression,
 RT purification, characterization and mutagenesis of the A-chain;
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDORIBOSOMAL OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; A025548; A025548.2;
 DR Interpro; IPR000772; R1CIN_B_LECTIN.
 DR Interpro; IPR001574; R1P.
 DR Pfam; PF00652; R1CIN_B_LECTIN; 5.
 DR Pfam; PF00161; R1P; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; R1CIN; 2.
 DR PROSITE; PS0231; R1CIN_B_LECTIN; 2.
 DR PROSITE; PS0231; R1CIN_B_LECTIN; 2.
 KM Hydrolyase; Toxin.
 FT SIGNAL 1
 FT CHAIN 549
 FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CINAMOMOIN II.
 SQ SEQUENCE 549 AA; 60648 MW; 02607F6607C44B0 CRC64;

Query Match 58.2%; Score 824.5; DB 10; Length 549;
 Best Local Similarity 59.6%; Pred. No. 3,76-61;
 Matches 188; Conservative 32; Mismatches 72; Indels 3; Gaps 2;

QY 1 DVTGASAPTYRIVGKNGKIVVDDDFDQNGIQLPKSKNDPQGLMTIKDCTTIS 60
 DB 285 NDPTCADPEFTYRISGNGLCVDYDCKXNNGNFIQLPFCQKQSDVWQMLTARDCTIS 344
 QY 61 NSGCLTGYTAGYVYMI FDCQAVREATIQIWDNGIILNPSNVLAAAGSISKTTLT 120
 DB 345 NGKCLTNGSAGDYVMIDRPTVLAASIQFANGIILNPSALVLAAGSINPPTLT 404
 QY 121 VQTLDTYLGQWLAGNDTAPREVTLYGFDLQENSGSVWVETDSQKQGNALYD 180
 DB 405 VQADTYASRQWLAGNTEPVTISVFNDCQWQAMWVBCSSFAED KMLVYD 463
 QY 181 GSIRPHODRCLSTDMHSGSIIISCSFSGSQQWFWFNDOTLNLKGLVADYK 238
 DB 466 GSIRPHODRCLSTDMHSGSIIISCSFSGSQQWFWFNDOTLNLKGLVADYK 523
 QY 239 QANPKLRRIIYPATGKQWMLPV 263
 DB 524 SNPSLHQLIWPATGKQWMLPV 548

RESULT 11

094BM3 PRELIMINARY; PRT; 581 AA.
 ID 094BM3
 AC 094BM3; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinamomoin I precursor
 DE EC 3.2.2.22 (EC N-Glycosylase)
 OS Cinamomum camphora (Camphor tree)
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 NX NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;

RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamon proteins and study of their expression patterns." RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases. CC -1- CATALYTIC ACTIVITY: ENDOPHYCOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA. CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. DR EMBL: AF001574; RIPO00772; R1P. DR InterPro: IPR001574; R1P. DR Pfam: PF00652; R1cin_B_lectin. 5. DR PRINTS: PR00161; R1P.1. DR SMART: SM00458; R1CIN.2. DR PROSITE: PS0231; R1CIN_B_LECTIN.2. DR HYDROLASE; Signal; Toxin. DR SIGNAL. 32. DR CHAIN. 1. 581. FT SEQUENCE. 581 AA; 64215 MW; 688318893630196 CRC64; QUERY MATCH. 58.2%; Score 824.5; DB 10; Length 581; Best Local Similarity 59.6%; Pred. No. 4e-61; Matches 158; Conservative 32; Mismatches 72; Indels 3; Gaps 2; QY 1 DVTGSAEPFVRIYVGRNKGVDVDDPHQNOIQLPKSNNDPQQLTKRIGTIR 60 DB 317 NDDTADPFPVIRISRNGLCDVADKYNNGNPQLMPCKNSDVMQMLTRDAIR 376 QY 61 NSCLTYGTYAGVYVMTFCNTAVREATIQIWDNGTIIINRSNLYLAASGIKGTLT 120 DB 377 MKCLITNGYASDGYVMTYDCTPTMASIYQFNANGIINFGSALVLSASGIRPTL 436 QY 121 VQTDYTLGGMLAGNDAPRATVYVGRFDCVNSGSGVYTCSSQKQKALYGD 180 DB 437 VQNTVYASQGLAGNTEPEFTVTSVFNDCVQANQDPAWTEKCSYKAGQ. NALYTPD 495 QY 181 GSIRPQND--QCLTSGRDSVYVNIYVSCGASGQVYVTEGALINTKGLANDVA 238 DB 496 GSIRPQNDPPAPACPLDINHPQSTILLISSCSPSRGRVWZMDGVVNLGLWMDV 555 QY 239 CANPRAIITVYVGRKQKQMLPY 263 DB 556 GSNPRLHQLIIMPATKKNHMLPI 580

RESULT 12
Q06076 PRELIMINARY; PRT; 528 AA.
AC Q06076 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 21, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 21, Last annotation update)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
AB Abrid (EC 3.2.2.22) (RNA N-glycosidase)
OS Abrid precatorius (Indian licoice) (Crab's eye)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abrusae; Abrus.
NCBI_Taxid=3816;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=3132798; PubMed=842133;
RA 1996; 1996; 1996; 1996; 1996; 1996; 1996; 1996; 1996; 1996;
RT Primary structure of the cDNA sequence determined by cDNA
RT sequencing; conservation and significance;
RT J. Mol. Biol. 229:263-267(1993)
CC -1- CATALYTIC ACTIVITY: ENDOPHYCOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: M98346; AAA3262.1;
DR HSSP: P11140; LAM.
DR InterPro: IPR000772; R1cin_B_lectin.
DR InterPro: IPR001574; R1P.

DR Pfam: PF00652; R1cin_B_lectin; 6.
DR Pfam: PF001574; RIPO00772; R1P.
DR PRINTS: PR00161; R1P.1.
DR SMART: SM00458; R1CIN.2.
DR PROSITE: PS0231; R1CIN_B_LECTIN.2.
DR PROSITE: PS0275; SHGA_R1CIN.1.
KW Hydrolase; Toxin.
FT NON TER 1
FT NON TER 528
SQ SEQUENCE. 528 AA; 58870 MW; 626242F89F360F8 CRC64;
QUERY MATCH. 53.8%; Score 722; DB 10; Length 528; Best Local Similarity 54.8%; Pred. No. 6.3e-50; Matches 143; Conservative 44; Mismatches 72; Indels 2; Gaps 2; QY 5 CSAS-EPTVRIYVGRNKGVDVDDPHQNOIQLPKSNNDPQQLTKRIGTIR 63 DB 269 CSSEYEPVRIYVGRNKGVDVDDPHQNRRIAMKCKORLEKQMLTKSDLTRSNK 326 QY 64 CLTYGTYAGVYVMTFCNTAVREATIQIWDNGTIIINRSNLYLAASGIKGTLT 123 DB 329 CLTIGTYAGVYVMTYDCTPTMASIYQFNANGIINFGSALVLSASGIRPTL 388 QY 124 LDYTLGGMLAGNDAPRATVYVGRFDCVNSGSGVYTCSSQKQKALYGD 183 DB 389 NEYLMQGMETNNTSPFTVTSVFNDCVQANQDPAWTEKCSYKAGQ. NALYTPD 447 QY 184 RPYQNDQCLTSGRDSVYVNIYVSCGASGQVYVTEGALINTKGLANDVA 243 DB 448 RSYQNTNCLTSGRDSVYVNIYVSCGASGQVYVTEGALINTKGLANDVA 507 QY 244 LERITVYVGRKQKQMLPY 264 DB 508 LKQILIMVYVGRNKGVDVDDPHQNRRIAMKCKORLEKQMLTKSDLTRSNK 528

RESULT 13
Q8SA43 PRELIMINARY; PRT; 382 AA.
ID Q8SA43
AC Q8SA43
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
AB Abrid isoform G (EC 3.2.2.22) (RNA N-glycosidase)
OS Abrid precatorius (Indian licoice) (Crab's eye)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abrusae; Abrus.
NCBI_Taxid=3816;
RN [1]
RS SEQUENCE FROM N.A.
RX Cook J.P.; Roberts L.N.; Lord M.;
RA Tissue=leaf;
RT New isoform of Abrid - Abrid G;
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOPHYCOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF179626; ALU7434.1;
DR InterPro: IPR000772; R1cin_B_lectin.
DR InterPro: IPR001574; R1P.
DR Pfam: PF00652; R1cin_B_lectin. 6.
DR Pfam: PF00161; R1P.1.
DR SMART: SM00458; R1CIN.2.
DR PROSITE: PS0231; R1CIN_B_LECTIN.2.
DR PROSITE: PS0275; SHGA_R1CIN.1.
KW Hydrolase; Toxin.
FT NON TER 1
FT NON TER 382
FT CHAIN. 1. 382. FT ABRIN A CHAIN.
FT ABRIN B CHAIN.
SQ SEQUENCE. 382 AA; 42743 MW; B08A3A1813ADEE CRC64;

Query Match 52.8%; Score 748.5; DB 10; Length 382;
Best Local Similarity 54.3%; Pred. No. 5,9e-55;
Matches 139; Conservative 41; Mismatches 75; Indels 1; Gaps 1;

QY 9 EPTVRI VARNRGEVYVDDPFDGNOQLAPSKSNNDPNQWLTIRKDTIRNSGCTTY 68
DB 128 EPTVRI VARNRGEVYVDDPFDGNOQLAPSKSNNDPNQWLTIRKDTIRNSGCTTY 187
QY 69 GTVAGYVYVFPDCAVREAVTQWMDKFTINPBNLVLAASGIGKTTLYQTLDTY 128
DB 188 GTVAGYVYVFPDCAVREAVTQWMDKFTINPBNLVLAASGIGKTTLYQTLDTY 247
QY 129 GQGNLAGNDTAPREVITVGFEDLCNESNGSVWETCSQXQKQKALYDPSIRPK 188
DB 248 GQGNLAGNDTAPREVITVGFEDLCNESNGSVWETCSQXQKQKALYDPSIRPK 306
QY 189 ODQCLTSGRDSYVTVINIVSGSAGSQWPTVEGATINLKTGLADPAQANR 248
DB 307 ODQCLTSGRDSYVTVINIVSGSAGSQWPTVEGATINLKTGLADPAQANR 366
QY 249 IYPATGKQNMALPEV 264
DB 367 IYPATGKQNMALPEV 382

RESULT 14

ID Q9M69 PRELIMINARY; PRT; 547 AA.
AC Q9M69; 01-OCT-2000 (TREMBL) 15, Created
DT 01-OCT-2000 (TREMBL) 15, Last sequence update
DE 01-MAR-2003 (TREMBL) 23, Last annotation update
PR Preprogastrin (SC 3.2.2.22) (rRNA N-glycosidase).
GN AAG.
OS Arabidopsis thaliana (Indian floricane) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Eudicotyledons; Magnoliopsida; Liliales; Asparagus; Iridaceae;
CC Eucrocid; Fabaceae; Papilionoideae; Abruseae; Abrus.
NCBI_Taxid=3816;

RP SEQUENCE FROM N.A.
RX MEDLINE-20102702; PubMed-10636890;
RA Liu C.L., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Hwang M.J.,
RN Primary structure and function analysis of the Arabidopsis
RT Arabidopsis thaliana (Crab's eye) protein, a member of the
FT Alpha-Helix H. Impey, Proc. Natl. Acad. Sci. USA 97:1901 (2000).
CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DB EMBL; AF190173; AF283093.1; .
DB HSSP; P11146; IABR.
DB InterPro; IPR000772; R1Cin_B_lectin.
DB Pfam; PF00652; R1Cin_B_lectin.6.
DB Pfam; PF00165; R1P_1.
DB PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; R1CIN.2.
DR PROSITE; PS02231; R1CIN_B_LECTIN.2.
DR PROSITE; PS00275; SHIGA_R1CIN.1.
KW Hydroxylase; Toxin.
SQ SEQUENCE 547 AA; 61248 MW; 35543252354ALBD CRC64;

Query Match 52.8%; Score 748.5; DB 10; Length 547;
Best Local Similarity 54.0%; Pred. No. 1e-54;
Matches 141; Conservative 40; Mismatches 78; Indels 2; Gaps 2;

QY 5 CSAS-EPTVRI VARNRGEVYVDDPFDGNOQLAPSKSNNDPNQWLTIRKDTIRNSG 63
DB 288 CSAS-EPTVRI VARNRGEVYVDDPFDGNOQLAPSKSNNDPNQWLTIRKDTIRNSG 347

QY 64 CLTGYAGYVYVFPDCAVREAVTQWMDKFTINPBNLVLAASGIGKTTLYQTL 123
DB 348 CLTGYAGYVYVFPDCAVREAVTQWMDKFTINPBNLVLAASGIGKTTLYQTL 407
QY 124 LDVTLGQGNLAGNDTAPREVITVGFEDLCNESNGSVWETCSQXQKQKALYDPS 183
DB 408 LDVTLGQGNLAGNDTAPREVITVGFEDLCNESNGSVWETCSQXQKQKALYDPS 466
QY 184 PRKQNDQCLTSGRDSYVTVINIVSGSAGSQWPTVEGATINLKTGLADPAQANR 243
DB 467 PRKQNDQCLTSGRDSYVTVINIVSGSAGSQWPTVEGATINLKTGLADPAQANR 526
QY 244 IRRITVATGKQNMALPEV 264
DB 527 IRRITVATGKQNMALPEV 547

RESULT 15

ID Q9M28 PRELIMINARY; PRT; 573 AA.
AC Q9M28; 01-MAR-2002 (TREMBL) 20, Created
DT 01-MAR-2002 (TREMBL) 20, Last sequence update
DE 01-MAR-2003 (TREMBL) 23, Last annotation update
PR Ribosome-inactivating protein IBAR (EC 3.2.2.22) (rRNA N-glycosidase)
GN Arabidopsis thaliana (Dutch iris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Eudicotyledons; Magnoliopsida; Liliales; Asparagus; Iridaceae;
CC Irid.
NCBI_Taxid=3816;

RP SEQUENCE FROM N.A.
RX van Damme E.J.M., Peumans W.J.,
RN "Iris (iris holandica var. professor Blauw) plants express both type
RT 1 and type 2 ribosome-inactivating proteins in bulb tissue."
FT Shmida, Plant Cell Physiol. 43:1005-1010 (2002).
CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DB EMBL; AF256084; AL55093.1; .
DB InterPro; IPR001574; R1P.
DB Pfam; PF00652; R1Cin_B_lectin.6.
DB Pfam; PF00165; R1P_1.
DB PRINTS; SM00458; SHIGARICIN.
DR SMART; SM00458; R1CIN.2.
DR PROSITE; PS02231; R1CIN_B_LECTIN.2.
DR PROSITE; PS00275; SHIGA_R1CIN.1.
KW Hydroxylase; Toxin.
FT NON TER
SQ SEQUENCE 573 AA; 63759 MW; 1414A3BACD4F5C CRC64;

Query Match 48.0%; Score 679.5; DB 10; Length 573;
Best Local Similarity 48.2%; Pred. No. 1e-48;
Matches 133; Conservative 40; Mismatches 89; Indels 3; Gaps 3;

QY 1 DWTYVCAEPTVRI VARNRGEVYVDDPFDGNOQLAPSKSNNDPNQWLTIRKDTIRNSG 60
DB 311 DWTYVCAEPTVRI VARNRGEVYVDDPFDGNOQLAPSKSNNDPNQWLTIRKDTIRNSG 370
QY 61 WSCITVYGTAGYVYVFPDCAVREAVTQWMDKFTINPBNLVLAASGIGKTTLY 120
DB 371 WSCITVYGTAGYVYVFPDCAVREAVTQWMDKFTINPBNLVLAASGIGKTTLY 429
QY 122 WQTLDTLGGTNLAGNDTAPREVITVGFEDLCNESNGSVWETCSQXQKQKALYDPS 179
DB 430 WQTLDTLGGTNLAGNDTAPREVITVGFEDLCNESNGSVWETCSQXQKQKALYDPS 488
QY 180 DGSIRKQNDQCLTSGRDSYVTVINIVSGSAGSQWPTVEGATINLKTGLADPAQANR 239
DB 489 DGSIRKQNDQCLTSGRDSYVTVINIVSGSAGSQWPTVEGATINLKTGLADPAQANR 548

